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Felipe Figueiredo

Instituto Nacional de Traumatologia e Ortopedia

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- **Mecanismo de busca**, mantido pelo governo dos EUA (NLM¹ e NIH²)
- Acessa primariamente a base MEDLINE, entre outras
- Referências dos artigos são indexadas e catalogadas para busca
- Links para o conteúdo dos artigos (externos)
- Sugere artigos similares
- Exporta referências para gerenciadores bibliográficos (Mendeley, EndNote, etc)

¹National Library of Medicine

²National Institutes of Health

Definition

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- Índice
- Abstract
- Link para artigo completo (em geral, site da editora)

De acordo com a Wikipédia

Disciplinas: Medicine, nursing, pharmacy, dentistry, veterinary medicine, health care, biology, biochemistry, molecular evolution, biomedicine, history of medicine, health services research, AIDS, toxicology and environmental health, molecular biology, complementary medicine, behavioral sciences, chemical sciences, bioengineering, health policy development, environmental science, marine biology, plant and animal science, biophysics

Definition

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Disponíveis:

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1. [Viral variants that initiate and drive maturation of V1V2-directed HIV-1 broadly neutralizing antibodies.](#)
Bhiman JN, Anthony C, Doria-Rose NA, Karimanzira O, Schramm CA, Khoza T, Kitchin D, Botha G, Gorman J, Garrett NJ, Abdool Karim SS, Shapiro L, Williamson C, Kwong PD, Mascola JR, Morris L, Moore PL. Nat Med. 2015 Oct 12. doi: 10.1038/nm.3963. [Epub ahead of print]
PMID: 26457756

2. [The use of the NIS reporter gene for optimizing oncolytic virotherapy.](#)
Miller A, Russell SJ. Expert Opin Biol Ther. 2015 Oct 12:1-18. [Epub ahead of print]
PMID: 26457362

3. [Transcriptional regulation of gilthead seabream bone morphogenetic protein \(BMP\) 2 gene by bone- and cartilage-related transcription factors.](#)
Marques CL, Leonor Cancela M, Laizé V. Gene. 2015 Oct 8. pii: S0378-1119(15)01212-3. doi: 10.1016/j.gene.2015.10.005. [Epub ahead of print]

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Abstract

Nat Med. 2015 Oct 12. doi: 10.1038/nm.3963. [Epub ahead of print]

Viral variants that initiate and drive maturation of V1V2-directed HIV-1 broadly neutralizing antibodies.

Bhiman JN^{1,2}, Anthony C³, