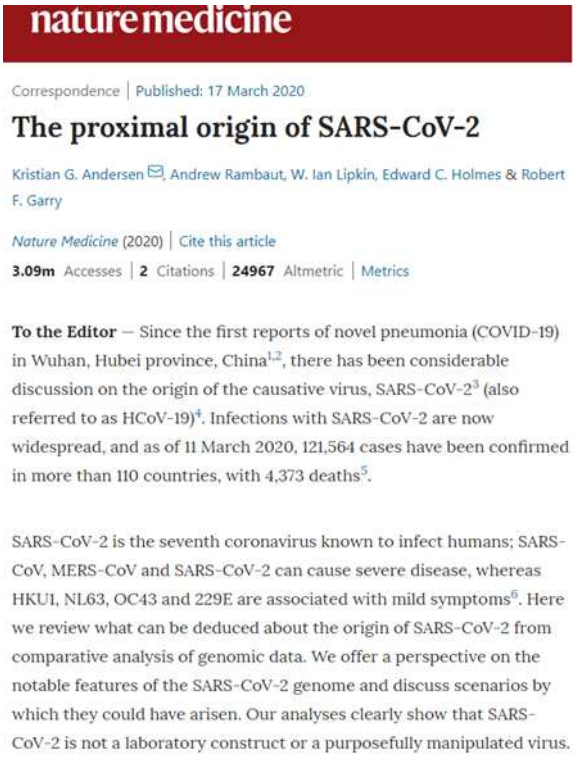
COVID 19. SOBRE VIRUS, ASESINOS Y ESTRATEGIAS

Máximo Sandín

Parece una obviedad afirmar que la crisis mundial que se ha desatado como consecuencia de la pandemia producida por el covid 19 no tiene precedentes en la historia. Lo que no es tan evidente es porqué si esta pandemia se produce como se afirma desde el ámbito científico, es decir, por el "salto" espontáneo del virus de algún animal al hombre, no se han producido continuamente epidemias de origen viral a lo lago de la historia.

En cualquier caso, esta situación ha originado un consenso social sobre las causas y consecuencias de la "aparición del coronavirus" generado por una abrumadora y permanente avalancha de información por parte de todos los medios de comunicación. Los expertos, que aportan la voz de la Ciencia, nos hablan de un "virus asesino" pero que utiliza una perversa "estrategia": no matar a todos los que infecta para poder seguir reproduciéndose.

Sin embargo, la atribución de cualidades, incluso de intenciones a un ente biológico que en estado libre es inerte, a una molécula de ADN o (en este caso) de ARN empaquetado con una densidad casi cristalina en una cápsida proteica envuelta en una capa de lípidos, un ente que no se puede considerar un ser vivo, produce una cierta desconfianza en estas interpretaciones científicas por muy prestigiosos que sean sus emisores. Pero lo que lleva la desconfianza al límite de la sospecha es cuando la prestigiosa revista científica Nature (*Nature Medicine* 17 de marzo) publica un artículo en elque concluye que el virus covid 19 "no es un virus obtenido en un laboratorio o manipulado a propósito", un estupor que puede equivaler al producido porque en una revista de astrofísica se publicase un artículo destinado a demostrar que la Tierra no es plana.



nature medicine

Correspondence | Published: 17 March 2020

The proximal origin of SARS-CoV-2

Kristian G. Andersen ✉, Andrew Rambaut, W. Ian Lipkin, Edward C. Holmes & Robert F. Garry

Nature Medicine (2020) | Cite this article

To the Editor — Since the first reports of novel pneumonia (COVID-19) in Wuhan, Hubei province, China[1,2], there has been considerable discussion on the origin of the causative virus, SARS-CoV-2[3] (also referred to as HCoV-19)[4]. Infections with SARS-CoV-2 are now widespread, and as of 11 March 2020, 121,564 cases have been confirmed in more than 110 countries, with 4,373 deaths[5].

SARS-CoV-2 is the seventh coronavirus known to infect humans; SARS-CoV, MERS-CoV and SARS-CoV-2 can cause severe disease, whereas HKU1, NL63, OC43 and 229E are associated with mild symptoms[6]. Here we review what can be deduced about the origin of SARS-CoV-2 from comparative analysis of genomic data. We offer a perspective on the notable features of the SARS-CoV-2 genome and discuss scenarios by which they could have arisen. Our analyses clearly show that SARS-CoV-2 is not a laboratory construct or a purposefully manipulated virus.

La pregunta que surge es ¿por qué una revista tan prestigiosa se dedica a contradecir un supuesto infundio que ni siquiera debería de ser tenido en cuenta científicamente por proceder del campo de lo que se suele calificar de “conspiranoico”?

Aunque en la situación actual pueda no parecer oportuno poner en duda las informaciones oficiales, dado que la prioridad es acabar con la pandemia, nunca está de más (puede ser fundamental) entender por qué se ha producido, por lo que propongo al lector que me acompañe para intentar disipar estas inquietudes recurriendo a datos científicos, es decir, no interpretaciones, que nos permitan hacernos una idea de qué está pasando.

Las informaciones que llegan al gran público se basan, fundamentalmente, en explicaciones y opiniones de expertos que, se supone, hay que creerse en base al principio de autoridad. En nuestro caso, pretendo que sea el lector el que obtenga sus propias conclusiones de los datos que voy a exponer. Para facilitar este trabajo no voy a utilizar referencias bibliográficas que obligan a verificar las afirmaciones buscando los artículos citados, sino, directamente, copiando las portadas de dichos artículos.

Veamos pues:

NATIONAL AERONAUTICS AND SPACE ADMINISTRATION

ASTROBIOLOGY
LIFE IN THE UNIVERSE

A Changing View of Viruses in the Evolution and Ecology of Life

Presenter: Mark Young (Montana State University)

October 26, 2009 11:00 AM Pacific
Viruses are the most abundant life-like entities on the planet. Studies over the past twenty years by environmental virologists have significantly changed our view of the role of viruses in the biosphere. It is becoming increasingly likely that viruses or virus-like entities are major players in earth's early life and in the present day ecology and evolution of life.

We are interested in the isolation and molecular characterization of archaeal viruses from high temperature environments. High temperature (>80C) acidic environments (pH<3.0) have proven to be a rich source of viruses replicating in crenarchaeal hosts (viruses replicating in host from the domain Archaea). We have isolated and characterized a number of these unusual viruses. Using both culture-dependent and culture-independent approaches, a broad diversity of virus particle morphologies and genome compositions have been detected. Like most crenarchaeal viruses isolated to date, the viral open reading frames (ORFs) have little to no similarity to proteins in the public databases. However, despite this lack of homology, these viruses have particle structures reminiscent of viruses of Eukarya and Bacteria, suggesting an evolutionary relationship between viruses from all domains of life.

Se ha calculado que el número de bacterias en la Tierra es aproximadamente un *nonillón* (es decir, un uno seguido de treinta ceros). Pues bien, se estima que el número de virus es entre cinco y veinticinco veces el número de bacterias. Como verán, los virus o entidades como virus" han jugado un papel importante en la evolución de la vida. Pero ésta es una larga historia. Vamos a limitarnos en este caso a su función ecológica:

Nature. 1999 Jun 10;399(6736):541-8.

nature

Marine viruses and their biogeochemical and ecological effects.

- Fuhrman JA.

Department of Biological Sciences, Wrigley Institute for Environmental Studies, University of Southern California, Los Angeles 90089-0371, USA. fuhrman@usc.edu

Viruses are the most common biological agents in the sea, typically numbering ten billion per litre. They probably infect all organisms, can undergo rapid decay and replenishment, and influence many biogeochemical and ecological processes, including nutrient cycling, system respiration, particle size-distributions and sinking rates, bacterial and algal biodiversity and species distributions, algal bloom control, dimethyl sulphide formation and genetic transfer. Newly developed fluorescence and molecular techniques leave the field poised to make significant advances towards evaluating and quantifying such effects

En aguas marinas superficiales se han contado hasta 10.000 millones de virus por litro. Su función es el control de la base de la red trófica marina. Como los virus son inertes y se mueven pasivamente, cuando las colonias de bacterias y algas crecen desmesuradamente, pudiendo llegar a impedir el paso de los rayos del sol a los fondos

marinos, los virus las destruyen hasta que su densidad hace posible el paso de los rayos de sol. Por cierto, los productos sulfurosos derivados de este proceso contribuyen a la nucleación de las nubes.

Veamos en los suelos (disculpen el tamaño de las letras):

APPLIED AND ENVIRONMENTAL MICROBIOLOGY, Nov. 2003, p. 6628–6633 Vol. 69, No. 11
0099-2240/03/$08.00+0 DOI: 10.1128/AEM.69.11.6628–6633.2003

Sampling Natural Viral Communities from Soil for Culture-Independent Analyses

Kurt E. Williamson,[1] K. Eric Wommack,[1]* and Mark Radosevich[2]

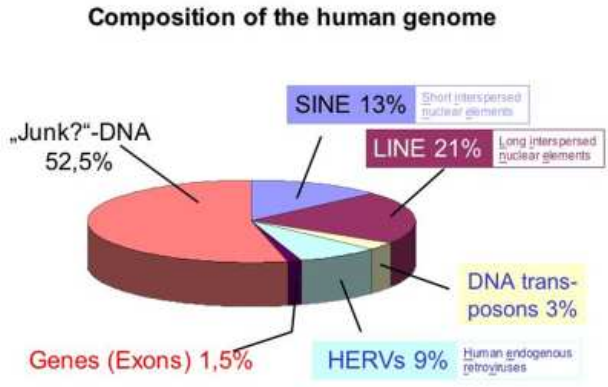
Department of Plant and Soil Sciences, University of Delaware, Newark, Delaware 19716,[1] and Department of Biosystems Engineering and Environmental Science, University of Tennessee, Knoxville, Tennessee 37996[2]

Received 3 April 2003/Accepted 12 August 2003

An essential first step in investigations of viruses in soil is the evaluation of viral recovery methods suitable for subsequent culture-independent analyses. In this study, four elution buffers (10% beef extract, 250 mM glycine buffer, 10 mM sodium pyrophosphate, and 1% potassium citrate) and three enumeration techniques (plaque assay, epifluorescence microscopy [EFM], and transmission electron microscopy [TEM]) were compared to determine the best method of extracting autochthonous bacteriophages from two Delaware agricultural soils. Beef extract and glycine buffer were the most effective in eluting viable phages inoculated into soils (up to 29% recovery); however, extraction efficiency varied significantly with phage strain. Potassium citrate eluted the highest numbers of virus-like particles from both soils based on enumerations by EFM (mean, 5.3 × 10^8 g of dry $soil^{-1}$), but specific soil-eluant combinations posed significant problems to enumeration by EFM. Observations of virus-like particles under TEM gave confidence that the particles were, in fact, phages, but TEM enumerations yielded measurements of phage abundance (mean, 1.5×10^8 g of dry $soil^{-1}$) that were about five times lower. Clearly, the measurement of phage abundance in soils varies with both the extraction and enumeration methodology; thus, it is important to assess multiple extraction and enumeration approaches prior to undertaking ecological studies of phages in a particular soil.

En los suelos su número es variable, en todo cado astronómico, En este estudio han arrojado cifras medias de 5,3-10e8 y también están implicados en el control de las comunidades bacterianas.

En cuanto a su presencia en los organismos, se considera que un 10% del genoma humano está compuesto por retrovirus endógenos, es decir, virus que a lo largo de la evolución han ido insertando sus secuencias génicas en nuestro genoma. Pero si tenemos en cuenta las secuencias derivadas de virus (elementos móviles como trasposones y retrotrasposones , elementos repetidos cortos y largos, intrones…) nos encontramos con que la inmensa mayor parte de nuestros genomas están constituidos por virus y sus derivados que controlan la expresión de los genes codificantes de proteínas.



Pero, es más, lo que se consideraba el genoma, es decir los genes codificantes de proteínas, que constituyen el 1,5% de la totalidad del genoma está constituido por virus y sus derivados:

Proc Natl Acad Sci U S A. 2004 Nov 30; 101(48): 16825–16830. PMCID: PMC534736
Published online 2004 Nov 16. doi: 10.1073/pnas.0406985101 PMID: 15546984
Evolution

Coding sequences of functioning human genes derived entirely from mobile element sequences

Roy J. Britten*

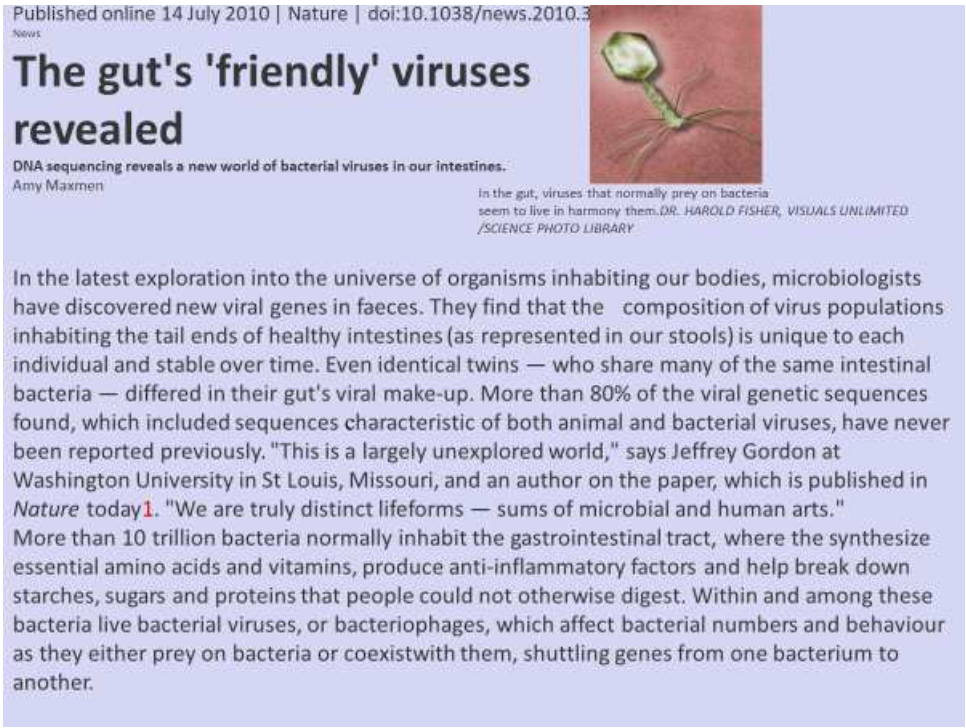
ABSTRACT Go to:

Among all of the many examples of mobile elements or "parasitic sequences" that affect the function of the human genome, this paper describes several examples of functioning genes whose sequences have been almost completely derived from mobile elements. There are many examples where the synthetic coding sequences of observed mRNA sequences are made up of mobile element sequences, to an extent of 80% or more of the length of the coding sequences. In the examples described here, the genes have named functions, and some of these functions have been studied. It appears that each of the functioning genes was originally formed from mobile elements and that in some process of molecular evolution a coding sequence was derived that could be translated into a protein that is of some importance to human biology. In one case (AD7C), the coding sequence is 99% made up of a cluster of *Alu* sequences. In another example, the gene BNIP3 coding sequence is 97% made up of sequences from an apparent human endogenous retrovirus. The Syncytin gene coding sequence appears to be made from an endogenous retrovirus envelope gene.

A modo de curiosidad, por si le resulta interesante a alguien, señalaré que en éste artículo el candoroso autor no se explica por qué las secuencias del genoma derivadas de virus son eliminadas "por alguien" de las bases de datos públicas:

Other Transcript Coding Sequences Apparently Derived from ME.

Table 4 is a list of 49 examples of observed transcripts for which the coding sequences have been determined by computer programs, and these cds are made up from MEs at least to the extent of 80%. This collection was made by running REPEATMASKER against the NCBI collection of gene transcripts in February of 2004, but when checks were made in early March, all of the transcripts so marked had been removed from the collection. It seems likely that someone decided they were junk, which in a sense may be true, but from the point of view of this article they may be considered potentially useful and should be further examined.



Published online 14 July 2010 | Nature | doi:10.1038/news.2010.3

News

The gut's 'friendly' viruses revealed

DNA sequencing reveals a new world of bacterial viruses in our intestines.

Amy Maxmen

In the gut, viruses that normally prey on bacteria seem to live in harmony them.*DR. HAROLD FISHER, VISUALS UNLIMITED /SCIENCE PHOTO LIBRARY*

In the latest exploration into the universe of organisms inhabiting our bodies, microbiologists have discovered new viral genes in faeces. They find that the composition of virus populations inhabiting the tail ends of healthy intestines (as represented in our stools) is unique to each individual and stable over time. Even identical twins — who share many of the same intestinal bacteria — differed in their gut's viral make-up. More than 80% of the viral genetic sequences found, which included sequences characteristic of both animal and bacterial viruses, have never been reported previously. "This is a largely unexplored world," says Jeffrey Gordon at Washington University in St Louis, Missouri, and an author on the paper, which is published in *Nature* today1. "We are truly distinct lifeforms — sums of microbial and human arts."

More than 10 trillion bacteria normally inhabit the gastrointestinal tract, where the synthesize essential amino acids and vitamins, produce anti-inflammatory factors and help break down starches, sugars and proteins that people could not otherwise digest. Within and among these bacteria live bacterial viruses, or bacteriophages, which affect bacterial numbers and behaviour as they either prey on bacteria or coexistwith them, shuttling genes from one bacterium to another.

Pero nuestro organismo no sólo contiene virus en forma de secuencias insertadas en los cromosomas. El número de virus completos que realizan funciones esenciales para nuestro organismo es de tal dimensión que sorprende a los propios investigadores. Miles de millones (más bien billones) de virus bacterianos coexisten con los billones de bacterias de nuestro tracto intestinal que son esenciales para nuestra vida. Los bacteriófagos o *fagos* regulan las poblaciones de bacterias e intercambian información

genética entre ellas. Es decir, los virus controlan las bacterias que controlan nuestro organismo.

