

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 por qué 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 largo 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 el que 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.

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:

Marine viruses and their biogeochemical and ecological effects.

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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):

Sampling Natural Viral Communities from Soil for Culture-Independent Analyses

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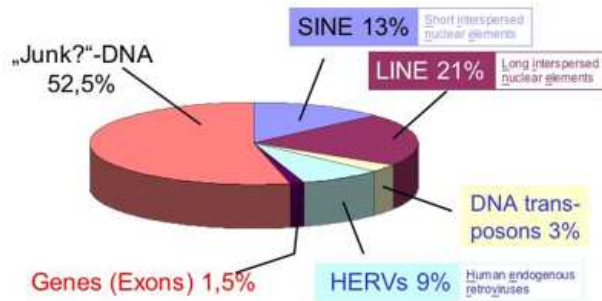
ABSTRACT

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, 5.3×10^4 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, 1.5×10^4 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 $5,3 \times 10^4$ por gramo de suelo seco. Estando también 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.

Composition of the human genome



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, ahora se sabe que también está constituido por virus y sus derivados:

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

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Contributed by Roy J. Britten, September 20, 2004

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 87% 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.

Mobile elements form the majority of the human genome, but that is unimportant compared to all of the functional effects these "parasites" have had on our evolution. Insertions have influenced the regulation of transcription of some genes and the termination of transcription. Hundreds of examples have been recognized where individual exons have sequences that are similar or identical to fragments of mobile element (ME) sequences (1, 2). In many of these cases a single exon is involved, and its transcription yields a variant mRNA (3). The suggestion is that MEs are a source of variation as a result of the insertion of fragments of sequence into functioning genes. Here, I am using MEs (*noni lenis*) to represent any repeated sequence present in many copies in the genome. Smit (4) has made a list of 19 examples of human genes "probably derived from transposable elements."

have been theoretical proposals (10) of the evolutionary role of variety and change in these relationships, particularly in the control of gene expression. There is direct evidence for the evolutionarily significant role of mobile elements/repeats (11–13) and evidence for strong associations and functions including the regulation of transcription. The cases described in this paper add to this earlier evidence in that, in these cases, nearly the entire coding sequences of genes have apparently been derived from ME sequences.

A survey is in process to determine the fraction of the coding sequences recognized at present in available genomes that are derived from ME sequences. The early results turned up the AD7C or neural thread protein gene, which sparked interest because it is apparently derived entirely from a cluster of *Alu* repeated sequences. The investigators pointed out that the coding sequence contained regions of sequence similarity to four *Alu* sequences (14). Table 1 describes this and several other cases.

Methods

A collection of coding sequences was made from the NCBI file seq_gene.md. These were examined by REPEATMASKER, and those that were reported to be almost completely similar in sequence to mobile elements were set aside for further study. The examples examined in the first part of this paper were selected from this list on the basis of their known function. Some of the remainder of them are shown in Table 4.

Results and Discussion

AD7C. AD7C is a neuronal thread protein gene. It encodes a 41-kDa membrane spanning phosphoprotein that is useful in the diagnosis of early Alzheimer's disease (14, 15). The coding sequence is 1,128 nt long and REPEATMASKER shows that it consists of fragments of five (or four, see below) *Alu* sequences. All of the matches are with the reverse complements of the *Alu*

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 they 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 coexist with 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

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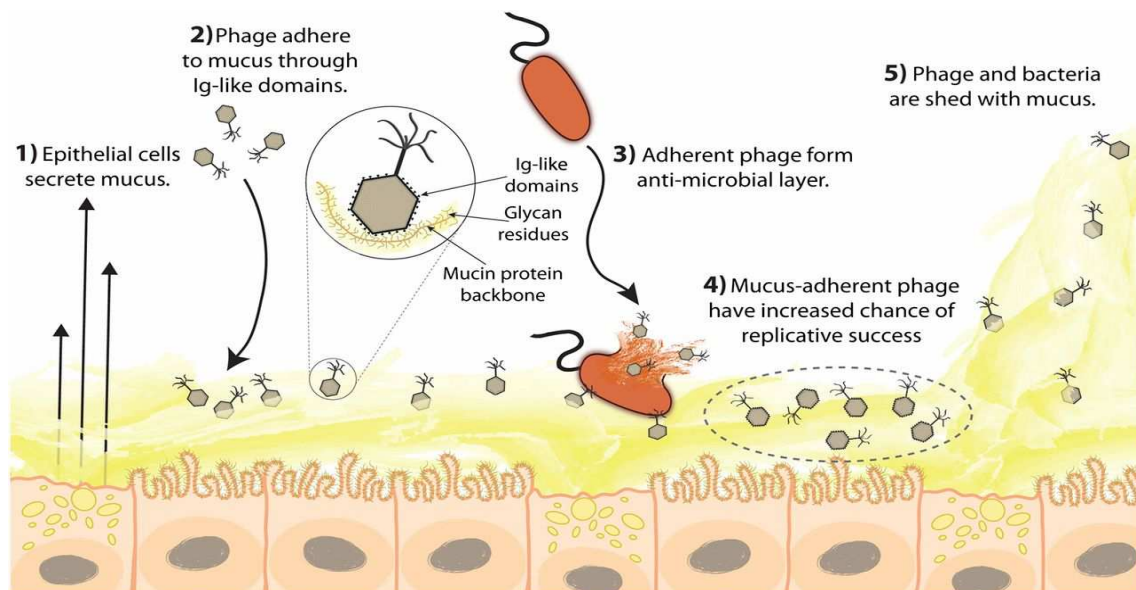
Edited by Richard E. Lenski, Michigan State University, East Lansing, MI, and approved April 18, 2013 (received for review March 28, 2013)

