Voimmeko ennustaa koronapandemian jatkoa?

Petri Lehenkari

Eturistiriidat

- Ei ole

Sidosryhmät

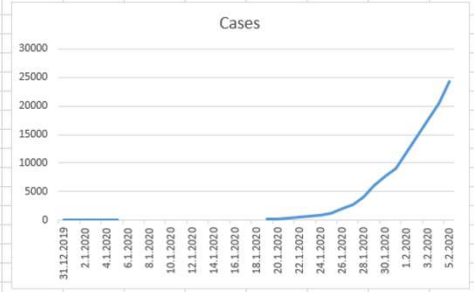
- PPSHP
- OY

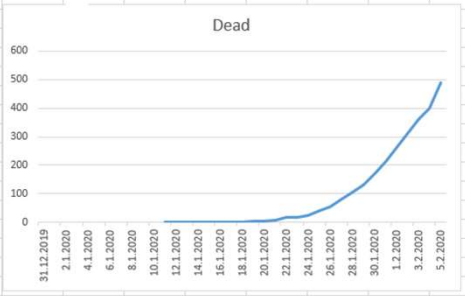
Voimmeko ennustaa koronapandemian jatkoa?

Kyllä, mutta…

”Tulevaisuuden ennustaminen on menneisyyden ennustamista vaikeampaa”

	päivä	varmisteti	kuolleet	kuolleisuus	
31.12.2019	0	27		0	
3.1.2020	3	44		0	
5.1.2020	5	59		0	
11.1.2020	11		1	#DIV/0!	
18.1.2020	18		2	#DIV/0!	
19.1.2020	19	201	3	0,014925	
20.1.2020	20	221	4	0,0181	
21.1.2020	21	446	9	0,020179	
22.1.2020	22	581	17	0,02926	
23.1.2020	23	650	18	0,027692	
24.1.2020	24	830	25	0,03012	
25.1.2020	25	1287	41	0,031857	
26.1.2020	26	2000	56	0,028	
27.1.2020	27	2744	80	0,029155	
28.1.2020	28	4000	106	0,0265	
29.1.2020	29	6000	132	0,022	
30.1.2020	30	7700	170	0,022078	0,025254
31.1.2020	31	9000	213	0,023667	
3.2.2020	34	17351	361	0,020806	
4.2.2020	35	20400	400	0,019608	
5.2.2020	36	24300	490	0,020165	





- Tammikuussa 2020 aloin kerätä julkisuudessa ilmoitettuja lukuja koronaviruksesta, laitoin nämä ilmoitustaululle Oulun lääkikseen ja ne poistettiin sieltä

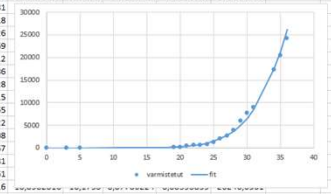
”Always listen to the good guys”

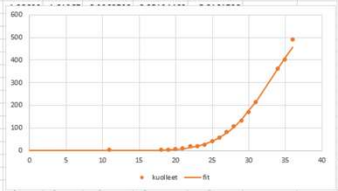
$$f(t) = A\exp g(t)$$
$$\ln f(t) = \ln A + g(t)$$
$$\equiv p_0 + p_1 t + p_2 t^2 + p_3 t^3 + p_4 t^4$$

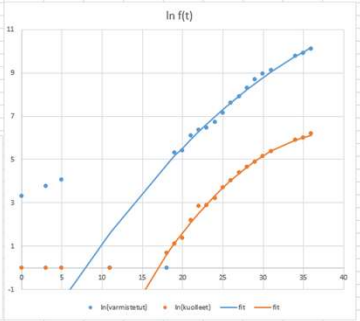
p0	##########	##########	##########	1,01475E+01
p1	6,18922E-01	2,95528E-01	6,18922E-01	##########
p2	##########		##########	5,63982E-02
p3				##########
p4				
RMS	0,27461697	0,62959266	0,27461697	0,17087989

p0	##########	##########	##########	##########
p1	##########	2,93758E-01	9,67399E-01	1,71360E+00
p2	##########		##########	##########
p3				3,37297E-04
p4				
RMS	0,1891902	1,72942755	0,18919016	0,17007927

	päivä	varmistet	kuolleet	kuolleisuu	ln(varmistetu	fit	diff	diff^2	fit
#########	0	27		0	3,29583687	-4,4899	-7,7857529	60,6179476	0,01122159
3.1.2020	3	44		0	3,78418963	-2,686	-6,4702298	41,8638731	0,06815027
5.1.2020	5	59		0	4,07753744	-1,5422	-5,6197588	31,581689	0,21390541
11.1.2020	11		1	#DIV/0!	#NUM!	1,60716	#NUM!	#NUM!	4,98863423
18.1.2020	18		2	#DIV/0!	#NUM!	4,74668	#NUM!	#NUM!	115,201184
19.1.2020	19	201	3	0,01493	5,30330491	5,14817	-0,1551345	0,0240667	172,116307
20.1.2020	20	221	4	0,0181					
21.1.2020	21	446	9	0,02018					
22.1.2020	22	581	17	0,02926					
23.1.2020	23	650	18	0,02769					
24.1.2020	24	830	25	0,03012					
25.1.2020	25	1287	41	0,03186					
26.1.2020	26	2000	56	0,028					
27.1.2020	27	2744	80	0,02915					
28.1.2020	28	4000	106	0,0265					
29.1.2020	29	6000	132	0,022					
30.1.2020	30	7700	170	0,02208					
31.1.2020	31	9000	213	0,02367					
3.2.2020	34	17351	361	0,02081					
4.2.2020	35	20400	400	0,01961					
5.2.2020	36	24300	490	0,02016					
				0,02401					







Cases

Juha Vaara <juha.t.vaara@gmail.com>
To Petri Lehenkari

You replied to this message on 11.2.2020 9.42.

coronavirus_deathtoll.xlsx
103 KB

ei,

tteessä sovitin sekä havaittujen tautitapausten että kuolleiden määrään käyriä. Otin ensin luonnollisen logaritmin datasta; jos kasvu olisi eksponentiaalista, luonnollinen logaritmi olisi suora (eli kaavani polynomissa olisi vain termit p0+p1*t).

autitapausten lukumäärä näyttäisi sopivan tuohon lineaariseen funktioon hyvin, mikä tarkoittaisi aika lailla eksponentiaalista kasvua. Pientä hidastumista on, koska p2-kertoimelle tulee negatiivinen arvo - mutta joka päivä tuleva lisädata näyttää, onko tuo merkityksellistä.

uolleiden määrän luonnollisen logaritmin sovituksessa täytyy pitää termit p0+p1*t+p2*t^2 mukana, muttei enää p3-termiä. Tämä tarkoittaa, että kuolleiden määrä kasvaisi merkitsevästi hitaammin kuin eksponentiaalisesti. Joko hoitomenetelmät kehittyvät tai tilastoja kaunistellaan ;-)

Juha

Petri Lehenkari <petri.lehenkari@oulu.fi> kirjoitti 5.2.2020 kello 8.50:

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3710332/

https://www.sciencedirect.com/science/article/pii/S0307904X16306278

tässä sulle vähän muuta mietittävää, kun on sapatilla, on hyvä hyppelehtiä vähän mukavuusalueen ulkopuolellakin?

J

p
<coronavirus_deathtoll.xlsx>

Reply Reply A

Applied Mathematical Modelling
Volume 43, March 2017, Pages 566-578

Understanding epidemics from mathematical models: Details of the 2010 dengue epidemic in Bello (Antioquia, Colombia)

Diana Paola Lizarralde-Bejarano [a], Sair Arboleda-Sánchez [b], María Eugenia Puerta-Yepes [a]

REVIEW
Virulence 4:4, 295–306; May 15, 2013; © 2013 Landes Bioscience

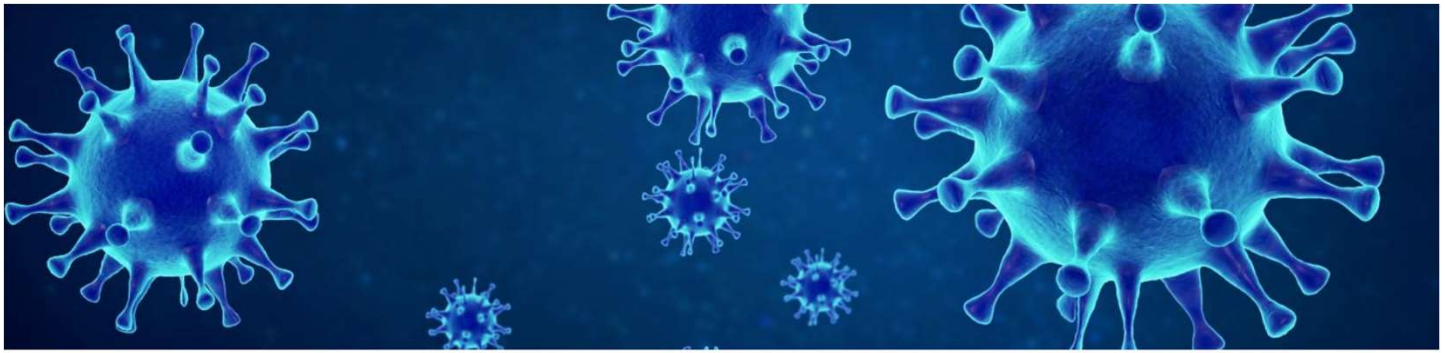
Mathematical modeling of infectious disease dynamics

Constantinos I. Siettos[1,*] and Lucia Russo[2]

[1]School of Applied Mathematics and Physical Sciences; National Technical University of Athens; Athens, Greece; [2]Consiglio Nazionale di Ricerce; Napoli, Italy

Johtopäätökset tilanteesta?

- https://www.oulu.fi/ltk/tie-ulos-covid-kriisist%C3%A4



Tie ulos COVID-kriisistä

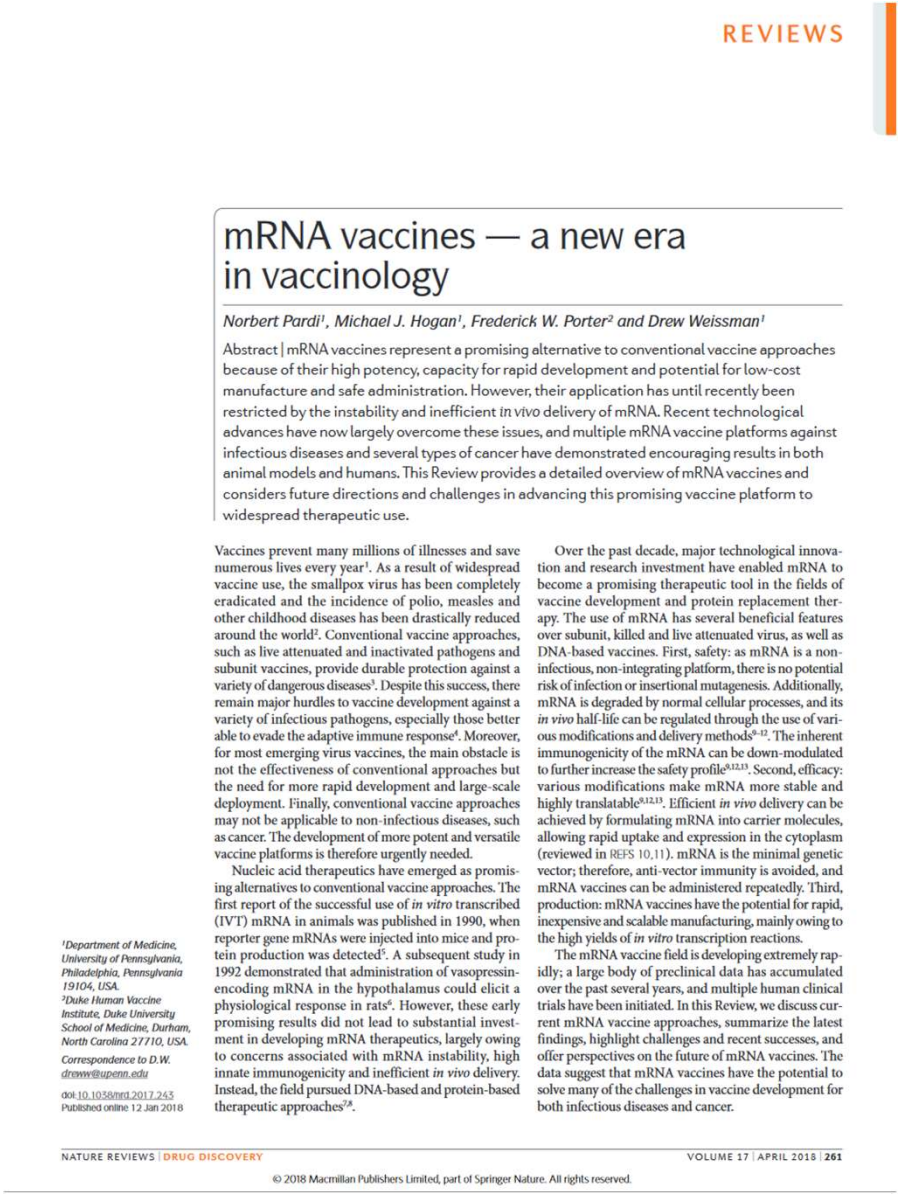
COVID-kriisi edellyttää, että kaikki ihmiset sairastavat jossain vaiheessa viruksen aiheuttaman sairauden. Suuren kuolleisuuden vuoksi sairastamisen suurina joukkoina voidaan sallia tapahtuvan vasta, kun kunnollinen rokotesuoja on saatu kattavasti väestöille ja varautuminen sairaalahoidossa riittäväksi. Ensivaiheessa tauti täytyy saada kokonaan pysäytettyä. Tämä edellyttää erityisiä toimia valtioilta ja erityisesti yksilöiltä. Sosiaalinen eristäytyminen ja suusuojaimet täytyy normalisoida arkielämään, sairaat ja epäillyt sairaat tulee eristää ja tauti poistaa kokonaan seuraamalla tartuntoja massatutkimusten avulla. Näin voidaan ostaa aikaa, ja laumasuojan vaativa sairastaminen voi alkaa vasta, kun rokotesuoja saadaan vähintään riskiryhmille.

Kirjoittaja: Petri Lehenkari (henkilökohtainen mielipidekirjoitus)

Solubiologian harrastus level III –miten ennustetaan rokoteaikataulua?

- Ennennäkemätön tilanne, jossa tarvitaan täysin uusi rokoteteknologia
- Perinteisten rokotteiden kehitys/tuotantoaikataulu n 10 vuotta
- Ratkaisu?

Nature –reviews julkaisu 2018!



mRNA vaccines — a new era in vaccinology

Norbert Pardi[1], Michael J. Hogan[1], Frederick W. Porter[2] and Drew Weissman[1]

Abstract | mRNA vaccines represent a promising alternative to conventional vaccine approaches because of their high potency, capacity for rapid development and potential for low-cost manufacture and safe administration. However, their application has until recently been restricted by the instability and inefficient *in vivo* delivery of mRNA. Recent technological advances have now largely overcome these issues, and multiple mRNA vaccine platforms against infectious diseases and several types of cancer have demonstrated encouraging results in both animal models and humans. This Review provides a detailed overview of mRNA vaccines and considers future directions and challenges in advancing this promising vaccine platform to widespread therapeutic use.

Vaccines prevent many millions of illnesses and save numerous lives every year[1]. As a result of widespread vaccine use, the smallpox virus has been completely eradicated and the incidence of polio, measles and other childhood diseases has been drastically reduced around the world[2]. Conventional vaccine approaches, such as live attenuated and inactivated pathogens and subunit vaccines, provide durable protection against a variety of dangerous diseases[3]. Despite this success, there remain major hurdles to vaccine development against a variety of infectious pathogens, especially those better able to evade the adaptive immune response[4]. Moreover, for most emerging virus vaccines, the main obstacle is not the effectiveness of conventional approaches but the need for more rapid development and large-scale deployment. Finally, conventional vaccine approaches may not be applicable to non-infectious diseases, such as cancer. The development of more potent and versatile vaccine platforms is therefore urgently needed.

Nucleic acid therapeutics have emerged as promising alternatives to conventional vaccine approaches. The first report of the successful use of *in vitro* transcribed (IVT) mRNA in animals was published in 1990, when reporter gene mRNAs were injected into mice and protein production was detected[5]. A subsequent study in 1992 demonstrated that administration of vasopressin-encoding mRNA in the hypothalamus could elicit a physiological response in rats[6]. However, these early promising results did not lead to substantial investment in developing mRNA therapeutics, largely owing to concerns associated with mRNA instability, high innate immunogenicity and inefficient *in vivo* delivery. Instead, the field pursued DNA-based and protein-based therapeutic approaches[7,8].

Over the past decade, major technological innovation and research investment have enabled mRNA to become a promising therapeutic tool in the fields of vaccine development and protein replacement therapy. The use of mRNA has several beneficial features over subunit, killed and live attenuated virus, as well as DNA-based vaccines. First, safety: as mRNA is a non-infectious, non-integrating platform, there is no potential risk of infection or insertional mutagenesis. Additionally, mRNA is degraded by normal cellular processes, and its *in vivo* half-life can be regulated through the use of various modifications and delivery methods[9–12]. The inherent immunogenicity of the mRNA can be down-modulated to further increase the safety profile[8,12,13]. Second, efficacy: various modifications make mRNA more stable and highly translatable[8,12,13]. Efficient *in vivo* delivery can be achieved by formulating mRNA into carrier molecules, allowing rapid uptake and expression in the cytoplasm (reviewed in REFS 10,11). mRNA is the minimal genetic vector; therefore, anti-vector immunity is avoided, and mRNA vaccines can be administered repeatedly. Third, production: mRNA vaccines have the potential for rapid, inexpensive and scalable manufacturing, mainly owing to the high yields of *in vitro* transcription reactions.

The mRNA vaccine field is developing extremely rapidly; a large body of preclinical data has accumulated over the past several years, and multiple human clinical trials have been initiated. In this Review, we discuss current mRNA vaccine approaches, summarize the latest findings, highlight challenges and recent successes, and offer perspectives on the future of mRNA vaccines. The data suggest that mRNA vaccines have the potential to solve many of the challenges in vaccine development for both infectious diseases and cancer.

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dreww@upenn.edu

doi:10.1038/nrd.2017.243
Published online 12 Jan 2018

doi:10.1038/nrd.2017.243

mRNA rokotteiden kuljettimen optimointi

Table 1 | **mRNA vaccine complexing strategies for *in vivo* use**

Delivery system type	Route of delivery	Species	Target
Commercial transfection reagent	i.n.	Mouse	OVA[145]
Protamine	i.d.	Mouse, ferret, pig and human	Influenza virus[18,52], melanoma[150], non-small-cell lung cancer[200], prostate cancer[36,52,151], rabies virus[56], OVA[36,52,155] and Lewis lung cancer[155]
Protamine liposome	i.v.	Mouse	Lung cancer[201]
Polysaccharide particle	s.c.	Mouse and rabbit	Influenza virus[98]
Cationic nanoemulsion	i.m.	Mouse, rabbit, ferret and rhesus macaque	Influenza virus[96], RSV[50], HIV-1 (REFS 50,97), HCMV[50], *Streptococcus* spp.[100], HCV and rabies virus[87]
Cationic polymer	s.c. and i.n.	Mouse	Influenza virus[99], andHIV-1 (REFS 110,111)
Cationic polymer liposome	i.v.	Mouse	Melanoma[202,203], pancreatic cancer[204]
Cationic lipid nanoparticle	i.d., i.v. and s.c.	Mouse	HIV-1 (REF. 109) and OVA[152]
Cationic lipid, cholesterol nanoparticle	i.v., s.c. and i.s.	Mouse	Influenza virus[59,108], melanoma[59,141], Moloney murine leukaemia virus, OVA, HPV andc olon cancer[59]
Cationic lipid, cholesterol, PEG nanoparticle	i.d., i.m. and s.c.	Mouse, cotton rat and rhesus macaque	Zika virus[20,85,112], influenza virus[22,94,95,205], RSV[19], HCMV, rabies virus[87] and melanoma[153]
Dendrimer nanoparticle	i.m.	Mouse	Influenza virus, Ebola virus, *Toxoplasma gondii*[89] and Zika virus[88]

HCMV, human cytomegalovirus; HCV, hepatitis C virus; HPV, human papillomavirus; i.d., intradermal; i.m., intramuscular; i.n., intranasal; i.s., intrasplenic; i.v., intravenous; OVA, ovalbumin-expressing cancer models; PEG, polyethylene glycol; RSV, respiratory syncytial virus; s.c., subcutaneous.

doi:10.1038/nrd.2017.243

mRNA rokotteiden farmakologian optimointi

Box 1 | **Strategies for optimizing mRNA pharmacology**

A number of technologies are currently used to improve the pharmacological aspects of mRNA. The various mRNA modifications used and their impact are summarized below.

- Synthetic cap analogues and capping enzymes[26,27] stabilize mRNA and increase protein translation via binding to eukaryotic translation initiation factor 4E (EIF4E)
- Regulatory elements in the 5′-untranslated region (UTR) and the 3′-UTR[23] stabilize mRNA and increase protein translation
- Poly(A) tail[25] stabilizes mRNA and increases protein translation
- Modified nucleosides[9,48] decrease innate immune activation and increase translation
- Separation and/or purification techniques: RNase III treatment (N.P. and D.W., unpublished observations) and fast protein liquid chromatography (FPLC) purification[13] decrease immune activation and increase translation
- Sequence and/or codon optimization[29] increase translation
- Modulation of target cells: co-delivery of translation initiation factors and other methods alters translation and immunogenicity

doi:10.1038/nrd.2017.243

Immunisaatioreaktion teoria

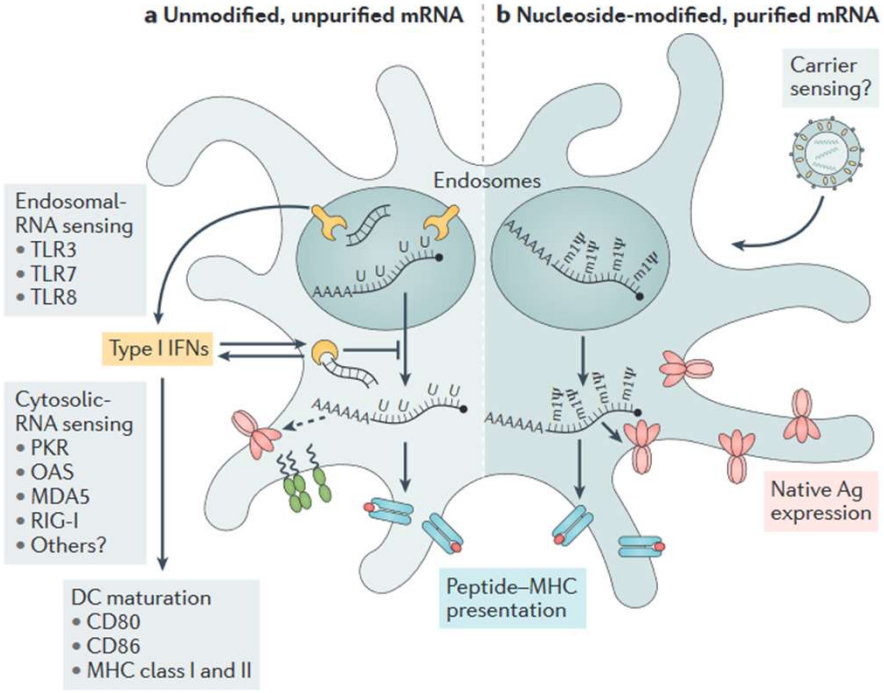


Figure 1 | **Innate immune sensing of mRNA vaccines.** Innate immune sensing of two types of mRNA vaccine by a dendritic cell (DC), with RNA sensors shown in yellow, antigen in red, DC maturation factors in green, and peptide–major histocompatibility complex (MHC) complexes in light blue and red; an example lipid nanoparticle carrier is shown at the top right. A non-exhaustive list of the major known RNA sensors that contribute to the recognition of double-stranded and unmodified single-stranded RNAs is shown. Unmodified, unpurified (part **a**) and nucleoside-modified, fast protein liquid chromatography (FPLC)-purified (part **b**) mRNAs were selected for illustration of two formats of mRNA vaccines where known forms of mRNA sensing are present and absent, respectively. The dashed arrow represents reduced antigen expression. Ag, antigen; PKR, interferon-induced, double-stranded RNA-activated protein kinase; MDA5, interferon-induced helicase C domain-containing protein 1 (also known as IFIH1); IFN, interferon; m1Ψ, 1-methylpseudouridine; OAS, 2′-5′-oligoadenylate synthetase; TLR, Toll-like receptor.

doi:10.1038/nrd.2017.243

Syöpä on liian vaikea sairaus mRNA rokotteille –samoin HIV mutta RNA virukset helppo!

Table 2 | **Clinical trials with mRNA vaccines against infectious diseases**

Sponsoring institution	Vaccine type (route of administration)	Targets	Trial numbers (phase)	Status
Argos Therapeutics	DC EP with autologous viral Ag and CD40L mRNAs (i.d.)	HIV-1	• NCT00672191 (II) • NCT01069809 (II) • NCT02042248 (I)	• Completed[105] • Completed; results NA • Completed; results NA
CureVac AG	RNActive viral Ag mRNA (i.m., i.d.)	Rabies virus	NCT02241135 (I)	Active[56,91]
Erasmus Medical Center	DC loaded with viral Ag mRNA with TriMix (i.nod.)	HIV-1	NCT02888756 (II)	Recruiting
Fundació Clínic per la Recerca Biomèdica	Viral Ag mRNA with TriMix (NA)	HIV-1	NCT02413645 (I)	Active
Massachusetts General Hospital	DC loaded with viral Ag mRNA (i.d.)	HIV-1	NCT00833781 (II)	Completed[104]
McGill University Health Centre	DC EP with autologous viral Ag and CD40L mRNAs (i.d.)	HIV-1	NCT00381212 (I/II)	Completed[102]
Moderna Therapeutics	Nucleoside-modified viral Ag mRNA (i.m.)	Zika virus	NCT03014089 (I/II)	Recruiting[85]
		Influenza virus	NCT03076385 (I)	Ongoing[22]

The table summarizes the clinical trials registered at ClinicalTrials.gov as of 5 May 2017. Ag, antigen; CD40L, CD40 ligand; DC, dendritic cell; EP, electroporated; i.d., intradermal; i.m., intramuscular; i.nod., intranodal; NA, not available.

doi:10.1038/nrd.2017.243

Rokotteen muistijälki?

- Innate Immunity

- Adaptive immunity

1. Antibodies
2. Cellular memory

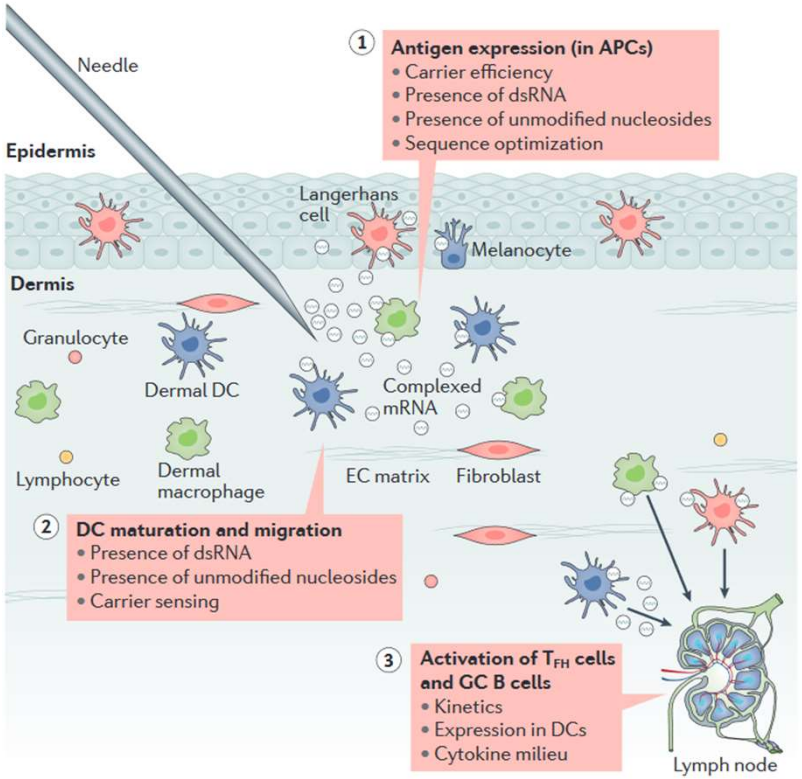


Figure 3 | **Considerations for effectiveness of a directly injected mRNA vaccine.** For an injected mRNA vaccine, major considerations for effectiveness include the following: the level of antigen expression in professional antigen-presenting cells (APCs), which is influenced by the efficiency of the carrier, by the presence of pathogen-associated molecular patterns (PAMPs) in the form of double-stranded RNA (dsRNA) or unmodified nucleosides and by the level of optimization of the RNA sequence (codon usage, G:C content, 5′ and 3′ untranslated regions (UTRs) and so on); dendritic cell (DC) maturation and migration to secondary lymphoid tissue, which is increased by PAMPs; and the ability of the vaccine to activate robust T follicular helper (T_{FH}) cell and germinal centre (GC) B cell responses — an area that remains poorly understood. An intradermal injection is shown as an example. EC, extracellular.

doi:10.1038/nrd.2017.243

Table 4 | **Leading mRNA vaccine developers: research focus, partners and therapeutic platforms**

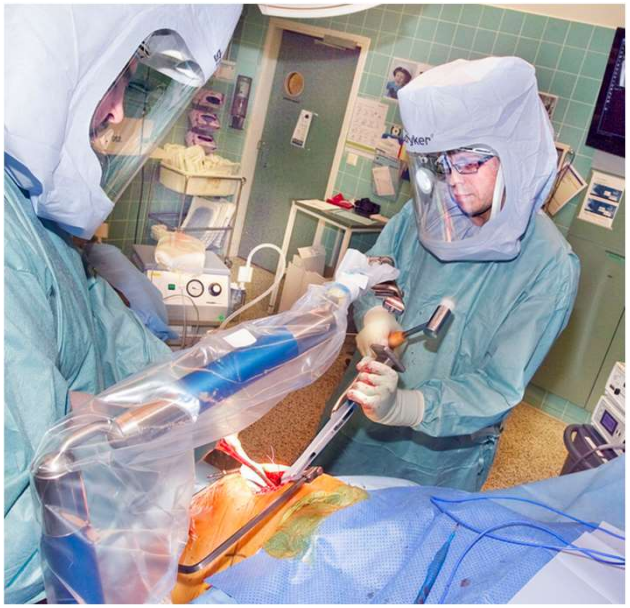
Institution	mRNA technology	Partners	Indication (disease target)
Argos Biotechnology	mRNA neoantigens (Arcelis platform)	NA	Individualized cancer vaccines, HIV-1
BioNTech RNA Pharmaceuticals GmbH	Nucleoside-modified mRNA (IVAC Mutanome, FixVAC)	Genentech/Roche	Individualized cancer vaccines
		Bayer AG	Veterinary vaccines
CureVac AG	Sequence-optimized, purified mRNA (RNActive, RNArt, RNAdjuvant)	Boehringer Ingelheim GmbH	Cancer vaccines (lung cancer)
		Johnson & Johnson	Viral vaccines
		Sanofi Pasteur	Infectious disease vaccines
		BMGF	Infectious disease vaccines
		IAVI	HIV vaccines
eTheRNA Immunotherapies	Purified mRNA (TriMix)	NA	Cancer (melanoma, breast), viral vaccines (HBV and/or HPV)
GlaxoSmithKline/ Novartis	Self-amplifying mRNA (SAM) (alphavirus replicon)	NA	Infectious disease vaccines
Moderna Therapeutics	Nucleoside-modified mRNA	Merck & Co.	Individualized cancer vaccines, viral vaccines
		BMGF, DARPA, BARDA	Viral vaccines (influenza virus, CMV, HMPV, PIV, chikungunya virus, Zika virus)
University of Pennsylvania	Nucleoside-modified, purified mRNA	NA	Infectious disease vaccines

BARDA, Biomedical Advanced Research and Development Authority; BMGF, Bill & Melinda Gates Foundation; CMV, cytomegalovirus; DARPA, Defense Advanced Research Projects Agency; HBV, hepatitis B virus; HMPV, human metapneumovirus; HPV, human papillomavirus; IAVI, International AIDS Vaccine Initiative; NA, not available; PIV, parainfluenza virus.

doi:10.1038/nrd.2017.243

Kasvomaskit

- Ortopedian harrastus
- Infektiotautien ylilääkäri Hannu Syrjälän kattava katsaus maskien vs suojahuppujen käytöstä
- Hyvin realistinen näkemys tehosta, hyödyistä ja haitoista, erityisesti aerosolitartunnoissa
- Hyvin inhorealistinen näkemys RCT tutkimusten soveltuvuudesta väestötutkimuksissa ja tilanteissa, joissa ei voida toteuttaa aitoa randomisaatiota!
- Kirurgien muistisääntö: craniumiin voi hengittää, thoraxiin voi aivastaa, vatsaonteloon voi vaikka paskantaa, niveleen vain katsahtaa (V Koivukangas)