¿Algunos virus más? Veamos:

Bacteriophage adhering to mucus provide a non–host-derived immunity

Jeremy J. Barr[a,1], Rita Auro[a], Mike Furlan[a], Katrine L. Whiteson[a], Marcella L. Erb[b], Joe Pogliano[b], Aleksandr Stotland[a], Roland Wolkowicz[a], Andrew S. Cutting[a], Kelly S. Doran[a], Peter Salamon[c], Merry Youle[d], and Forest Rohwer[a]

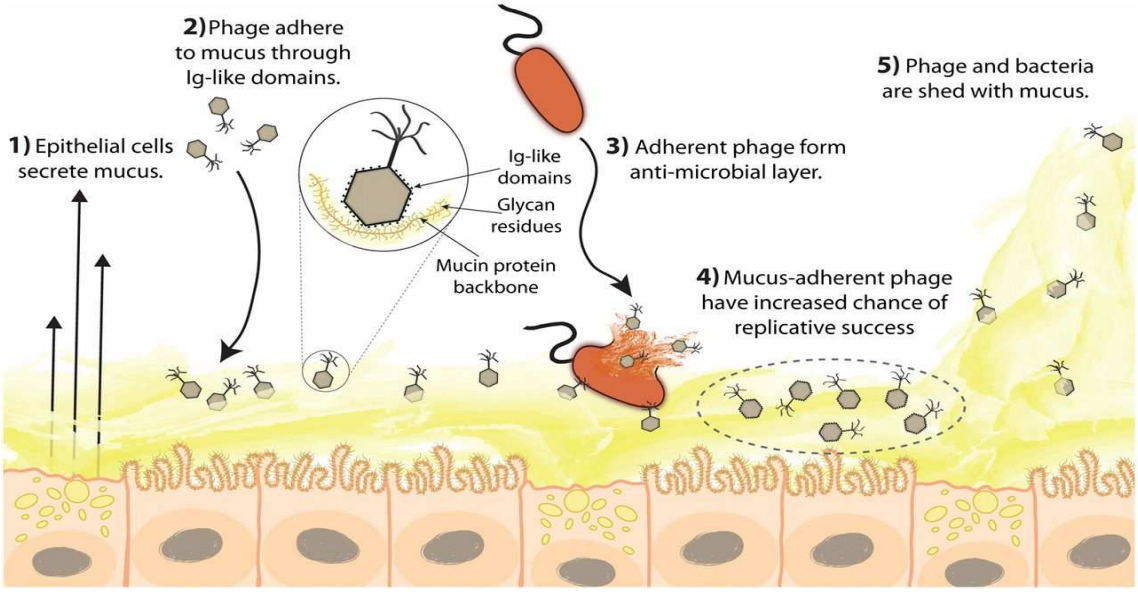
[a]Department of Biology, San Diego State University, San Diego, CA 92182; [b]Division of Biological Sciences, University of California, San Diego, CA 92093; [c]Department of Mathematics and Statistics, San Diego State University, San Diego, CA 92182; and [d]Rainbow Rock, Ocean View, HI 96737

Edited by Richard E. Lenski, Michigan State University, East Lansing, MI, and approved April 18, 2013 (received for review March 28, 2013)

Mucosal surfaces are a main entry point for pathogens and the principal sites of defense against infection. Both bacteria and phage are associated with this mucus. Here we show that phage-to-bacteria ratios were increased, relative to the adjacent environment, on all mucosal surfaces sampled, ranging from cnidarians to humans. In vitro studies of tissue culture cells with and without surface mucus demonstrated that this increase in phage abundance is mucus dependent and protects the underlying epithelium from bacterial infection. Enrichment of phage in mucus occurs via binding interactions between mucin glycoproteins and Ig-like protein domains exposed on phage capsids. In particular, phage Ig-like domains bind variable glycan residues that coat the mucin glycoprotein component of mucus. Metagenomic analysis found these Ig-like proteins present in the phages sampled from many

epithelium may respond by increased production of antimicrobial agents, hypersecretion of mucin, or alteration of mucin glycosylation patterns to subvert microbial attachment (29–31).

Also present in the mucus environment are bacteriophage (phage), the most common and diverse biological entities. As specific bacterial predators, they increase microbial diversity through Red Queen/kill-the-winner dynamics (32, 33). Many phages establish conditional symbiotic relationships with their bacterial hosts through lysogeny. As integrated prophages, they often express genes that increase host fitness or virulence (34–36) and protect their host from lysis by related phages. As free phage, they aid their host strain by killing related competing strains (37–39). Phages participate, along with their bacterial hosts, in tripartite symbioses with metazoans that affect meta-



Una enorme cantidad de bacteriófagos adheridos a las mucosas del organismo impiden que penetren bacterias externas, que no deberían estar ahí, es decir también protegen nuestro organismo.

Si se me permite una opinión, da la sensación de que algo se ha estado haciendo mal con los virus. Con la condición de los virus cuando se descubrieron asociados a enfermedades. Pero, veamos algunas de esas asociaciones:

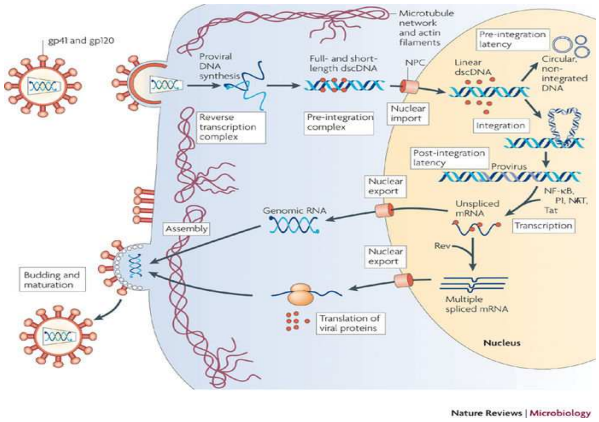
J. Virol., 10 1995, 6408-6416, Vol 69, No. 10

Retrovirus-like particles released from the human breast cancer cell line T47-D display type B- and C-related endogenous retroviral sequences

W Seifarth, H Skladny, F Krieg-Schneider, A Reichert, R Hehlmann and C Leib-Mosch
III Medizinische Klinik, Klinikum Mannheim, Universitat Heidelberg, Mannheim, Germany.

The human mammary carcinoma cell line T47-D releases retrovirus-like particles of type B morphology in a steroid-dependent manner (I. Keydar, T. Ohno, R. Nayak, R. Sweet, F. Simoni, F. Weiss, S. Karby, R. Mesa-Tejada, and S. Spiegelman, Proc. Natl. Acad. Sci. USA 81:4188-4192, 1984). Furthermore, reverse transcriptase (RT) activity is found to be associated with particle preparations. Using a set of degenerate primers derived from a conserved region of retroviral pol genes, we repeatedly amplified three different retroviral sequences (MLN, FRD, and FTD) from purified T47-D particles in several RT-PCR experiments. Screening of a human genomic library and Southern blot analysis revealed that these sequences are of endogenous origin.

Según este artículo, el cáncer de mama emite partículas retrovirales. Se sabe que los virus endógenos pueden saltar del genoma ante algún tipo de agresión ambiental. Es por eso, por lo que, en muchas ocasiones, se ha señalado a virus como agente causal de distintas enfermedades cuando en realidad son consecuencia. Y es por eso, por lo que en tejidos enfermos se observa la presencia de partículas virales



Y así, se ha sugerido un origen viral a enfermedades como artritis o esquizofrenia, a pesar de que nunca ha sido reportada una epidemia de estas enfermedades.

VIRUS-LIKE PARTICLES IN SYNOVIAL FLUIDS FROM PATIENTS WITH RHEUMATOID ARTHRITIS

G. STRANSKY, J. VERNON, W. K. AICHER, L. W. MORELAND, R. E. GAY, S. GAY

Rheumatology, Volume 32, Issue 12, December 1993, Pages 1044–1048,
https://doi.org/10.1093/rheumatology/32.12.1044
Published: 01 December 1993 **Article history ▾**

Abstract

Based on the elevated expression of oncogenes in proliferating transformed-appearing synoviocytes we searched for the possible involvement of a viral agent in the pathogenesis of RA. We report the detection of virus-like particles with retro viral C type morphology in SF, which lack the typical morphologic as well as immunohistochemical features of the human T-lymphotropic and immunodeficiency viruses.

Schizophr Res. 2010 May;118(1-3):224-31. Epub 2010 Feb 13.

Neuroanatomic and cognitive abnormalities related to herpes simplex virus type 1 in schizophrenia.

Schretlen DJ, Vannorsdall TD, Winnick JM, Mushtaq Y, Hikida T, Sawa A, Yolken RH, Dickerson FB, Cascella NG.
Department of Psychiatry and Behavioral Sciences, Johns Hopkins University School of Medicine, Baltimore, Maryland, United States. dschret@jhmi.edu

Abstract

Herpes simplex virus 1 (HSV-1) tends to replicate in the temporal cortex and can damage the limbic system. The presence of serum antibodies to HSV-1 is associated with cognitive impairment in adults with schizophrenia, suggesting that cerebral gray matter abnormalities might distinguish patient subgroups defined by HSV-1 exposure. We assessed 43 adult outpatients with schizophrenia. The assessment included clinical interviews, neurocognitive testing, anatomic brain magnetic resonance imaging and measures of serum IgG antibodies specific to herpes simplex viruses 1 and 2. We then compared 25 patients who tested positive for antibodies to HSV-1 with 15 who were seronegative for both HSV-1 and HSV-2. The seropositive patients performed significantly worse than the seronegative patients on four neuropsychological measures of psychomotor speed, executive functioning, and explicit verbal memory.

Desde hace tiempo se sabe que los virus endógenos se expresan como parte constituyente de los genomas, es decir, son el genoma. Este hecho es de una gran trascendencia para el tema que nos ocupa. Retrovirus endógenos o partes de ellos se expresan en procesos tan importantes como producción de enzimas fundamentales o la formación de la placenta durante el embarazo.

PNAS **October 28, 2003** vol. 100 no. 22 **12841-12846**

An endogenous retroviral long terminal repeat is the dominant promoter for human β1,3-galactosyltransferase 5 in the colon

Catherine A. Dunn*,†, Patrik Medstrand‡, and Dixie L. Mager*,†,§

Abstract

LTRs of endogenous retroviruses are known to affect expression of several human genes, typically as a relatively minor alternative promoter. Here, we report that an endogenous retrovirus LTR acts as one of at least two alternative promoters for the human β1,3-galactosyltransferase 5 gene, involved in type 1 Lewis antigen synthesis, and show that the LTR promoter is most active in the gastrointestinal tract and mammary gland. Indeed, the LTR is the dominant promoter in the colon, indicating that this ancient retroviral element has a major impact on gene expression.

PNAS | **September 26, 2006** | vol. 103 | no. 39 | **14390-14395**

BIOLOGICAL SCIENCES / DEVELOPMENTAL BIOLOGY

Endogenous retroviruses regulate periimplantation placental growth and differentiation.

Kathrin A. Dunlap*, Massimo Palmarini, Mariana Varela, Robert C. Burghardt, Kanako Hayashi*, Jennifer L. Farmer*, and Thomas E. Spencer*, *Center for Animal Biotechnology and Genomics, Department of Animal Science, and Image Analysis Laboratory, Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, TX 77843; and Institute of Comparative Medicine, University of Glasgow Veterinary School, Glasgow G61 1QH, United Kingdom

Edited by George E. Seidel, Jr., Colorado State University, Fort Collins, CO, and approved August 8, 2006 (received for review May 10, 2006)

Endogenous retroviruses (ERVs) are fixed and abundant in the genomes of vertebrates. Circumstantial evidence suggests that ERVs play a role in mammalian reproduction, particularly placental morphogenesis, because intact ERV envelope genes were found to be expressed in the syncytiotrophoblasts of human and mouse placenta and to elicit fusion of cells *in vitro*.

Estos hallazgos nos hablan del papel fundamental que los virus juegan en los procesos de la vida, pero ¿cuál es la relación de estos fenómenos con el tema que nos ocupa? Veremos que es una relación de enorme importancia, por lo que les ruego presten la mayor atención a los dos artículos que siguen:

Virology
Volume 297, Issue 2,
5 June 2002, Pages 220-225

Developmental Expression of HERV-R (ERV3) and HERV-K in Human Tissue

Ann-Catrin Andersson[a, 1], Patrick J. W. Venables[b], Ralf R. Tönjes[c], Jürgen Scherer[c], Lars Eriksson[a] and Erik Larsson[a]

Abstract

The human endogenous retroviruses (HERVs), ERV3 (HERV-R) and HERV-K, are both known to be transcriptionally active in human placenta. In the case of ERV3 there is also indirect evidence for its participation in cellular differentiation. In this study we examined the expression of ERV3 (HERV-R) and HERV-K in human normal fetal tissues by *in situ* hybridization. The highest level of ERV3 *env* expression was detected in primitive adrenal cortex. Elevated levels of expression were also found in the following developing tissues: kidneys (tubules), tongue, heart, liver, and central nervous system. Tissue-specific expression was found for HERV-K *rec* (former *cORF*) but not for *pol/int* transcripts. The highest *rec* expression was found in placenta and levels slightly higher than sense control were found in the rest of the tissues examined. *Pol/Int* was not possible to quantitate. It appears that ERV3 is expressed in an organ-specific way during embryogenesis and might suggest a possible role in the development and differentiation of human tissues.

En los tejidos embrionarios se expresan (participan en el desarrollo) una multitud de retrovirus endógenos. Como se puede ver, se expresan en placenta, cortex adrenal, riñones, lengua, corazón, hígado, y sistema nervioso central así como en el resto de los tejidos. Pero veamos en tejidos adultos:

J Virol. 2005 January; 79(1): 341–352.

Comprehensive Analysis of Human Endogenous Retrovirus Transcriptional Activity in Human Tissues with a Retrovirus-Specific Microarray

Wolfgang Seifarth,1*† Oliver Frank,1† Udo Zeilfelder,1 Birgit Spiess,1 Alex D. Greenwood,2,3 Rüdiger Hehlmann,1 and Christine Leib-Mösch1,2

ABSTRACT

In the present study, we have investigated the transcriptional activity of representative members of 20 HERV families in 19 different normal human tissues. Qualitative evaluation of chip hybridization signals and quantitative analysis by real-time RT-PCR revealed distinct HERV activity in the human tissues under investigation, suggesting that HERV elements are active in human cells in a tissue-specific manner. Most active members of HERV families were found in mRNA prepared from skin, thyroid gland, placenta, and tissues of reproductive organs. In contrast, only few active HERVs were detectable in muscle cells. Human tissues that lack HERV transcription could not be found, confirming that human endogenous retroviruses are permanent components of the human transcriptome. Distinct activity patterns may reflect the characteristics of the regulatory machinery in these cells, e.g., cell type-dependent occurrence of transcriptional regulatory factors.

En individuos adultos normales los retrovirus endógenos se expresan en todos los tejidos **confirmando que son componentes permanentes del transcriptoma humano.**

Y ahora, vamos a ver cómo se han fabricado ciertas vacunas:

En la web de la INTERNATIONAL FEDERATION OF PHARMACEUTICAL AND MANUFATURERS & ASSOCIATIONS http://www.ifpma.org/influenza/index.aspx?47exponían muy ufanos la siguiente información:

No la busquen, porque ha desaparecido de la web. Y por buenas razones, porque cultivar virus humanos en embriones de otros animales en los que se expresan multitud de virus endógenos, conduce a que se produzcan hibridaciones con sus virus correspondientes con lo que se producen virus infectivos de características diferentes a las originales.

Desde hace tiempo se nos informaba de que la gripe estacional provenía “de las aves” y que cada año “mutaba”, muy posiblemente con la elaboración de cada nueva vacuna. Con cada nueva hibridación.

Por ejemplo, en esta vacuna contra la fiebre amarilla:

J Virol. 2003 January; 77(2): 1105–1111.

Identification and Characterization of Avian Retroviruses in Chicken Embryo-Derived Yellow Fever Vaccines: Investigation of Transmission to Vaccine Recipients

Althaf I. Hussain,1 Jeffrey A. Johnson,1 Marcos da Silva Freire,2 and Walid Heneine1*

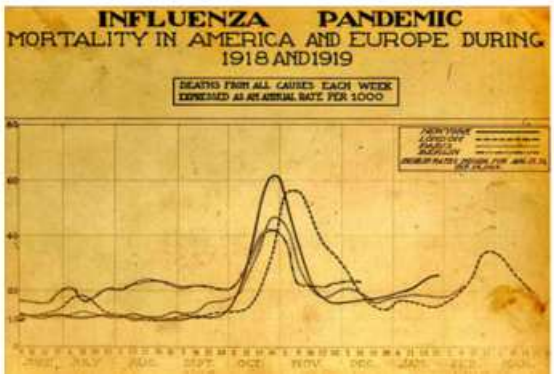
All currently licensed yellow fever (YF) vaccines are propagated in chicken embryos. Recent studies of chick cell-derived measles and mumps vaccines show evidence of two types of retrovirus particles, the endogenous avian retrovirus (EAV) and the endogenous avian leukosis virus (ALV-E), which originate from the chicken embryonic fibroblast substrates. In this study, we investigated substrate-derived avian retrovirus contamination in YF vaccines currently produced by three manufacturers (YF-vax [Connaught Laboratories], Stamaril [Aventis], and YF-FIOCRUZ [FIOCRUZ-Bio-Manguinhos]). Testing for reverse transcriptase (RT) activity was not possible because of assay inhibition. However, Western blot analysis of virus pellets with anti-ALV RT antiserum detected three distinct RT proteins in all vaccines, indicating that more than one source is responsible for the RTs present in the vaccines.

Estas terribles consecuencias de unas prácticas peligrosas se pueden considerar fruto del desconocimiento de unos descubrimientos relativamente recientes. Por tanto, no intencionadas. Permítanme exponerles algunas prácticas llevadas a cabo con perfecto conocimiento de lo que se estaba haciendo y que dejo a su interpretación:

Tal vez el lector se pregunte ¿qué sentido tiene resucitar un virus que causó cerca de cincuenta millones de muertos? Un virus que no “surgió” en España, a pesar de que con intención de ocultar la mortalidad que causó en los soldados al final de la primera guerra mundial, se denominó “gripe española” porque en nuestro país sí se declaró el estado de epidemia.

Pero su origen fue, al parecer, en los soldados norteamericanos. Hace tiempo me encontré con esta información que, a pesar de no provenir de canales “oficiales” resulta congruente con lo que hemos visto anteriormente;

THE 1918 INFLUENZA EPIDEMIC WAS A VACCINE-CAUSED DISEASE
http://www.drcarley.com/
E. McBean (Vaccination The Silent Killer p28)
Very few people realize that the worst epidemic ever to hit America, the Spanish Influenza of 1918 was the after effect of the massive nation-wide vaccine campaign.
If we check back in history to that 1918 flu period, we will see that it suddenly struck just after the end of World War I when our soldiers were returning home from overseas. That was the first war in which all the known vaccines were forced on all the servicemen.



Si este es el caso, se trataría del resultado del desconocimiento de los virus existentes enlos sustratos y de los métodos utilizados para elaborar vacunas, que en el caso de las iniciales eran muy rudimentarios y peligrosos.

Pero en los siguientes casos, es evidente que no se trata de desconocimiento. La excusa de que se trata de determinar su virulencia resulta poco creíble. Los dos anteriores conatos de pandemia que no llegaron a serlo fueron los producidos por la "gripe aviar" o H5N1 que resultó de alta mortalidad pero de difícil transmisión y a continuación la "gripe porcina" H1N1 que resultó de fácil transmisión pero poco virulenta. Las letras H y N se refieren a la hematoglutinina, una proteína componente del sistema de coagulación de la sangre y a la neuramidasa, una enzima que controla la formación y mantenimiento de la vaina de mielina de las neuronas, que forman la cápsida del virus de la gripe.

Y, hablando de cápsidas de virus, en *Nature*, en Noviembre de 2015, Declan Butler escribía un artículo con el título: *"El virus de murciélago diseñado suscita debate sobre investigaciones arriesgadas"*. En Marzo de 2020, dicho autor añadió a la portada de su artículo, se supone que "espontáneamente", un comentario en que se desmentía concluyendo que "los científicos creen que un animal es la fuente más probable del coronavirus". Sin embargo, en dicho artículo había informaciones muy interesantes que vamos a enunciar: ***"Los investigadores crearon un virus quimérico hecho con una proteína de superficie SHC014 y el núcleo de un virus SARS que ha sido adaptado para crecer en ratón e imitar la enfermedad humana. La quimera infectó células respiratorias, probando que la proteína de superficie SHC014 es la estructura necesaria para unirse a un receptor llave en las células e infectarlas".*** Es decir, la elaboración de virus "híbridos" de animal y humano resulta muy laboriosa (recordemos que, según nos informan, el COVID 19 tiene secuencias de murciélago y pangolín), porque hay que modificar en el virus animal la proteína de la envuelta del virus para que éste se una a un receptor

específico que tienen las células, en este caso, humanas, que en cada especie es distinta para cada virus diferente.

***NATURE* | NEWS**

Engineered bat virus stirs debate over risky research

Lab-made coronavirus related to SARS can infect human cells.

- Declan Butler

12 November 2015

Article tools

An experiment that created a hybrid version of a bat coronavirus — one related to the virus that causes SARS (severe acute respiratory syndrome) — has triggered renewed debate over whether engineering lab variants of viruses with possible pandemic potential is worth the risks.

In an article published in *Nature Medicine*[1] on 9 November, scientists investigated a virus called SHC014, which is found in horseshoe bats in China. The researchers created a chimaeric virus, made up of a surface protein of SHC014 and the backbone of a SARS virus that had been adapted to grow in mice and to mimic human disease. The chimaera infected human airway cells — proving that the surface protein of SHC014 has the necessary structure to bind to a key receptor on the cells and to infect them. It also caused disease in mice, but did not kill them.

Este tipo de "experimento científico", si se le puede llamar así, se ha producido en otras ocasiones. Por ejemplo, en la revista *Science* del 2 de Diciembre de 2011, Martin Enserink firma un artículo con el siguiente título: "***Estudios controvertidos dan alas a un virus mortal de la gripe***". El autor explica que *"El virus es una cepa del H5N1 de la gripe aviar que ha sido alterado genéticamente y ahora es fácilmente transmitido entre hurones, los animales cuya respuesta a la gripe es más similar a la humana"*.

Science 2 December 2011:
Vol. 334 no. 6060 pp. 1192-1193
DOI: 10.1126/science.334.6060.1192

•NEWS & ANALYSIS
INFECTIOUS DISEASES

Controversial Studies Give a Deadly Flu Virus Wings
•Martin Enserink

ROTTERDAM, NETHERLANDS—Locked up in the bowels of a medical faculty building here and accessible to only a handful of scientists lies a humanmade flu virus that scientists say could change world history if it were ever set free.
The virus is an H5N1 avian influenza strain that has been genetically altered and is now easily transmissible between ferrets, the animals that most closely mimic the human response to flu. Flu researchers believe it's likely that the pathogen, if it emerged in nature or were released, would trigger an infl uenza pandemic, quite possibly with many millions of deaths.
In an office on the 17th floor, virologist Ron Fouchier of Erasmus Medical Center calmly concedes that his team has created what is "probably one of the most dangerous viruses you can make." But he says the research, which has been submitted for publication, promises major public health benefits. Knowing exactly what could turn H5N1 into a virus with pandemic potential is useful because scientists can look out for such changes in the wild and prepare countermeasures.

La pregunta que surge es: ¿Por qué, para qué se llevan a cabo estos experimentos? La absurda respuesta es invariable: "para estudiarlos por si surgen un día en la naturaleza". Pero ¿no hemos visto lo complejo que es fabricarlos? ¿Cómo nos pueden decir que lo que ellos hacen puede pasar espontáneamente en la naturaleza?
Pero quizás, el "experimento" que nos puede resultar más clarificador es uno que figura en el artículo publicado en la revista *Nature* en Octubre de 2005. El título es: ***"Informe especial. El virus de la gripe de 1918 ha sido resucitado"***. Se consiguió el genoma completo del virus de la gripe de 1918, al parecer de un soldado enterrado y congelado en Alaska.

Nature **437**, 794-795 (6 October 2005) | doi:10.1038/437794a; Published online 5 October 2005

Special ReportThe 1918 flu virus is resurrected

Abstract

The recreation of one of the deadliest diseases known could help us to prevent another pandemic. Or it might trigger one, say critics. Andreas von Bubnoff investigates whether the benefits outweigh the risks.

It is thought to have killed 50 million people, and yet scientists have brought it back to life. In this issue of *Nature*, scientists publish an analysis of the full genome sequence of the 1918 human influenza virus. And in this week's *Science*, researchers describe how they used that sequence to recreate the virus and study its effects in mice.

Some scientists have already hailed the work as giving unprecedented insight into the virus. But others have raised concerns that the dangers of resurrecting the virus are just too great. One biosecurity expert told *Nature* that the risk that the recreated strain might escape is so high, it is almost a certainty. And the publication of the full genome sequence gives any rogue nation or bioterrorist group all the information they need to make their own version of the virus.

Jeffery Taubenberger of the Armed Forces Institute of Pathology in Rockville, Maryland, is the lead author of the sequencing study. He says the work was necessary and the risks were low. The paper on page 889 gives details of the final three genes; the sequences of the rest have already been published.