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-

BIOLOGY



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, seguramente, debido a que se descubrieron asociados a enfermedades. Pero, veamos algunas de esas asociaciones:

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

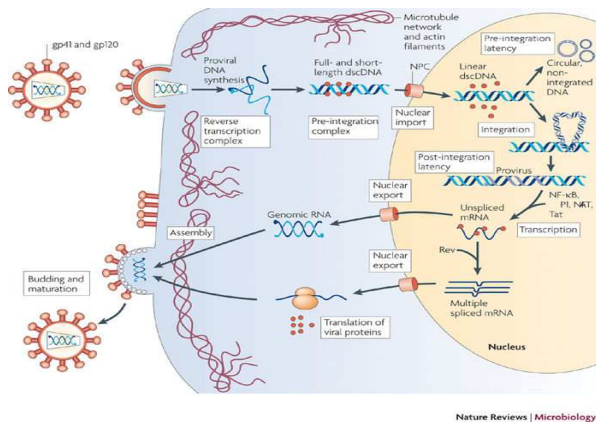
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Retrovirus-like particles released from the human breast cancer cell line T47-D display type B- and C-related endogenous retroviral sequences

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.

Rheumatology

- Oxford Journals
- Medicine
- Rheumatology
- Volume 32, Number 12
- Pp. 1044-1048
- **VIRUS-LIKE PARTICLES IN SYNOVIAL FLUIDS FROM PATIENTS WITH RHEUMATOID ARTHRITIS**
- G. STRANSKY, J. VERNON, W. K. AICHER, L. W. MORELAND, R. E. GAY and S. GAY
- Division of Clinical Immunology and Rheumatology, The University of Alabama at Birmingham Birmingham, Alabama, USA
- 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.

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.

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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 β 1,3-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 β 1,3-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.

BIOLOGICAL SCIENCES / DEVELOPMENTAL BIOLOGY

Endogenous retroviruses regulate periimplantation placental growth and differentiation.

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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:

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

Ann-Catrin Andersson¹, Patrick J. W. Venables², Ralf R. Tönjes³, Jürgen Scherer⁴, Lars Eriksson⁵ and Erik Larsson⁶

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 lo

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 Zeifelder,¹ Birgit Spiess,¹ Alex D. Greenwood,^{2,3} Rüdiger Hehlmann,¹ and Christine Leib-Mösch,^{1,2}

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 MANUFACTURERS & ASSOCIATIONS <http://www.ifpma.org/influenza/index.aspx?47> exponían muy ufanos, la siguiente información:

Vaccine Manufacture : Egg-Based Vaccine Production



Currently commercialized seasonal influenza vaccines rely upon the supply of embryonated chicken eggs as the substrate for virus propagation. Seed virus strains bearing the recommended hemagglutinin

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. Esta técnica, 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:

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 Heneine^{1*}

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 son las 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:

Special Report The 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.

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;

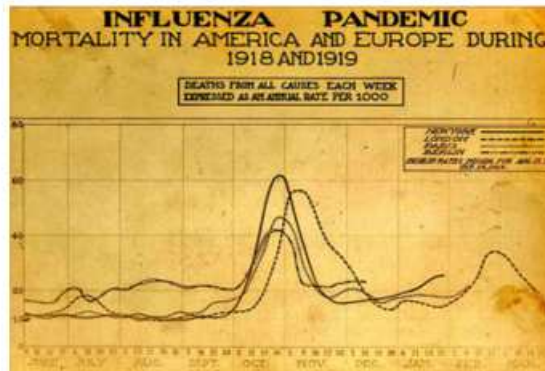
THE 1918 INFLUENZA EPIDEMIC WAS A VACCINE-CAUSED DISEASE

<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 en los sustratos y de los métodos utilizados para elaborar vacunas, que en el caso de las iniciales, eran muy rudimentarios y peligrosos.

Pero en el siguiente caso, 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 virulento. Las letras H y N se refieren a la hemaglutinina, 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 ahora un experimento inocente:

Experimental Infection of Pigs with the Human 1918 Pandemic Influenza Virus

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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.

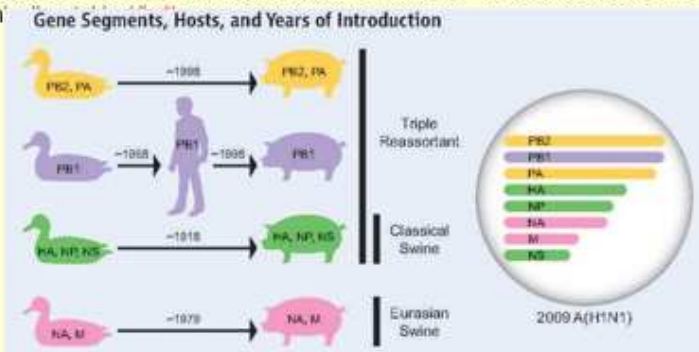
Veamos con atención las consecuencias de este “experimento”:

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

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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 antigenic.



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.