Lehenkarin ennustukset 4/2020

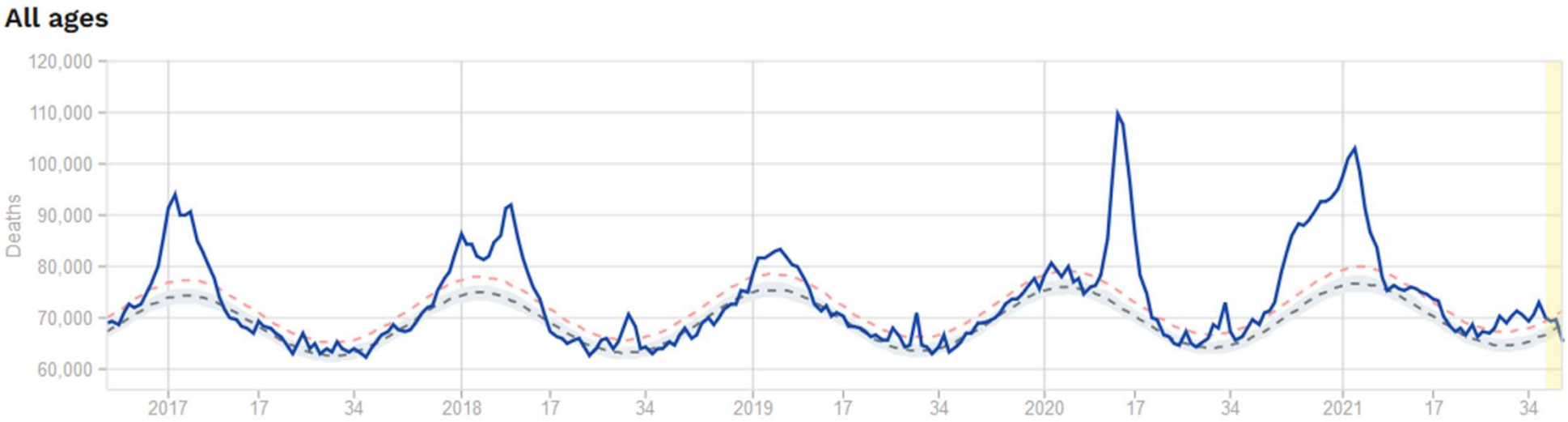
- 1. **Suusuojaimista** vaahtosin jo tuolloin, nyt ne ovat arkipäivää ja teho suurin piirtein tiedetään
- 2. **COVID kriisi edellyttää sitä, että kaikki ihmiset sairastavat jossain vaiheessa sairauden. Ensivaiheessa tauti täytyy saada kokonaan pysäytettyä.** (oletus endeemisyydestä)
- 3. **COVID -virus on osoittautunut n 10 kertaa ärhäkämmäksi kuin tavallinen influenssavirus**
- 4. totesin, että **WHO ja THL myös etsivät** tuolloin ja näyttää että vielä nytkin **kantaansa** ja tilannekuva muuttuu koko ajan
- 5. Ennustin myös näin: aikaisemman kokemuksen perusteella voidaan arvioida, **ettei mikään lääke tule olemaan kovin tehokas**; näyttää että tämäkin pitää paikkaansa, tosin perus- ja tehohoidon osaaminen on parantunut ja ennuste tätä kautta

- 6. Ennustin myös, että Suomessa on mahdollista, että meillä toteutuu totalitaariseen karanteeniin verrattava tilanne, ja kokonaiskuolleisuus jää välille 100-2000, ilokseni voin todeta, että haarukan keskivälille näytetään tässä vaiheessa jäävän
- 7. Edelleen on totta myös seuraava: jos jokainen ihminen rajoittaa sosiaalista kontaktointia totaalisesti 2 vko ajaksi, ihmiskunta selviää tilanteesta 4 viikossa.
- 8. Ennustin myös näin: On kiistämätön lääketieteellinen tosiasia, että ainoa lopullinen tie ulos COVID –viruksen kanssa yhteiselossa on se, että lähes me kaikki jossain vaiheessa sairastamme taudin ja tieto viruksen nujertamisesta tulee osaksi immuunijärjestelmämme muistia. Laumaimmuniteetti vaatii erittäin suurta väestötason immunisaatiota. Rokotteella voidaan valmistaa elimistöä tähän ja lieventää taudin kuvaa merkittävästi. Siksi heti alkuvaiheessa rokotekehitys on osattu nostaa ensisijaiseksi ja se on alkuvaiheen infektioneston ja rajaamisen jälkeen todellinen tie ulos tilanteesta.
- **Ja rokotusten aikataulusta ennustin vastoin kaikkia asiantuntijoita näin: Arvioin, että massarokotukset alkavat vuoden 2020 lopussa ja ne saadaan tehtyä vuoden 2021 loppuun mennessä.**

- 9. Totesin myös näin: ”asiantuntemus eri instituutioissa ei paikallistasolla kerta kaikkiaan riitä, joten **rajoittamistoimien tulee olla valtakunnan tasoisesti johdettuja, mutta sovellettuja ja kohdennettuja paikallisesti.** Näinhän tässä nyt on onneksi toimittu. On hyvä hahmottaa, että tämä tilanne ei kestä ikuisesti mutta se ei myöskään ole ihan nopeasti ohi. Ensimmäinen aalto on todennäköisesti otettu vastaan kesään 2020 mennessä, mutta rajoitukset jatkuvat kesän 2020 yli kaikkialla. Rokotukset alkavat loppuvuodesta 2020. COVID on selätetty kesällä 2021, se saattaa hiipiä muiden virusten mukana kausittain, mutta tämänkaltaista pandemiaa se ei kykene aiheuttamaan, vaan pandemian aiheuttaa jokin muu eliö, luultavimmin toinen RNAvirus. Yhteiskuntaa ei kannata romahduttaa yli vuodeksi, mutta työtä ja sairastamista tulee tehdä eri tavalla. Muutokset aikatauluissa mahdollisia.”
- 10. Viimeiseksi totesin näin: ”On hyvä hahmottaa, että tämä tilanne ei kestä ikuisesti mutta se ei myöskään ole ihan nopeasti ohi. Ensimmäinen aalto on todennäköisesti otettu vastaan kesään 2020 mennessä, mutta rajoitukset jatkuvat kesän 2020 yli kaikkialla. **Rokotukset alkavat loppuvuodesta 2020. COVID on selätetty kesällä 2021, se saattaa hiipiä muiden virusten mukana kausittain, mutta tämänkaltaista pandemiaa se ei kykene aiheuttamaan.”**

Tulevaisuus?

EUROMOMO -data

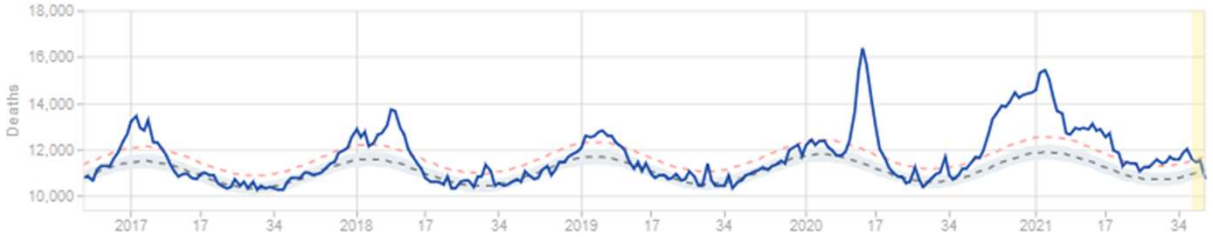


Weekly mortaility data

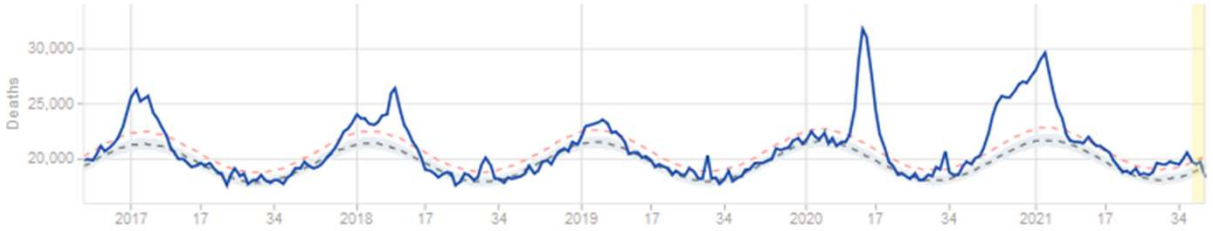
https://www.euromomo.eu/graphs-and-maps

https://www.euromomo.eu/graphs-and-maps

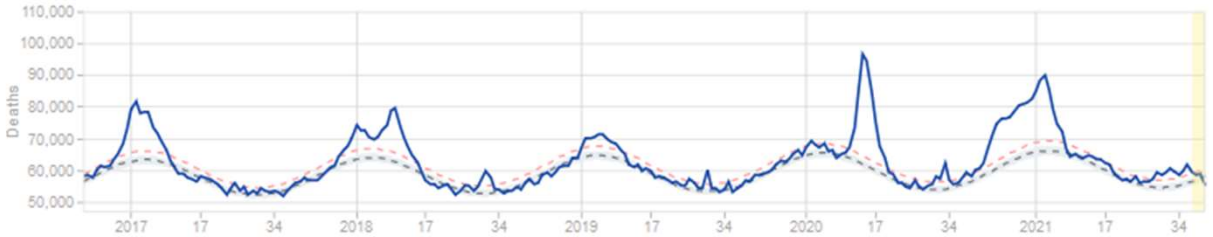
65-74 years



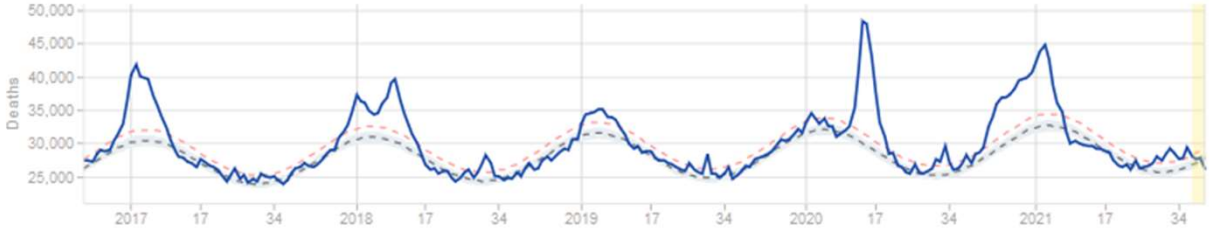
75-84 years



65+ years



85+ years



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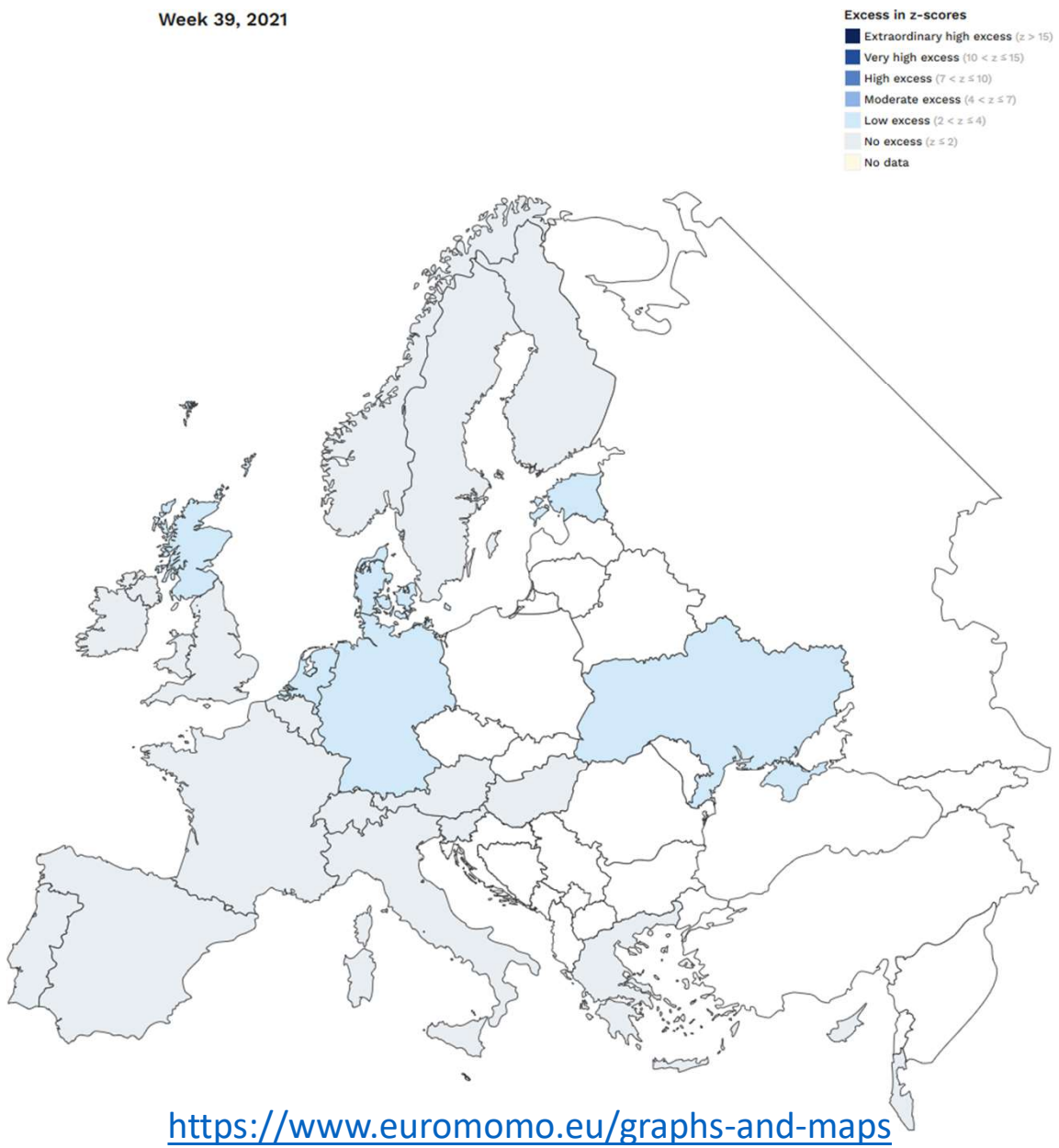

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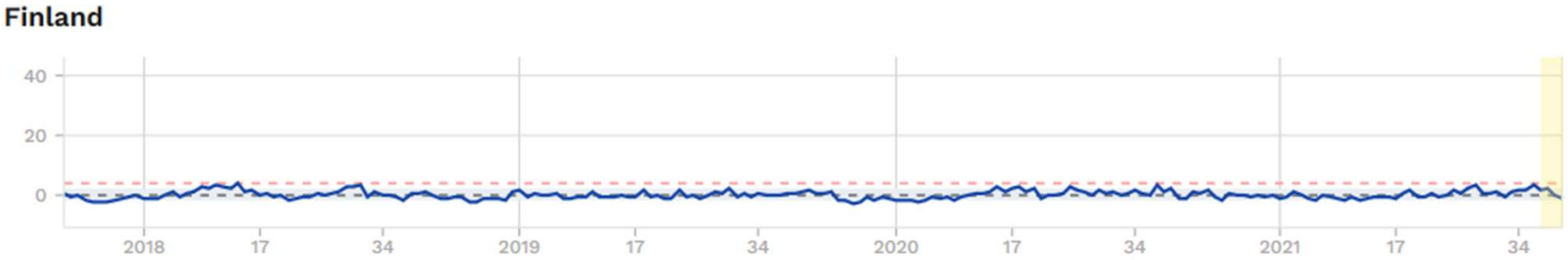

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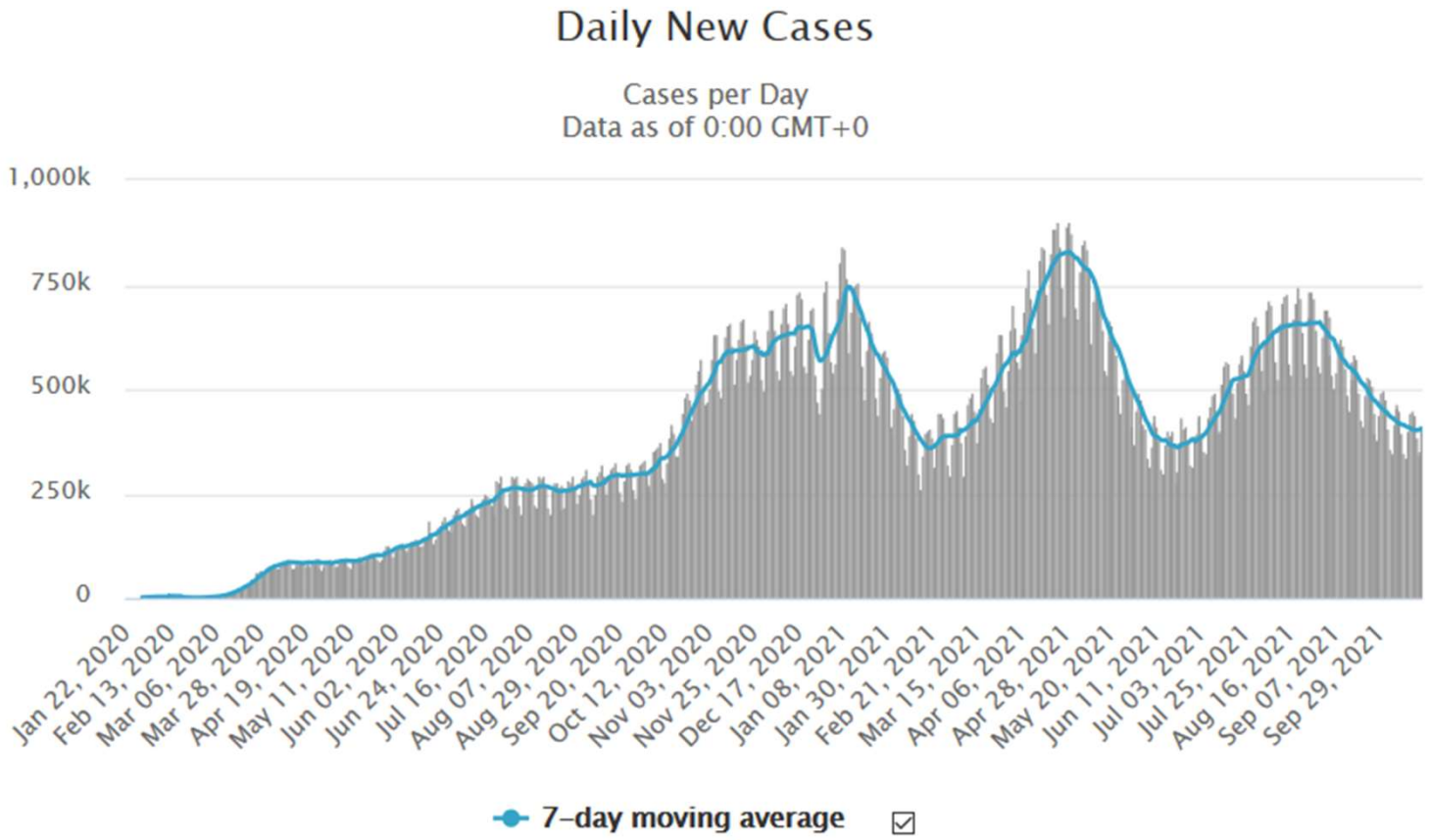
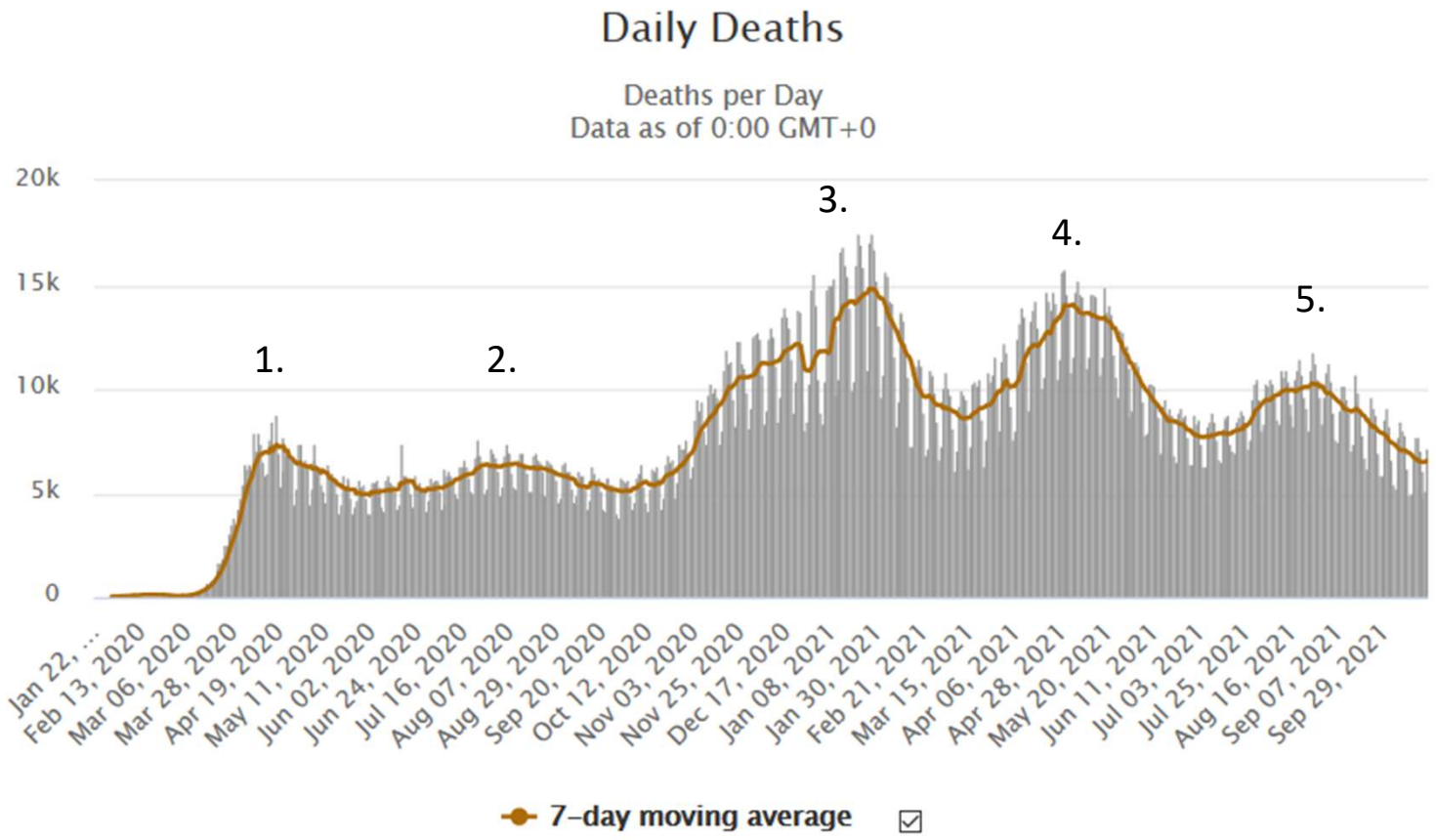
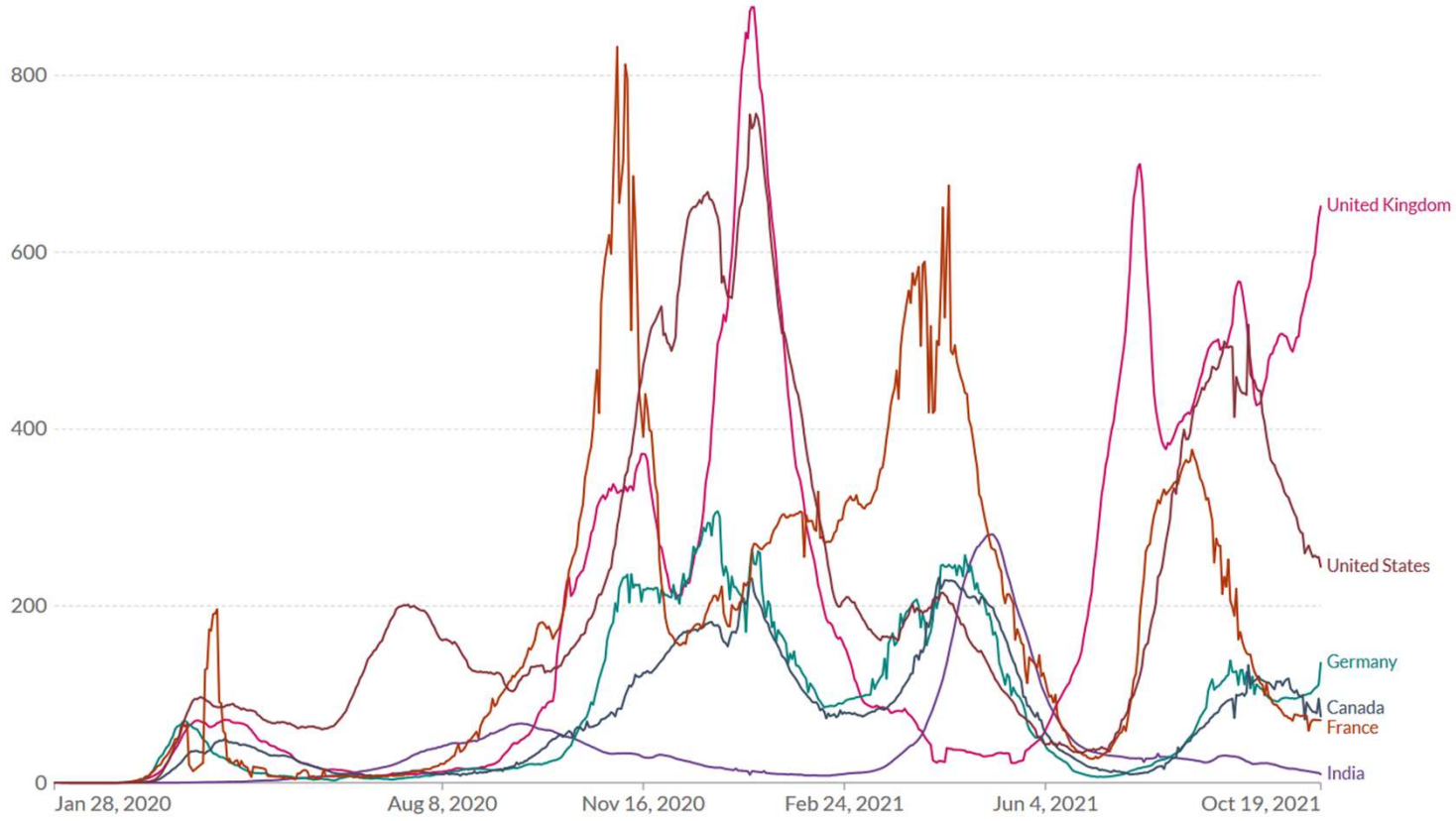


https://www.worldometers.info/coronavirus/

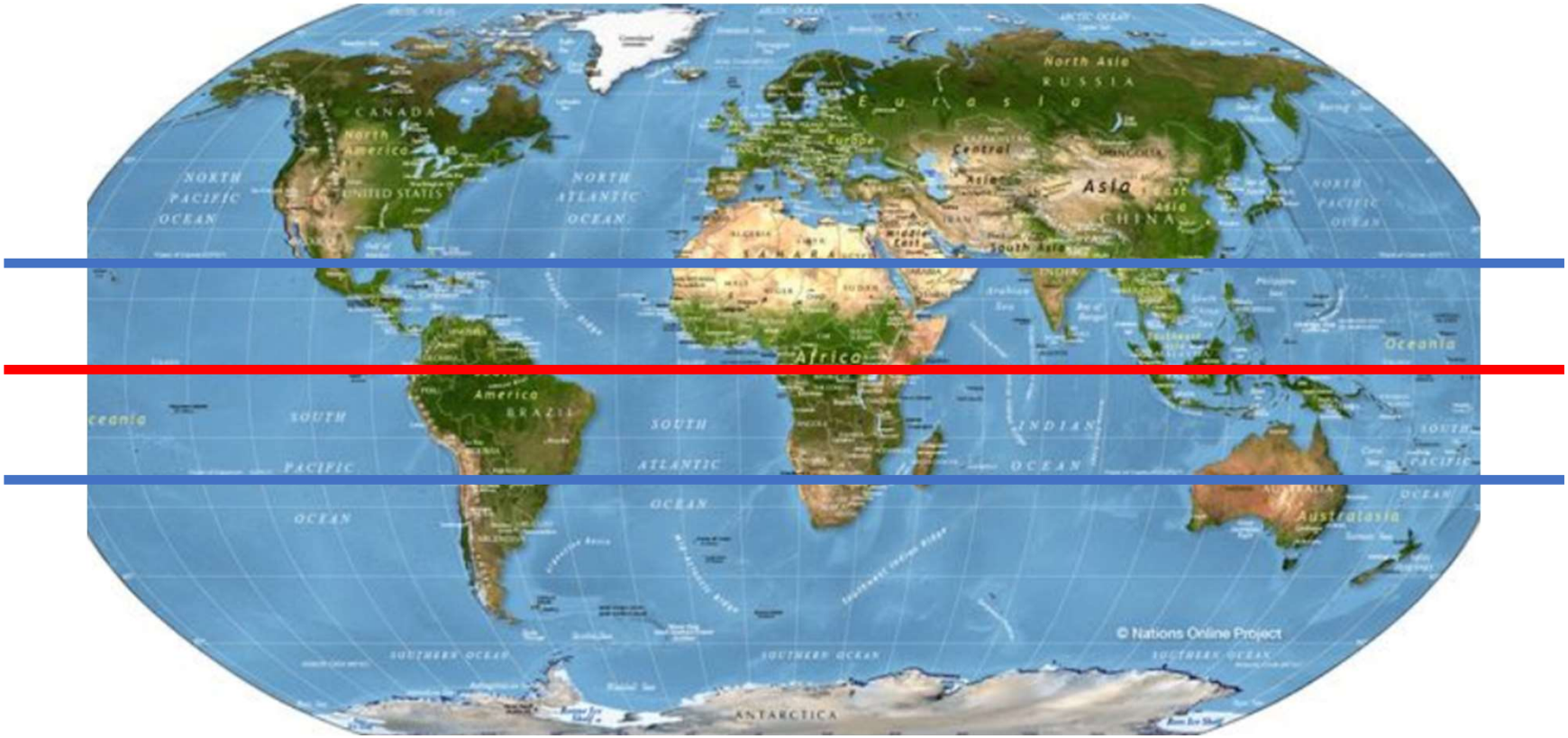


https://www.worldometers.info/coronavirus/

Daily new confirmed COVID-19 cases/1 million people



https://ourworldindata.org/covid-cases


North Asia
RUSSIA
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CANADA
North America
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Central Asia
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South Asia
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SOUTHERN OCEAN
ANTARCTICA

OVERVIEW

Seasonality of coronaviruses and other respiratory viruses in Canada: Implications for COVID-19

Philippe Lagacé-Wiens[1,2*], Jared Bullard[1,3,4], Roy Cole[5], Paul Van Caeseele[1,3,4]

Abstract

Background: Like endemic coronaviruses, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is believed to have emerged in humans from a zoonotic source and may ultimately develop a seasonal pattern. A seasonal pattern, particularly if combined with other seasonal outbreaks of respiratory virus infections, may have significant impacts on the healthcare system. We evaluated the seasonal pattern of existing endemic coronaviruses and several other common respiratory viruses to determine the potential impacts of added burden of respiratory disease should SARS-CoV-2 establish seasonality.

Methods: National surveillance data for laboratory confirmations of endemic coronaviruses, influenza A and B viruses, rhinovirus/enterovirus, human metapneumovirus, respiratory syncytial virus and parainfluenza virus for the past 10 years were obtained from the Government of Canada Open Data and FluWatch. Epidemic curves were generated from total case numbers and percent of samples testing positive for each respiratory virus by epidemiological week.

Results: In Canada, endemic coronaviruses and other common respiratory viruses cause annual seasonal outbreaks in the winter months. Should SARS-CoV-2 develop a seasonal pattern similar to endemic coronaviruses and respiratory viruses, co-circulation would be expected to peak between January and March. Peak endemic coronavirus activity occurs during the nadir of rhinovirus/enterovirus and parainfluenza activity.

Conclusion: Healthcare settings, assisted-living and long-term care homes, schools and essential services employers should anticipate and have contingencies for seasonal outbreaks of SARS-CoV-2 and co-circulating respiratory viruses during peak seasons. Given the likelihood of co-circulation, diagnostic multiplex testing targeting co-circulating pathogens may be more efficient than single target assays for symptomatic individuals if a seasonal pattern to coronavirus disease 2019 (COVID-19) is established.

Suggested citation: Lagacé-Wiens P, Bullard J, Cole R, Van Caeseele P. Seasonality of coronaviruses and other respiratory viruses in Canada: Implications for COVID-19. Can Commun Dis Rep 2021;47(3):132–8. https://doi.org/10.14745/ccdr.v47i03a02

Keywords: coronavirus, SARS-CoV-2, COVID-19, epidemiology, Canada, seasonality

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https://doi.org/10.14745/ccdr.v47i03a02

Mitkä kaikki virukset aiheuttavat flunssan kaltaisia oireita?

Bacterial [edit]

- Anthrax
- Brucellosis
- Cat scratch fever
- Legionellosis
- Leptospirosis
- Listeriosis
- Lyme disease
- Lymphogranuloma venereum
- Mastitis
- Salmonellosis
- Toxic Shock Syndrome
- Syphilis
- Tuberculosis
- Scrub typhus
- Rocky Mountain spotted fever

Viral [edit]

- Bornholm disease (Coxsackie B virus)
- Chickenpox
- Cytomegalovirus
- Eastern equine encephalitis virus
- California encephalitis virus
- Enteroviruses
- Hendra virus
- Hepatitis A, B, C, D, E
- Herpes
- HIV-1, -2
- Newcastle disease
- Human parainfluenza viruses
- Human rhinovirus
- Measles
- MERS coronavirus
- Human respiratory syncytial virus
- Rubella
- SARS coronavirus
- SARS coronavirus 2
- Slapped cheek syndrome
- Smallpox
- Togaviridae
- Venezuelan equine encephalitis

Huom: esim rhinoviruksia tunnetaan n 160 erilaista, arviolta niitä on kuitenkin satoja erilaisia!

Fungal [edit]

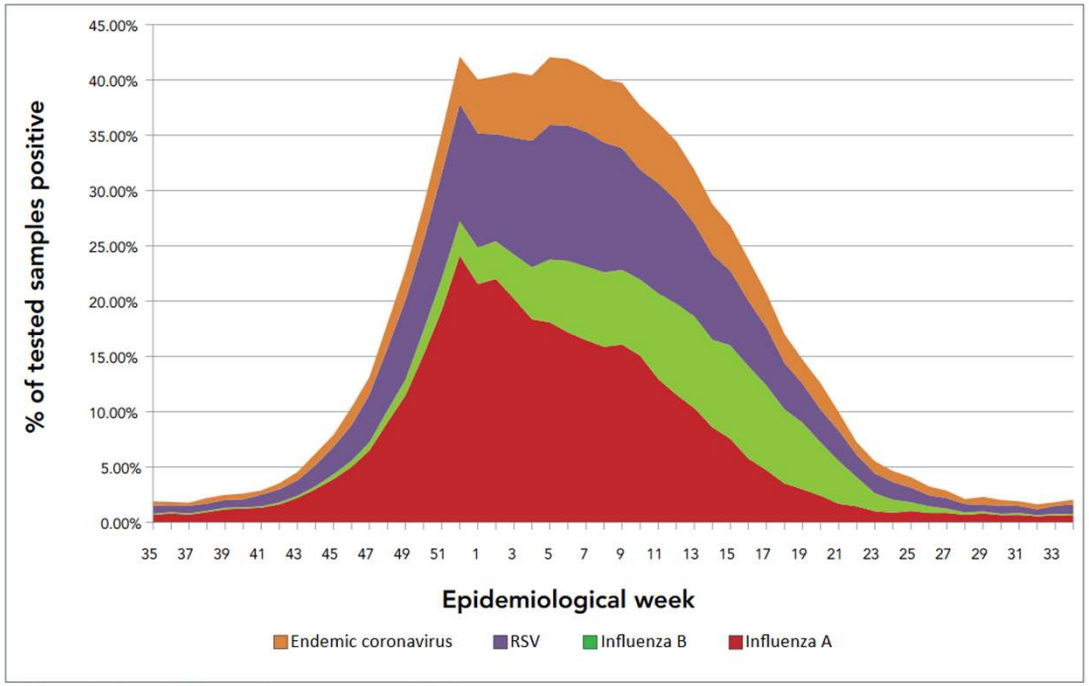
- Blastomycosis
- Coccidioidomycosis
- Histoplasmosis
- Stachybotrys chartarum

Protozoan [edit]

- Babesiosis
- Leishmaniasis
- Malaria
- Toxoplasmosis

https://en.wikipedia.org/wiki/List_of_infectious_diseases_causing_flu-like_syndrome

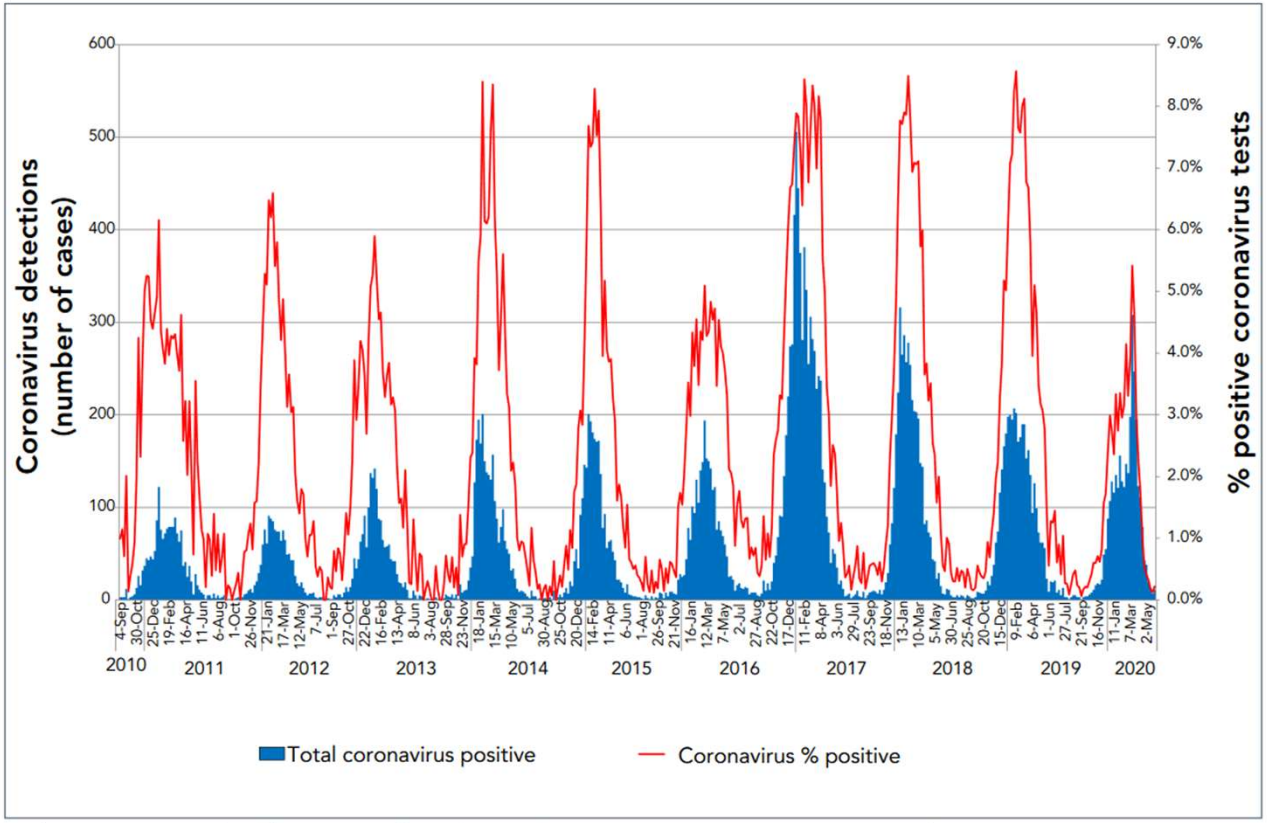
Figure 6: The 10-year averageof the proprotion of tests positive for endemic coronavirus, respiratory syncytial virus, influenza A or influenza B in reporting Canadian laboratories by epidemiological week



Abbreviation: RSV, respiratory syncytial virus
Note: Peak activity of these viruses, with >40% of tests positive for at least one of the viruses occurs between early January and early March
Data from Public Health Agency of Canada Open Data (https://open.canada.ca/en/open-data) and FluWatch (https://www.canada.ca/en/public-health/services/diseases/flu-influenza/influenza-surveillance.html)

https://doi.org/10.14745/ccdr.v47i03a02

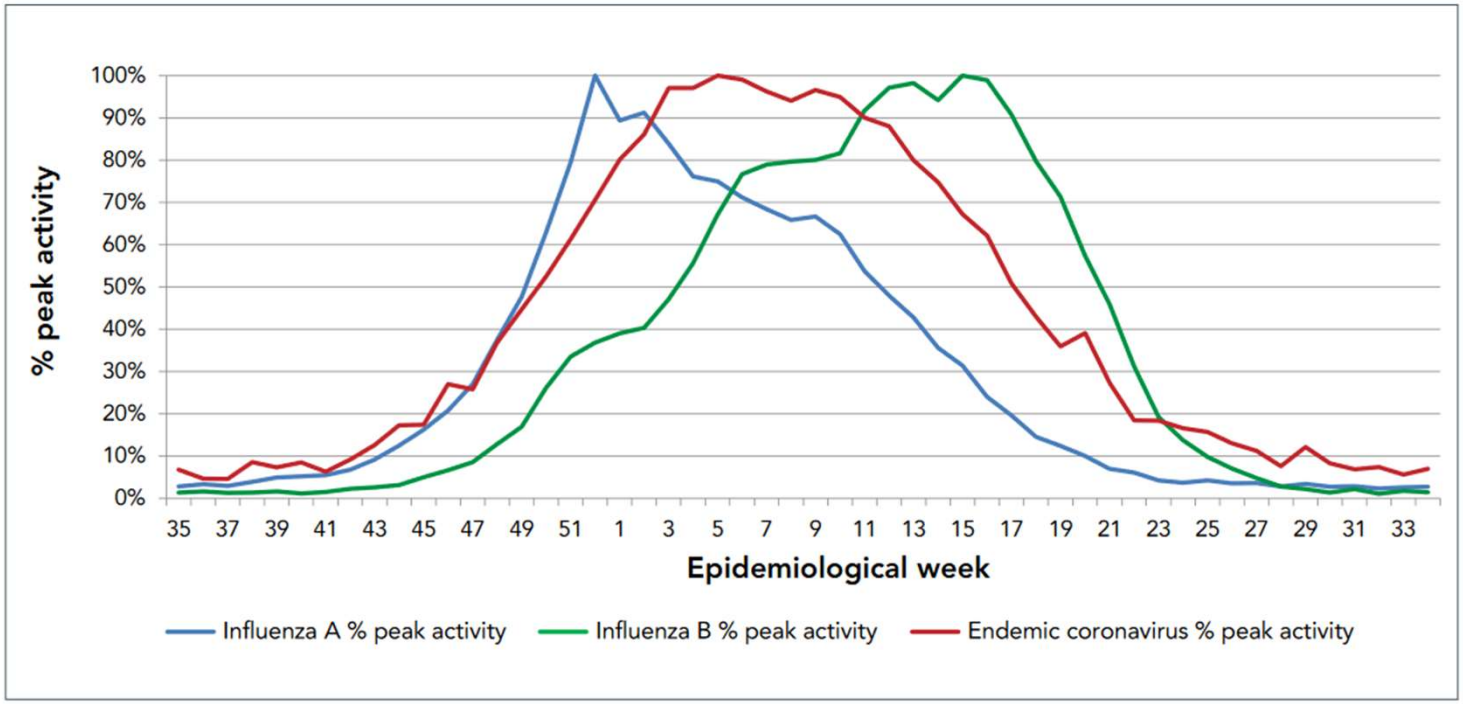
Figure 1: Seasonal pattern of endemic coronavirus detections and percent of coronavirus tests positive for endemic coronaviruses for the past ten years[a]



[a] The pattern is clearly seasonal; with epidemics occuring in winter months
Data from Public Health Agency of Canada Open Data (https://open.canada.ca/en/open-data) and FluWatch (https://www.canada.ca/en/public-health/services/diseases/flu-influenza/influenza-surveillance.html)

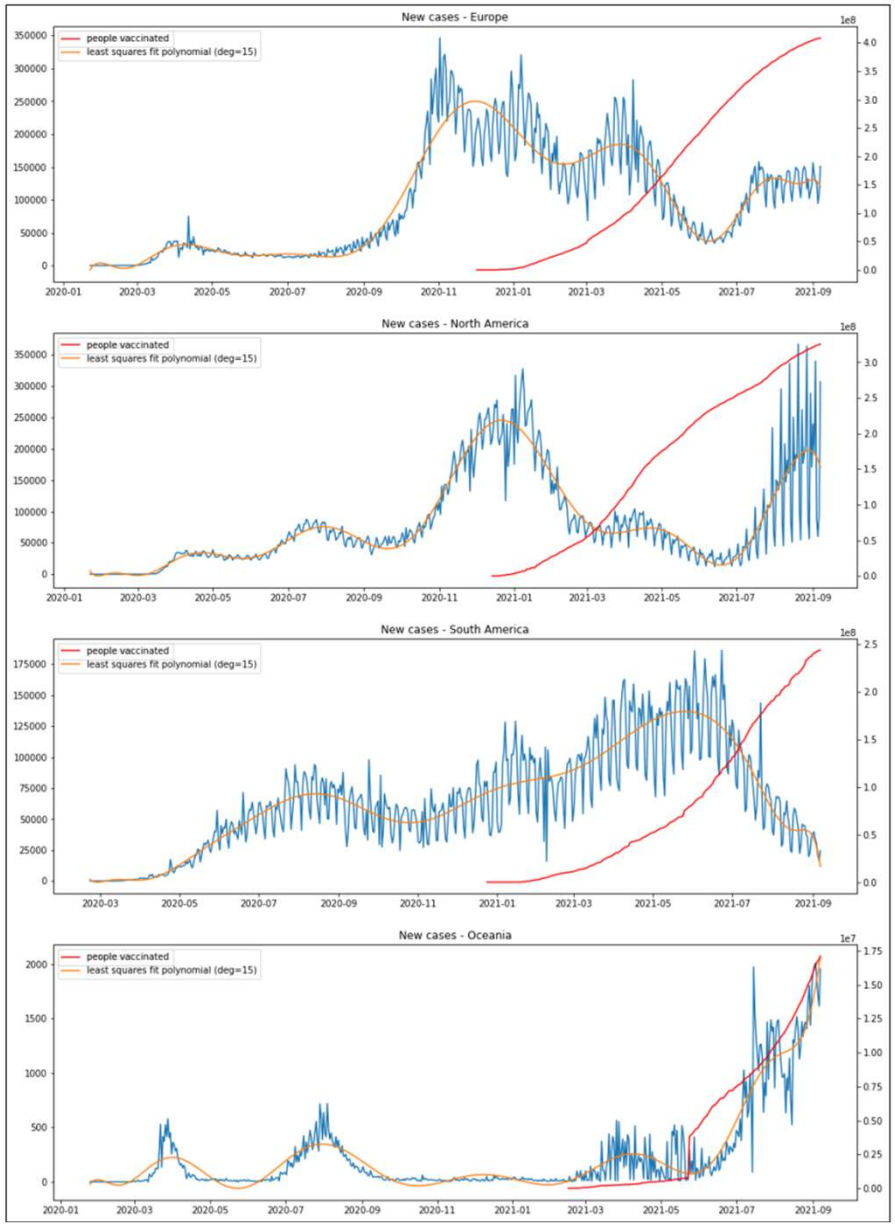
https://doi.org/10.14745/ccdr.v47i03a02

Figure 3: The 10-year average activity of influenza A, influenza B and endemic coronaviruses by epidemiological week



Note: Peak activity (100%) is defined as maximum percent-positive tests for each virus
Data from Public Health Agency of Canada Open Data (https://open.canada.ca/en/open-data) and FluWatch (https://www.canada.ca/en/public-health/services/diseases/flu-influenza/influenza-surveillance.html)

https://doi.org/10.14745/ccdr.v47i03a02



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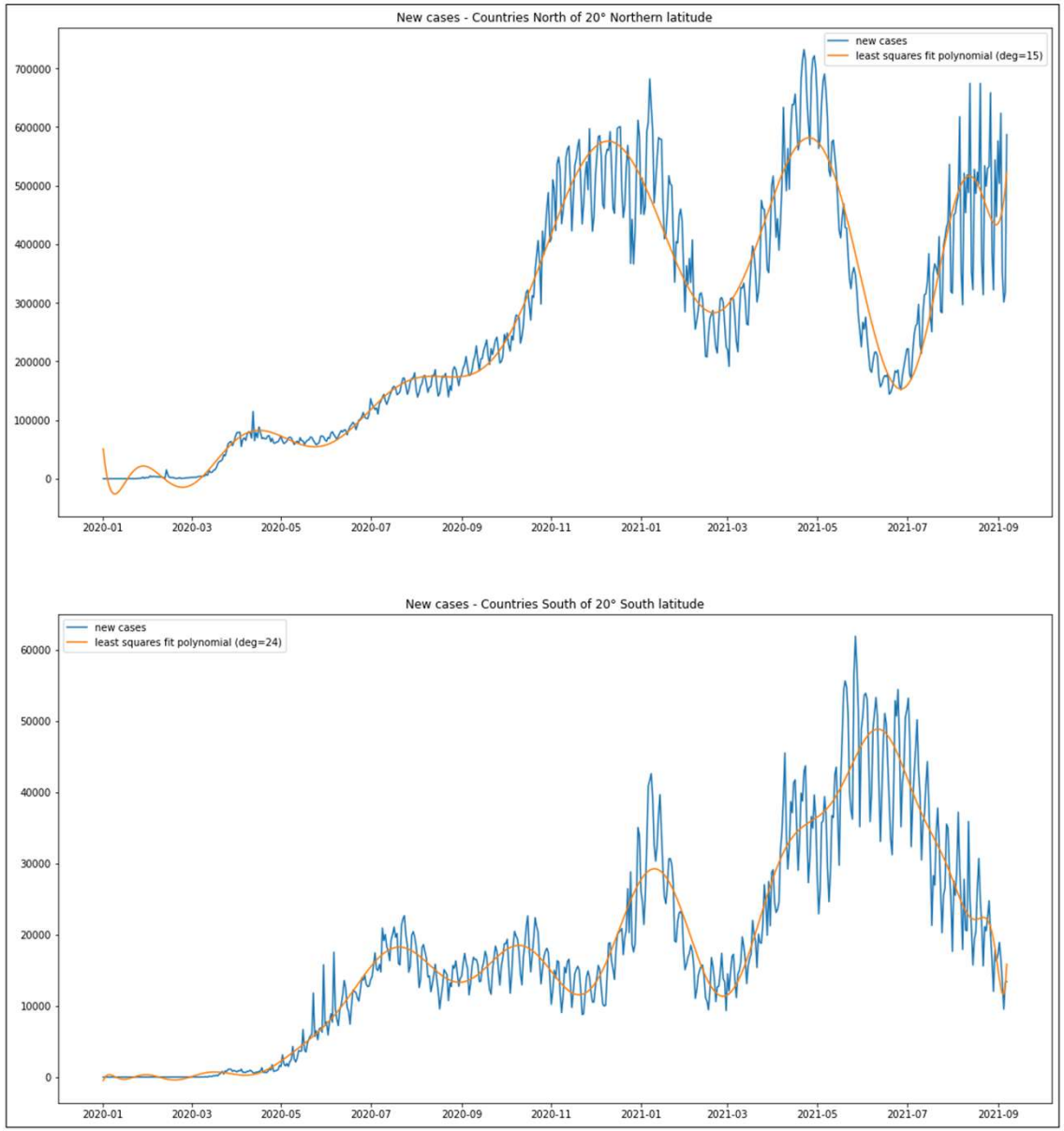

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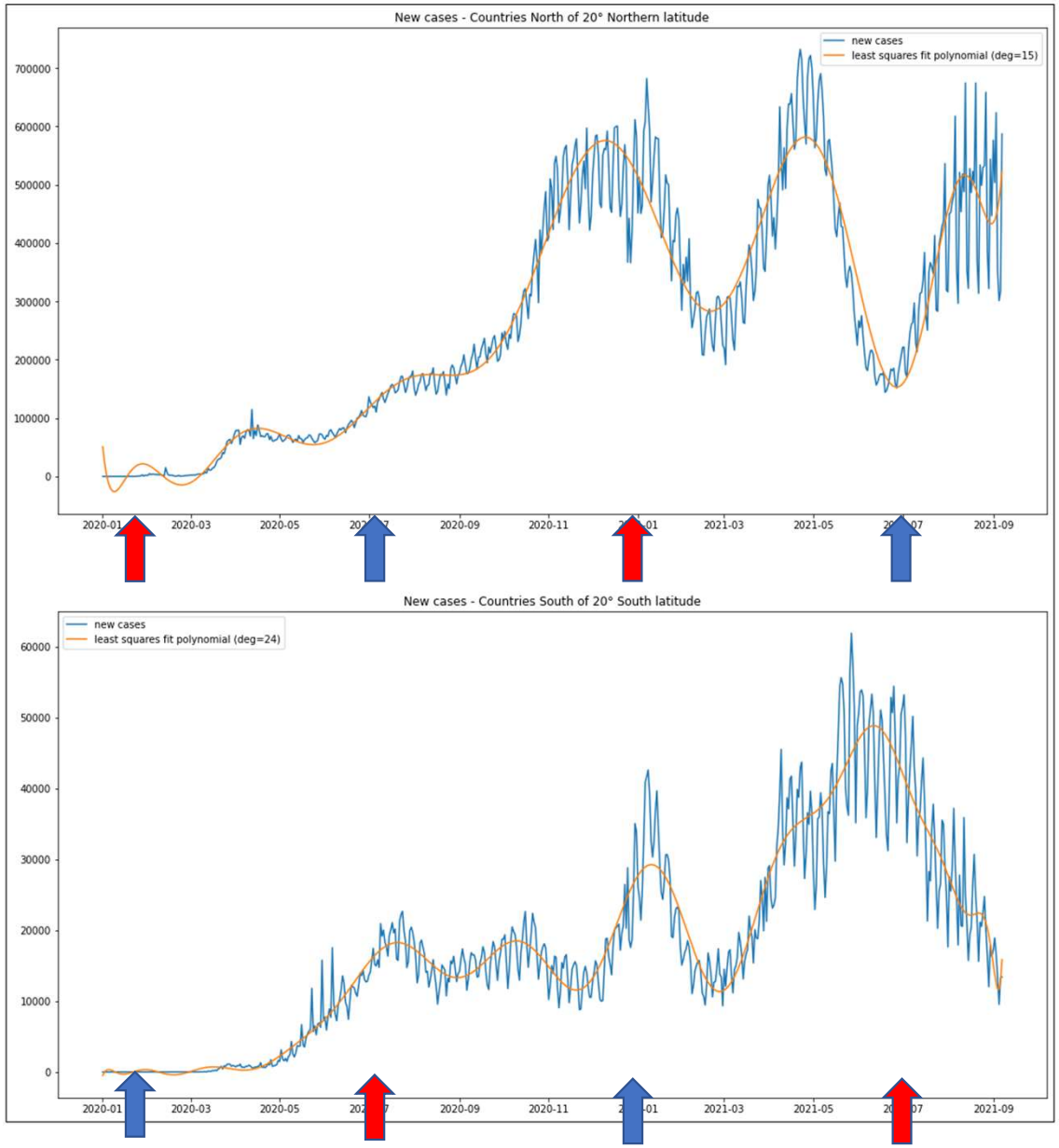


Tuukka Bogdanoff, Petri Lehenkari, Olli Silven

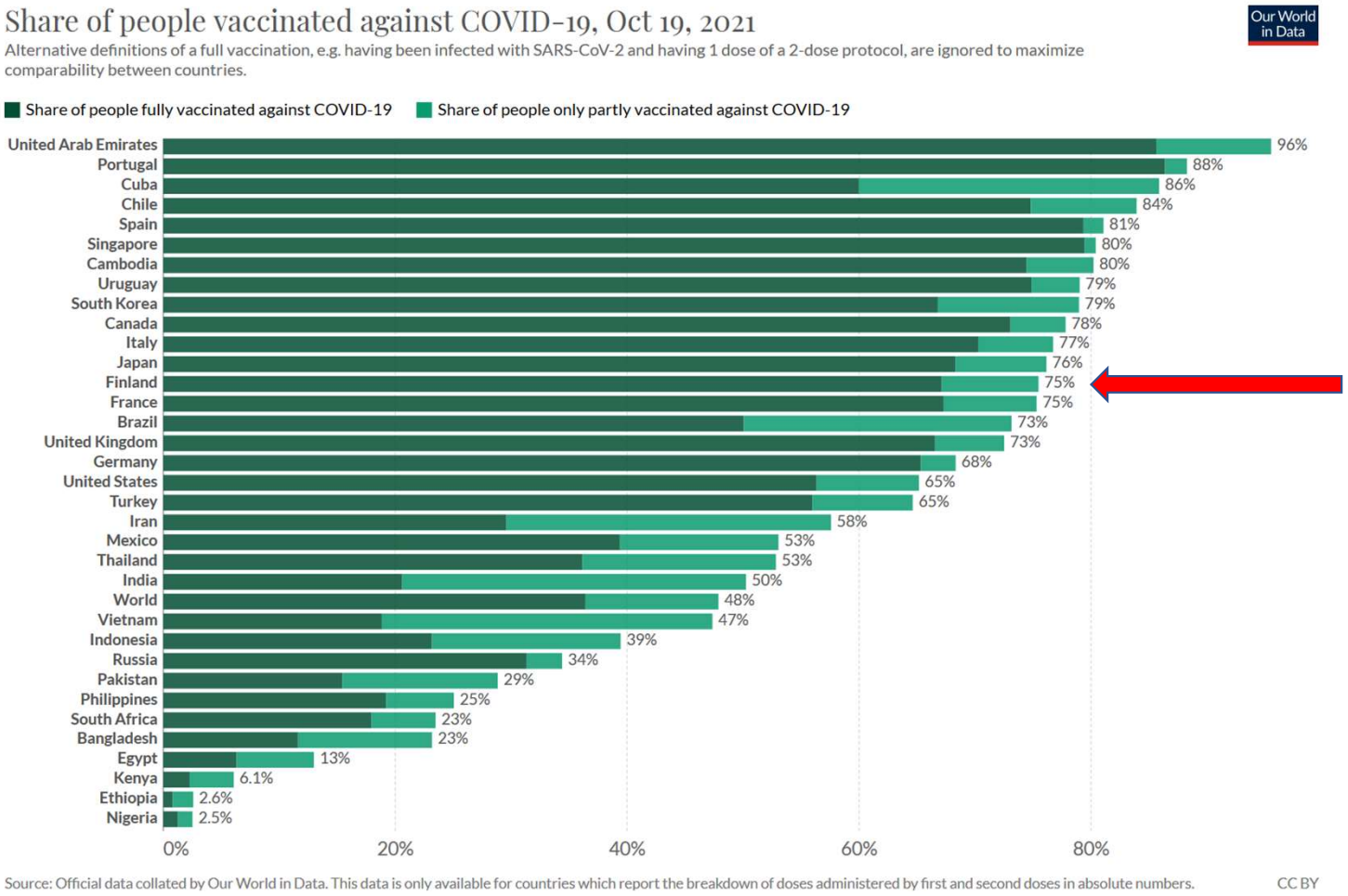
Ennustus 1: COVID-19 tulee olemaan viides endeeminen koronavirus, joka ilmaantuu infektiohuipuissa muiden virusten tapaan

Table 1: Currently circulating endemic human coronaviruses prior to zoonotic transfer to humans and emergence timeline based on molecular analysis

Endemic coronavirus	Reservoir	Intermediate host	Estimated emergence in humans	Discovery
NL63	Bats	Unknown	560–820 years ago	2004
229E	Bats	Camelids	~200 years ago	1966
HKU1	Rodents	Unknown	~1950s	2004
OC43	Rodents	Bovines	~1890	1967

https://doi.org/10.14745/ccdr.v47i03a02

Rokotuskattavuus maailmassa vaihtelee tällä hetkellä 2,5%-96%



Immunologinen muisti rokotetuilla säilyy hyvin vaikka vasta-ainepitoisuus laskisi

Original Article | Open Access

Decline in neutralising antibody responses, but sustained T-cell immunity, in COVID-19 patients at 7 months post-infection

Jun Chen, Xiaomin Liu, Xinyu Zhang, Yixiao Lin, Danping Liu, Jingna Xun, Zhenyan Wang, Ling Gu, Qian Li, Dan Yin, Junyang Yang, Hongzhou Lu,

First published: 26 July 2021 | https://doi.org/10.1002/cti2.1319

Ennustus 2: Rokotettu maailma selviää kohtuullisen hyvin vuosina 2021-2025, rokottamaton ei

- Rokottamilla 6 x enemmän tartuntoja (Suomessa jopa 11 x enemmän)
- Rokottamattomat joutuvat 17x todennäköisemmin sairaalahoitoon
- Rokotetuilla 11 x vähemmän kuolemia (CDC, USA)

MITÄ TÄMÄ TARKOITTAA KÄYTÄNNÖSSÄ?

Verrattuna tavalliseen influenssaan koronavirus on 10 x tappavampi, rokotus laskee riskin 1/10:n

=rokotettuna koronavirus on yhtä tappava kuin influenssa

Luonnollinen sairastamisen kautta saatu immuniteetti tasoittaa eroja jo nyt ja voimakkaammin ajan kuluessa, valistunut arvaus on että **2025 alkaen kuolleisuudessa ei ole eroja ja olemme immunoadaptoituneet virukseen globaalisti**

KYSYMYS: lakkaako rokotekattavuuden ollessa >80% koronavirus olemasta yleisvaarallinen tartuntatauti?

Yleisvaaralliset tartuntataudit

- EHEC-bakteerin aiheuttama tauti
- hepatiitti A
- hepatiitti E
- A-tyypin influenssaviruksen H5N1- tai H7N9-alatyypin taikka muun uuden tai harvinaisen alatyypin aiheuttama tauti
- isorokko
- kolera
- kuppa
- kurkkumätä
- lavantauti (Salmonella typhi)
- meningokokin aiheuttama vaikea yleisinfektio ja aivokalvontulehdus
- pernarutto
- pikkulavantauti (Salmonella paratyphi)
- polio
- rutto
- SARS ja MERS ja muu uuden koronavirustyypin aiheuttama vaikea infektio
- *salmonelloosi* (muu kuin lavantauti ja pikkulavantauti)
- shigellapunatauti
- tuberkuloosi
- tuhkarokko
- Ebola, Lassa, Marburg, Krimin-Kongon verenvuotokuume ja muut virusten aiheuttamat verenvuotokuumeet

https://thl.fi/fi/web/infektiotaudit-ja-rokotukset/seurantajarjestelmat-ja-rekisterit/tartuntatautirekisteri/ilmoitettavat-taudit-ja-mikrobit

Valvottavat tartuntataudit

- botulismi
- Creutzfeldt–Jakobin tauti
- ekinokokkoosi
- *hemofiluksen aiheuttama vaikea yleisinfektio ja aivokalvontulehdus*
- hepatiitti B
- hepatiitti C
- *hinkuyskä*
- hiv-infektio
- *sukupuoliteitse leviävät klamydiainfektiot*
- keltakuume
- legionelloosi
- listerioosi
- lepra ja *muu mykobakteeritauti kuin tuberkuloosi*
- malaria
- pneumokokin aiheuttama vaikea yleisinfektio ja aivokalvontulehdus
- *puutiaisaivokuume*
- vesikauhu (raivotauti)
- *rotavirusinfektio*
- sankkerit (LGV ja ulcus molle)
- sikotauti
- tetanus
- tippuri
- vihurirokko

https://thl.fi/fi/web/infektiotaudit-ja-rokotukset/seurantajarjestelmat-ja-rekisterit/tartuntatautirekisteri/ilmoitettavat-taudit-ja-mikrobit

Yleisvaaralliset tartuntataudit

Tartuntatauti on yleisvaarallinen, jos:

1. taudin tarttuvuus on suuri,
2. tauti on vaarallinen ja
3. taudin leviäminen voidaan estää toimenpiteillä, jotka kohdistuvat tautiin sairastuneeseen, taudinaiheuttajalle altistuneeseen tai tällaiseksi perustellusti epäiltyyn henkilöön.

- mahdollistaa tahdonvastaisen hoidon toteuttamisen (yleisvaaralliset tartuntataudit)
- vaikuttaa hoidon maksullisuuteen potilaalle (yleisvaaralliset ja valvottavat tartuntataudit)
- vaikuttaa tulomenetysten korvattavuuteen, mitkä määritellään muissa säädöksissä.

Ennustus 3: COVID-19 poistuu Suomessa yleisvaarallisten tartuntatautien listalta viimeistään kesällä 2022

- Vaikuttaa kaikkiin kansallisiin toimiin ja suhtautumiseen

COVID-19 ennustettiin jo hyvin seikkaperäisesti v 2015 Nature Medicine julkaisussa!

A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence

Vineet D Menachery[1], Boyd L Yount Jr[1], Kari Debbink[1,2], Sudhakar Agnihothram[3], Lisa E Gralinski[1], Jessica A Plante[1], Rachel L Graham[1], Trevor Scobey[1], Xing-Yi Ge[4], Eric F Donaldson[1], Scott H Randell[5,6], Antonio Lanzavecchia[7], Wayne A Marasco[8,9], Zhengli-Li Shi[4] & Ralph S Baric[1,2]

The emergence of severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome (MERS)-CoV underscores the threat of cross-species transmission events leading to outbreaks in humans. Here we examine the disease potential of a SARS-like virus, SHC014-CoV, which is currently circulating in Chinese horseshoe bat populations[1]. Using the SARS-CoV reverse genetics system[2], we generated and characterized a chimeric virus expressing the spike of bat coronavirus SHC014 in a mouse-adapted SARS-CoV backbone. The results indicate that group 2b viruses encoding the SHC014 spike in a wild-type backbone can efficiently use multiple orthologs of the SARS receptor human angiotensin converting enzyme II (ACE2), replicate efficiently in primary human airway cells and achieve *in vitro* titers equivalent to epidemic strains of SARS-CoV. Additionally, *in vivo* experiments demonstrate replication of the chimeric virus in mouse lung with notable pathogenesis. Evaluation of available SARS-based immune-therapeutic and prophylactic modalities revealed poor efficacy; both monoclonal antibody and vaccine approaches failed to neutralize and protect from infection with CoVs using the novel spike protein. On the basis of these findings, we synthetically re-derived an infectious full-length SHC014 recombinant virus and demonstrate robust viral replication both *in vitro* and *in vivo*. Our work suggests a potential risk of SARS-CoV re-emergence from viruses currently circulating in bat populations.

The emergence of SARS-CoV heralded a new era in the cross-species transmission of severe respiratory illness with globalization leading to rapid spread around the world and massive economic impact[3,4]. Since then, several strains—including influenza A strains H5N1, H1N1 and H7N9 and MERS-CoV—have emerged from animal populations, causing considerable disease, mortality and economic hardship for the afflicted regions[5]. Although public health measures were able to stop the SARS-CoV outbreak[4], recent metagenomics studies have identified sequences of closely related SARS-like viruses circulating in Chinese bat populations that may pose a future threat[1,6]. However, sequence data alone provides minimal insights to identify and prepare for future prepandemic viruses. Therefore, to examine the emergence potential (that is, the potential to infect humans) of circulating bat CoVs, we built a chimeric virus encoding a novel, zoonotic CoV spike protein—from the RsSHC014-CoV sequence that was isolated from Chinese horseshoe bats[1]—in the context of the SARS-CoV mouse-adapted backbone. The hybrid virus allowed us to evaluate the ability of the novel spike protein to cause disease independently of other necessary adaptive mutations in its natural backbone. Using this approach, we characterized CoV infection mediated by the SHC014 spike protein in primary human airway cells and *in vivo*, and tested the efficacy of available immune therapeutics against SHC014-CoV. Together, the strategy translates metagenomics data to help predict and prepare for future emergent viruses.

The sequences of SHC014 and the related RsWIV1-CoV show that these CoVs are the closest relatives to the epidemic SARS-CoV strains (**Fig. 1a**,**b**); however, there are important differences in the 14 residues that bind human ACE2, the receptor for SARS-CoV, including the five that are critical for host range: Y442, L472, N479, T487 and Y491 (ref. 7). In WIV1, three of these residues vary from the epidemic SARS-CoV Urbani strain, but they were not expected to alter binding to ACE2 (**Supplementary Fig. 1a**,**b** and **Supplementary Table 1**). This fact is confirmed by both pseudotyping experiments that measured the ability of lentiviruses encoding WIV1 spike proteins to enter cells expressing human ACE2 (**Supplementary Fig. 1**) and by *in vitro* replication assays of WIV1-CoV (ref. 1). In contrast, 7 of 14 ACE2-interaction residues in SHC014 are different from those in SARS-CoV, including all five residues critical for host range (**Supplementary Fig. 1c** and **Supplementary Table 1**). These changes, coupled with

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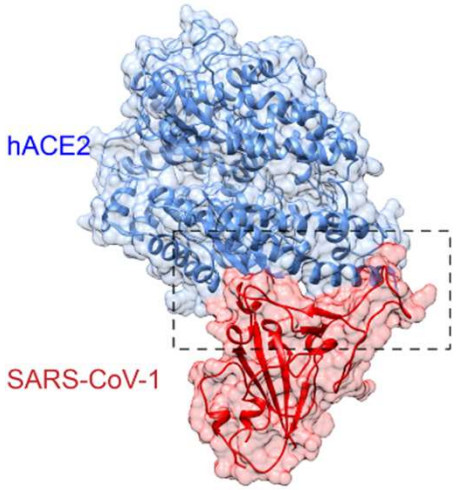
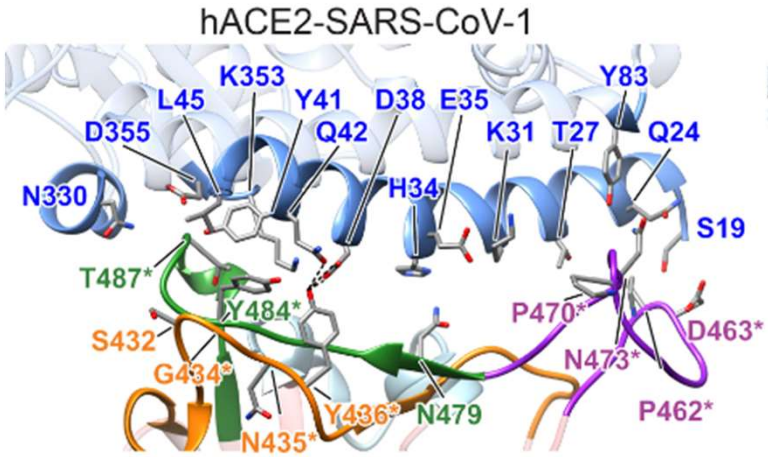
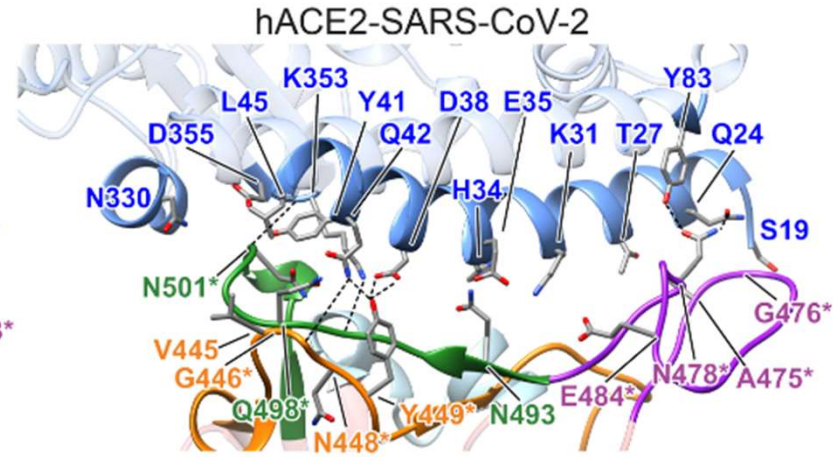
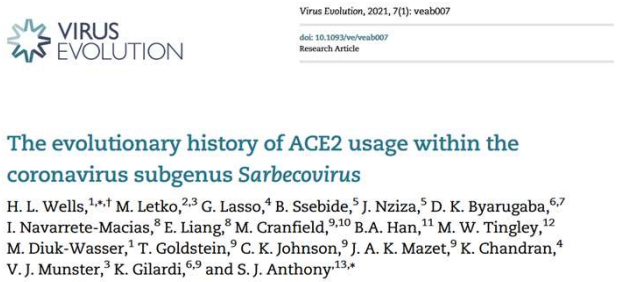
Received 12 June; accepted 8 October; published online 9 November 2015; corrected online 20 November 2015 (details online); doi:10.1038/nm.3985

ACE2 –reseptori?









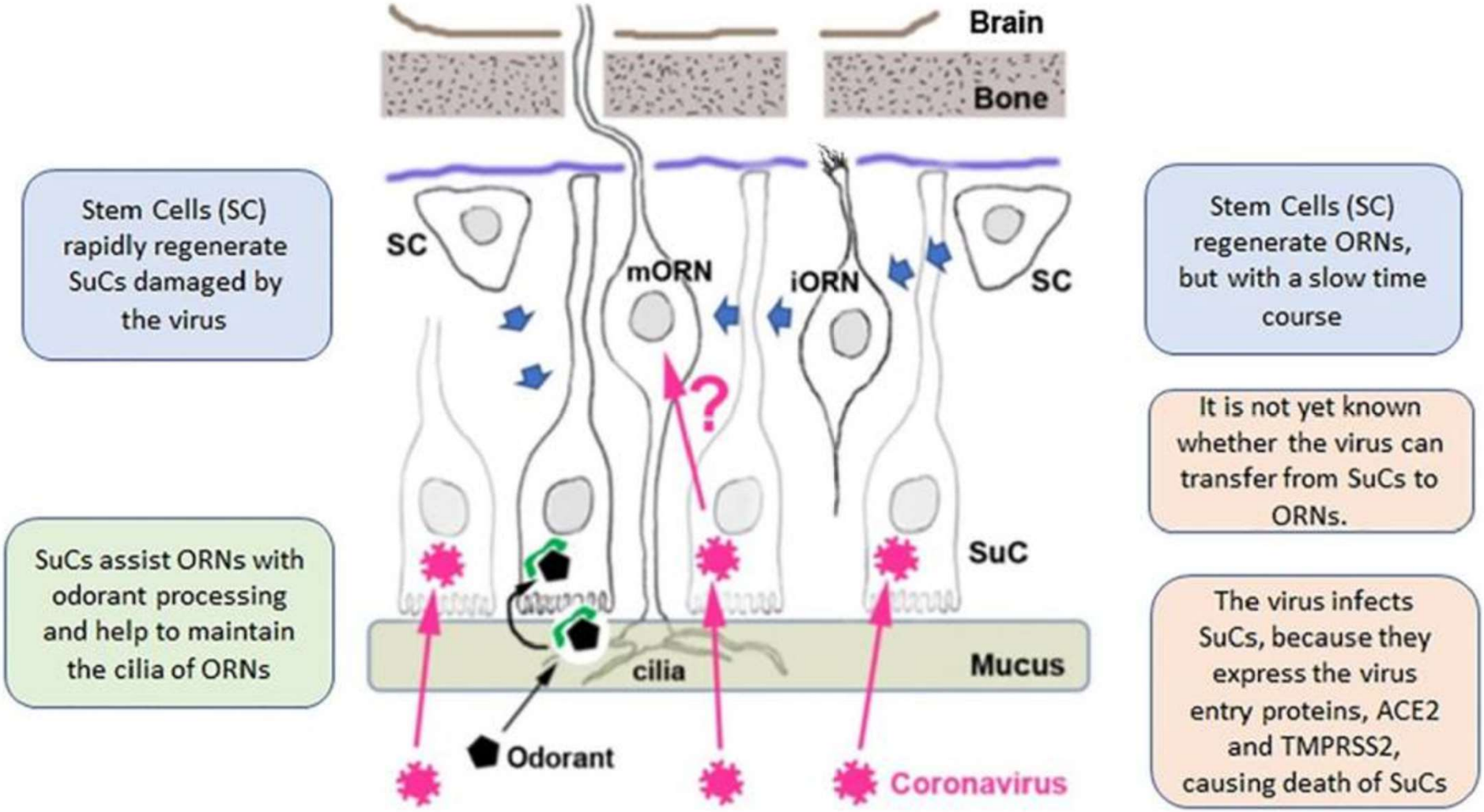
VIRUS EVOLUTION

Virus Evolution, 2021, 7(1): veab007

doi: 10.1093/ve/veab007
Research Article

The evolutionary history of ACE2 usage within the coronavirus subgenus *Sarbecovirus*

H. L. Wells,[1,*,†] M. Letko,[2,3] G. Lasso,[4] B. Ssebide,[5] J. Nziza,[5] D. K. Byarugaba,[6,7] I. Navarrete-Macias,[8] E. Liang,[8] M. Cranfield,[9,10] B.A. Han,[11] M. W. Tingley,[12] M. Diuk-Wasser,[1] T. Goldstein,[9] C. K. Johnson,[9] J. A. K. Mazet,[9] K. Chandran,[4] V. J. Munster,[3] K. Gilardi,[6,9] and S. J. Anthony[13,*]



Neuroscientist. 2020 Sep 11 : 1073858420956905.

Journal of Pathology
J Pathol 2004; **203**: 631–637
Published online in Wiley InterScience (www.interscience.wiley.com). **DOI:** 10.1002/path.1570

Rapid Communication

Tissue distribution of ACE2 protein, the functional receptor for SARS coronavirus. A first step in understanding SARS pathogenesis

I Hamming,[1] W Timens,[1]* MLC Bulthuis,[1] AT Lely,[2] GJ Navis[2] and H van Goor[1]
[1]*Department of Pathology and Laboratory Medicine, University Hospital Groningen, The Netherlands*
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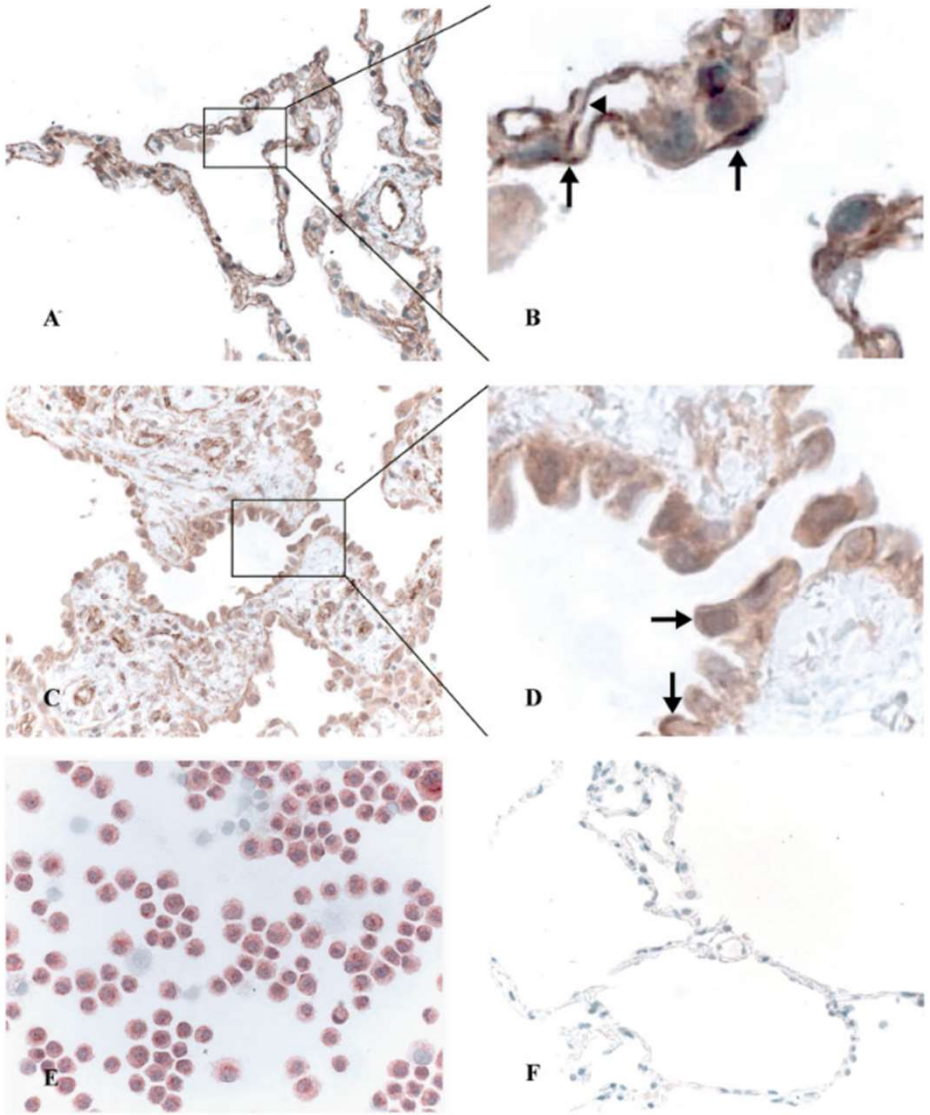


Figure 1. Normal lung tissue: overview (A) and larger magnification (B). Positive staining for ACE2 is clearly present on alveolar epithelial cells (arrow) and capillary endothelium (arrow-head). Fibrotic lung tissue (C) and larger magnification (D). Positive staining for ACE2 is clearly present on type II cells (arrow). Cultured lung type II alveolar epithelial cells (A549) are strongly positive for ACE2 (E). Control section stained with anti-ACE2 in the presence of the synthetic ACE2 peptide shows no staining of lung tissue (F)

DOI:10.1002/path.1570

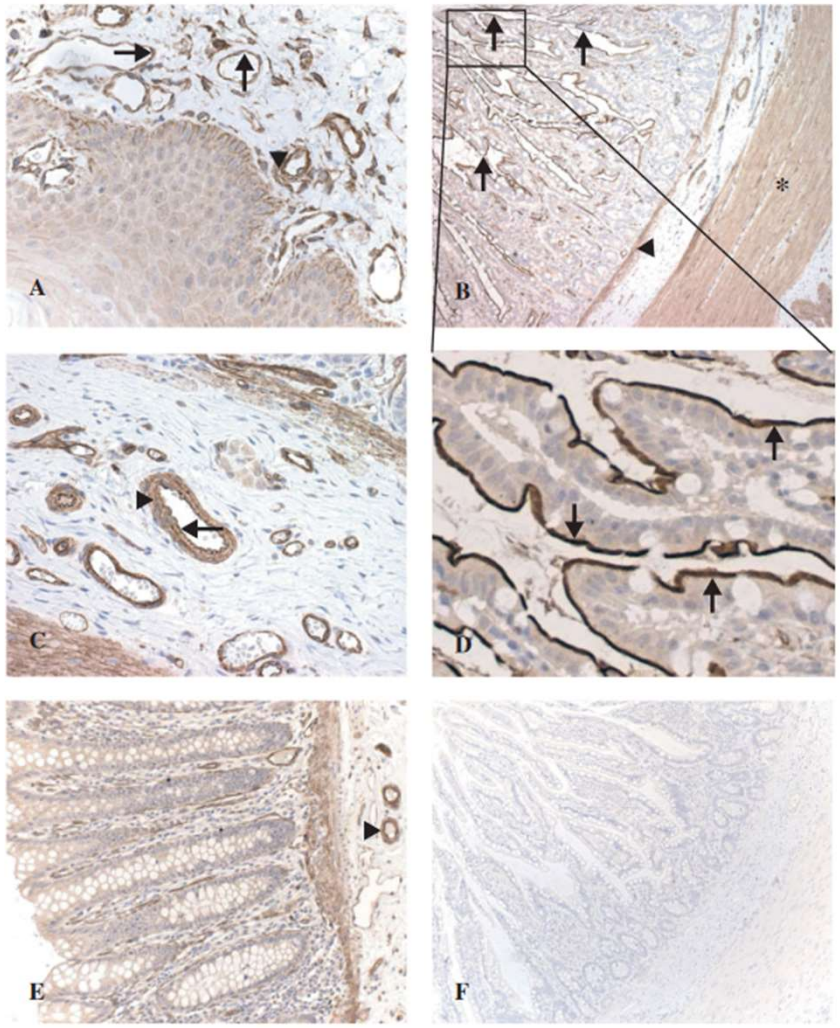


Figure 2. Overview of oral mucosa (A). Strong staining is observed in vascular endothelium (arrow) and vascular smooth cells (arrow-head). Granular ACE2 staining is present in the basal layer of the epithelium. In the small intestine (ileum) (B) staining can be seen in the villous brush border (arrow), the muscularis mucosae (arrow-head), and the muscularis propri In a larger magnification of the submucosa (C), strong staining is present in vascular endothelium (arrow) and vascular muscle cells (arrow-head). In a larger magnification of the villi (D), abundant staining is seen on the brush border of the ente (arrow). In the colon (E), ACE2 staining is present in endothelium and vascular smooth muscle cells from the blood (arrow-head) and in the muscular layers. Control section stained with anti-ACE2 in the presence of the synthetic ACE2 shows no staining in the small intestine (ileum) (F)

DOI:10.1002/path.1570

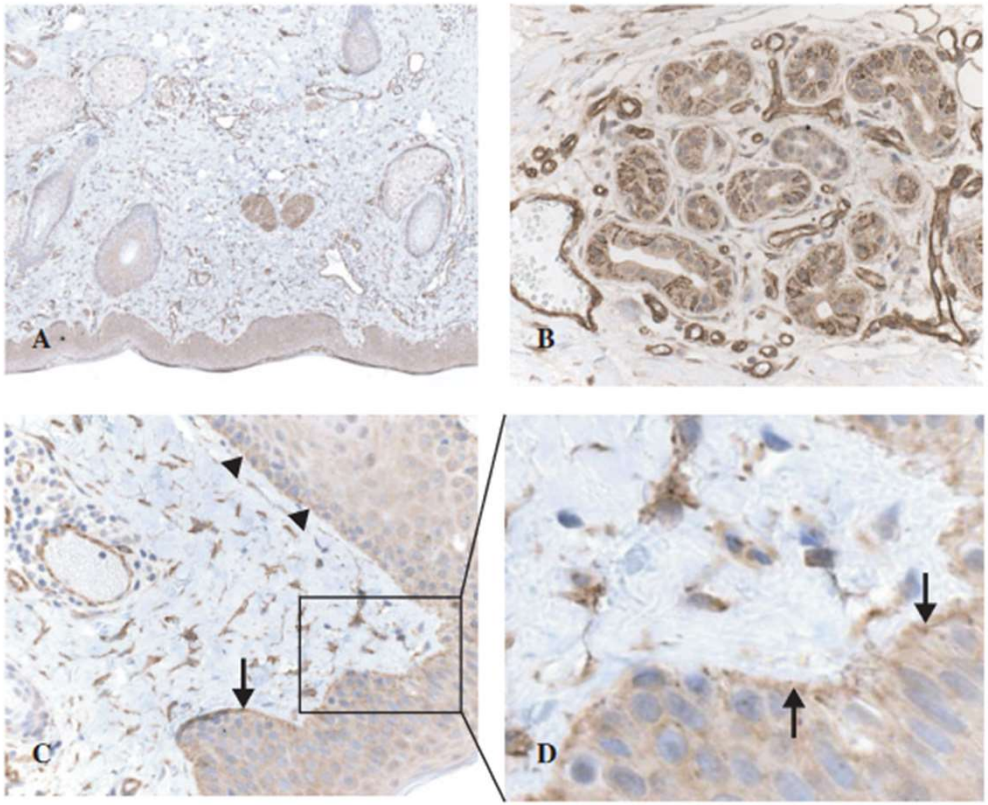


Figure 3. Skin tissue (A) with larger magnification (C, D). Staining is abundantly present in blood vessels/capillaries and in the basal layer of the epidermis (arrow) and hair follicles (arrow-head). Eccrine glands also express ACE2 (B)

DOI:10.1002/path.1570

Ennustus 4: COVID-19 tulee aiheuttamaan muita yleisiä kausiviruksia enemmän pitkäaikaishaittoja

Wanga V, Chevinsky JR, Dimitrov LV, et al. Long-Term Symptoms Among Adults Tested for SARS-CoV-2 — United States, January 2020–April 2021. MMWR Morb Mortal Wkly Rep 2021;70:1235–1241. DOI: http://dx.doi.org/10.15585/mmwr.mm7036a1external icon.

	SARS-CoV-2 test result, weighted % (95% CI)			
	Symptom prevalence among all persons receiving testing		Symptom prevalence among persons receiving testing who reported a symptom lasting >4 weeks since onset	
Symptom	Respondents who received a positive test result (n = 698)*	Respondents who received a negative test result (n = 2,437)*	Respondents who received a positive test result (n = 465)*	Respondents who received a negative test result (n = 1,058)*
Any symptom	65.9† (61.9–69.8)	42.9 (40.8–45.1)	—	—
1 symptom only	27.2† (23.7–30.8)	18.7 (17.0–20.4)	41.4 (36.5–46.3)	43.6 (40.3–46.9)
2 symptoms	14.0† (11.1–16.8)	9.5 (8.2–10.7)	21.2 (17.1–25.3)	22.1 (19.3–24.8)
≥3 symptoms	24.7† (21.0–28.3)	14.7 (13.2–16.3)	37.4 (32.5–42.4)	34.3 (31.1–37.5)
Fatigue/Tired/Weakness	22.5† (19.0–26.1)	12.0 (10.6–13.4)	34.2† (29.3–39.1)	28.0 (25.0–31.0)
Change in smell or taste	17.3† (14.1–20.4)	1.7 (1.1–2.3)	26.2† (21.8–30.7)	3.9 (2.6–5.3)
Shortness of breath or breathlessness	15.5† (12.4–18.7)	5.2 (4.2–6.2)	23.6† (19.1–28.1)	12.1 (9.9–14.2)
Cough	14.5† (11.6–17.4)	4.9 (4.0–5.9)	22.0† (17.8–26.2)	11.5 (9.4–13.6)
Headache	13.8† (10.9–16.7)	9.9 (8.6–11.2)	20.9 (16.7–25.1)	23.0 (20.2–25.8)
Problems sleeping	12.0† (9.3–14.7)	16.5 (14.8–18.1)	18.1† (14.2–22.1)	38.3 (35.1–41.6)
Joint or muscle pain	11.1 (8.4–13.9)	12.4 (10.9–13.9)	16.9† (12.9–20.9)	28.9 (25.8–32.0)
Cognitive dysfunction§	10.2† (7.7–12.8)	7.3 (6.1–8.4)	15.5 (11.8–19.3)	16.9 (14.4–19.4)
Chest pain or pressure	7.3† (5.2–9.4)	2.3 (1.6–2.9)	11.0† (7.9–14.2)	5.3 (3.7–6.8)
Change in mood	6.6 (4.6–8.7)	8.8 (7.6–10.0)	10.1† (7.1–13.1)	20.6 (17.9–23.2)
Postexertional malaise¶	6.1† (4.1–8.0)	2.4 (1.7–3.0)	9.2† (6.3–12.2)	5.5 (3.9–7.0)
Stomach pain	5.8 (3.9–7.7)	5.1 (4.1–6.1)	8.9 (6.0–11.7)	11.9 (9.7–14.1)
Hair loss	5.6 (3.7–7.5)	4.1 (3.3–5.0)	8.5 (5.6–11.3)	9.7 (7.6–11.7)
Diarrhea	5.3 (3.3–7.2)	3.3 (2.6–4.1)	8.0 (5.0–10.9)	7.8 (6.0–9.5)
Sore throat	4.9† (3.1–6.8)	1.7 (1.1–2.2)	7.5† (4.7–10.3)	3.9 (2.7–5.1)
Fever or chills	4.9† (3.0–6.8)	1.9 (1.4–2.5)	7.5 (4.7–10.3)	4.5 (3.2–5.8)
Palpitations (heart racing or pounding)	4.5 (2.7–6.3)	2.5 (1.9–3.2)	6.8 (4.1–9.5)	5.9 (4.3–7.5)
Nausea/Vomiting	4.1† (2.5–5.8)	1.9 (1.3–2.4)	6.3 (3.8–8.8)	4.3 (3.0–5.7)
Other symptom	1.3 (0.3–2.2)**	1.0 (0.6–1.5)	2.0 (0.5–3.4)**	2.4 (1.4–3.4)

Ennustus 5: Kiina avaa täysin kaiken sillä olevan tiedon Wuhanin viruslaboratorion toiminnasta ja viruksen leviämisestä

- viruksen väli-isäntä tai rekombinaatio/muuntumishistoria voidaan varmentaa
- palauttaa kansainvälisen yhteisön keskinäisen luottamuksen
- opimme vastaisen varalle suhtautumisen pandemiaan

Ennustus 6: mRNA rokotteet ovat tulleet jäädäkseen

- Parempi teho mm Influenssa –viruksiin!

Ennustus 7: 3.1. julistetaan pandemian uhrien muistopäiväksi

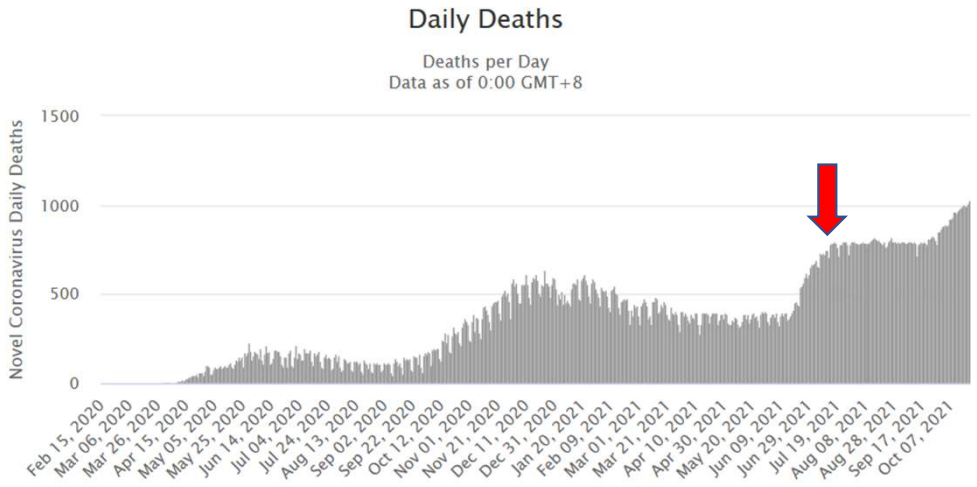
Ennustus 8: muut kuin koronaviruksen suoraan aiheuttamat laadullisten terveiden vuosien menetykset ylittävät koronavirusterveyshaitat jo v 2021

- Koronaviruksen hoito ja sulkutoimenpiteet viivästyttävät ja estävät hoitoa ja aiheuttaa terveyskuormitusta
- QALY –kertymä väestötasolla on negatiivinen pitkään, mutta koronaviruksen suoraan aiheuttama tautikuorma kohdistuu korkean rokotekattavuuden vuoksi hyvin pieneen ihmisryhmään ja muut haitat hyvin suureen ihmisryhmään
- Erityisen huolissani olen vaikutuksesta lapsiin ja nuoriin, parantumattomia sairauksia, mm syöpiä sairastaviin, joille hoitoon hakeutumisne viive tai palvelun tason aleneminen on elämän ja kuoleman kysymys

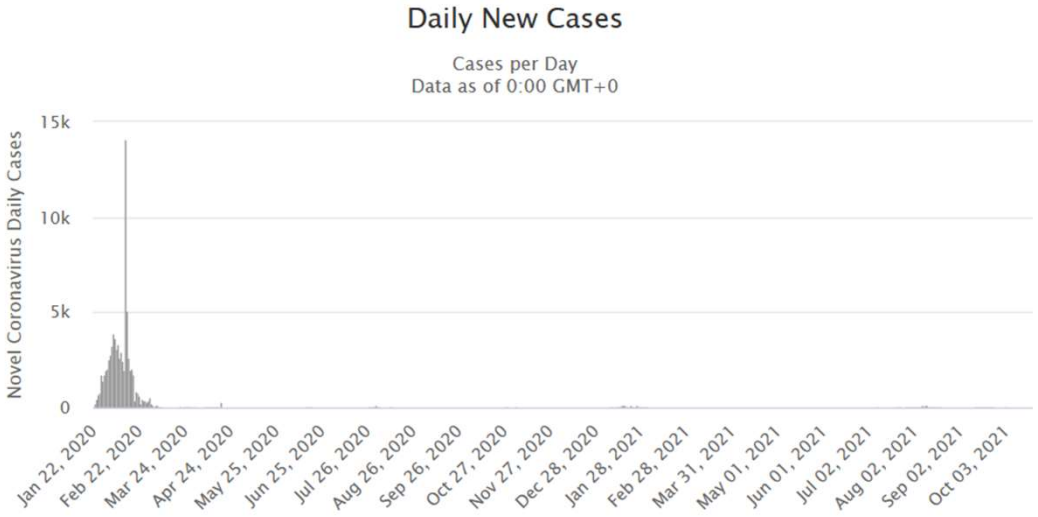
- Onko jo nyt Suomessa koronatoimien aiheuttama kuolleisuus suurempi kuin koronakuolleisuus?

Ennustus 9: saamme tietää todellisen koronakuolleisuuden ja sairastavuuden vasta kovista parametreistä, eli kuolleisuudesta, väestökehityksestä jne

Daily New Deaths in Russia



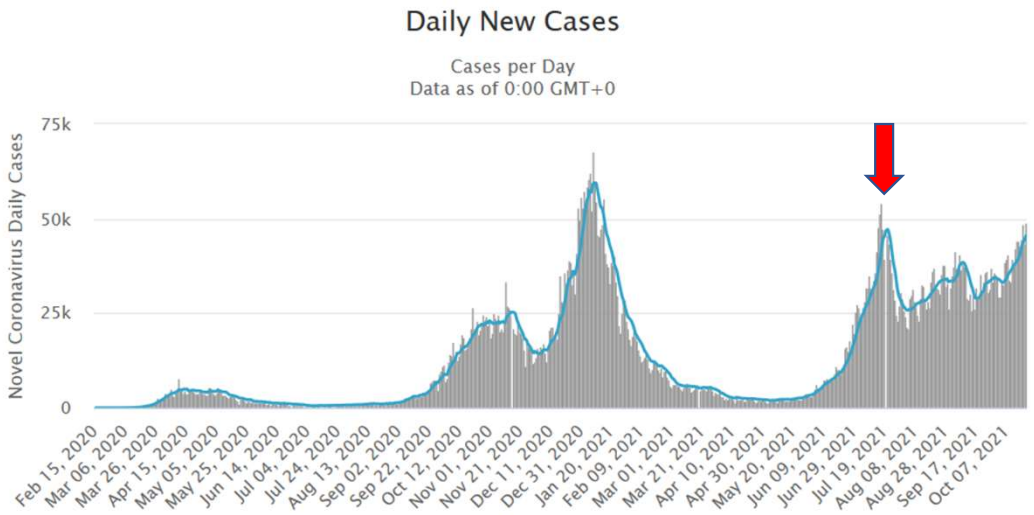
Daily New Cases in China

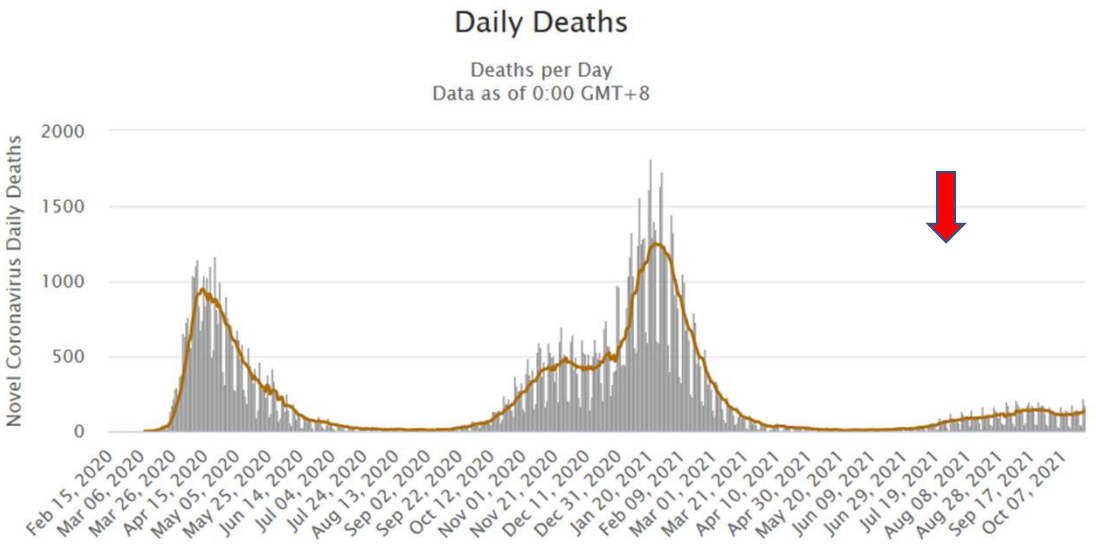


https://www.worldometers.info/coronavirus/

Indikaattorivaltioita kannattaa seurata!

Daily New Cases in the United Kingdom





https://www.worldometers.info/coronavirus/

Ennustus 10: Suomi

- Tapausten määrä nousee rajusti, mutta kokonaiskuolleisuus ei muutu
- Joudumme välillä tinkimään yökerhoelämästä ja matkustelusta ja käyttämään maskeja kun uusi variantti saapuu rokottamattomilta alueilta mutta **vessapaperia ei enää hamstrata**
- Kaikki rokotevastaiset, jotka sairastuvat, muuttuvat rokotemyönteisiksi
- Sairaaloiden kapasiteetti on koetuksella mutta kestää
- Poliitikot voivat jatkaa Instagram –postauksiaan ja jättää viruksen vastaiset toimet alueellisten viranomaisten ja THL:n huoleksi

Avoimeksi jääviä kysymyksiä?

- **Olisiko meidän mahdollista päästä vielä eroon viruksesta?**

-Kyllä olisi, mutta ei ole maailmanlaajuista konsensusta, että niin tehtäisiin

-taudin leviäminen eläimiin on teoreettinen toinen endeeminen virusvarasto, joten on mahdollista, ettei ihmisten koronasulku enää riitä

- **Miten maailman maiden heterogeeninen suhtautuminen vaikuttaa kaikkeen?**

-maailma tulee jakautumaan todella moneen eri kategoriaan, poliittinen ja taloudellinen epätasa-arvo voi lisääntyä, konfliktit voivat lisääntyä, tuotannon edellytykset ja talouden rakenteet vaurioitua pysyvästi, yksilön oikeudet ja asema voi muuttua

- **Mikä on kehitysmaiden osuus endeemisenä virusgeneraattorina?**

-pandemia on viides isku kehittyvien maiden kansanterveydelle, joilla ei ole varaa eikä kansalaisilla halua rokotteisiin (aliravitsemuksen ja puutteen aiheuttama sairauskuorma, onnettomuudet, ylipainon aiheuttamat sairaudet, muut tarttuvat taudit, nyt myös pandemia!)