Una nueva pregunta: Si tenemos en cuenta que el virus de la gripe de 1918 provocó, según se calcula, 50 millones de muertos, ¿Para qué se "resucita"? ¿Para estudiarlo? Veamos:

Journal of Virology, May 2009, p. 4287-4296, Vol. 83, No. 9
0022-538X/09/$08.00+0 doi:10.1128/JVI.02399-08

Experimental Infection of Pigs with the Human 1918 Pandemic Influenza Virus

Hana M. Weingartl,[1,2*] Randy A. Albrecht,[3] Kelly M. Lager,[4] Shawn Babiuk,[1,5] Peter Marszal,[1] James Neufeld,[1] Carissa Embury-Hyatt,[1] Porntippa Lekcharoensuk,[4,10] Terrence M. Tumpey,[6] Adolfo García-Sastre,[3,7,8] and Jürgen A. Richt[4,9*]

National Centre for Foreign Animal Disease, Canadian Food Inspection Agency, Winnipeg, Manitoba, Canada,[1] Department of Medical Microbiology,[2] Department of Immunology, University of Manitoba, Winnipeg, Manitoba, Canada,[5] Department of Microbiology,[3] Department of Medicine, Division of Infectious Diseases,[7] Emerging Pathogens Institute, Mount Sinai School of Medicine New York, New York,[8] National Animal Disease Center, ARS-USDA, Ames, Iowa,[4] Centers for Disease Control and Prevention, Influenza Division, Atlanta, Georgia,[6] Kansas State University, College of Veterinary Medicine, Manhattan, Kansas,[9] Department of Microbiology and Immunology, Faculty of Veterinary Medicine, Kasetsart University, Bangkok, Thailand,[10]

Received 19 November 2008/ Accepted 6 February 2009

Swine influenza was first recognized as a disease entity during the 1918 "Spanish flu" pandemic. The aim of this work was to determine the virulence of a plasmid-derived human 1918 pandemic H1N1 influenza virus (reconstructed 1918, or 1918/rec, virus) in swine using a plasmid-derived A/swine/Iowa/15/1930 H1N1 virus (1930/rec virus), representing the first isolated influenza virus, as a reference. Four-week-old piglets were inoculated intratracheally with either the 1930/rec or the 1918/rec virus or intranasally with the 1918/rec virus.

La respuesta puede estar en otro artículo muy interesante publicado en Science en Junio de 2009 titulado *Características antigénicas y genéticas del virus de la gripe de origen porcino 2009 A(H1N1) circulando en humanos.* El resultado: *"Han mostrado ser antigénicamente altamente similar al recientemente reconstruido virus 1918 A(H1N1) y* ***posiblemente comparta un antecesor común".*** **(?)**

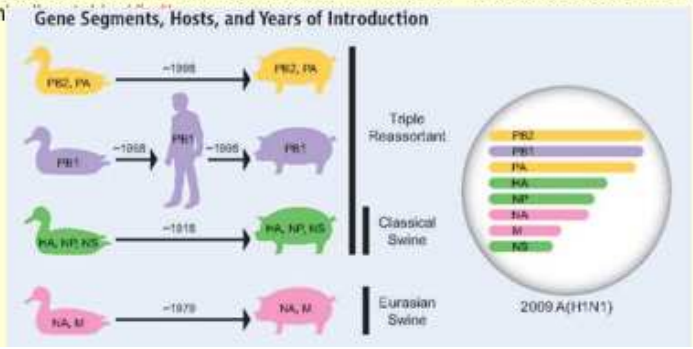
Science 10 July 2009:
Vol. 325. no. 5937, pp. 197 - 201
DOI: 10.1126/science.1176225

Antigenic and Genetic Characteristics of Swine-Origin 2009 A(H1N1) Influenza Viruses Circulating in Humans

Rebecca J. Garten,[1,*] C. Todd Davis,[1,*] Colin A. Russell,[2,3] Bo Shu,[1] Stephen Lindstrom,[1] Amanda Balish,[1] Wendy M. Sessions,[1] Xiyan Xu,[1] Eugene Skepner,[2] Varough Deyde,[1] Margaret Okomo-Adhiambo,[1] Larisa Gubareva,[1] John Barnes,[1] Catherine B. Smith,[1] Shannon L. Emery,[1] Michael J. Hillman,[1] Pierre Rivailler,[1] James Smagala,[1] Miranda de Graaf,[2,4] David F. Burke,[2] Ron A. M. Fouchier,[4] Claudia Pappas,[1] Celia M. Alpuche-Aranda,[5] Hugo López-Gatell,[5] Hiram Olivera,[5] Irma López,[5] Christopher A. Myers,[6] Dennis Faix,[6] Patrick J. Blair,[6] Cindy Yu,[7] Kimberly M. Keene,[8] P. David Dotson, Jr.,[8] David Boxrud,[10] Anthony R. Sambol,[11] Syed H. Abid,[12] Kirsten St. George,[13] Tammy Bannerman,[14] Amanda L. Moore,[15] David J. Stringer,[16] Patricia Blevins,[17] Gail J. Demmler-Harrison,[18] Michele Ginsberg,[19] Paula Kriner,[20] Steve Waterman,[21] Sandra Smole,[22] Hugo F. Guevara,[23] Edward A. Belongia,[24] Patricia A. Clark,[25] Sara T. Beatrice,[26] Ruben Donis,[1] Jacqueline Katz,[1] Lyn Finelli,[1] Carolyn B. Bridges,[1] Michael Shaw,[1] Daniel B. Jernigan,[1] Timothy M. Uyeki,[1] Derek J. Smith,[2,3,4]

Influenza pandemics occur when an influenza virus with a hemagglutinin (*HA*), against which there is little or no existing immunity, emerges in the human population and efficiently transmits from human to human. The genomes of the last three pandemic influenza viruses (1918 H1N1, 1957 H2N2, and 1968 H3N2) all originated in whole or in part from nonhuman reservoirs, and the *HA* genes of all of the pandemic viruses ultimately originated from avian influenza viruses.

A(H1N1) influenza viruses were first isolated from swine in 1930 (*1*). They have been shown to be antigenically highly similar to a recently reconstructed human 1918 A(H1N1) virus (*2*) and likely share a common ancestor (*3*, *4*). From 1930 to the late 1990s, these "classical swine influenza" viruses circulated in swine and remained relatively antigen



Resulta que las características del virus porcino (H1N1) "tienen una alta similaridad antigénica" con el virus humano 1918 reconstruido (H1N1). La explicación es que "posiblemente compartan un antecesor común" como si los virus anduvieran por el mundo casándose (o constituyendo parejas de hecho).

Las explicaciones sobre la "aparición" del covid 19 son del mismo nivel científico: "Probablemente pasó de un pangolín al hombre a través de un murciélago, pero no es seguro…" Espero que el lector tenga suficientes datos para deducir otra forma de "aparición" del coronavirus.

Bien: parece que hay suficientes informaciones para comprender cómo se produjo el covid 19. Sobre los autores y sus intenciones tendrán que investigar ustedes.

Villalbilla, Abril de 2020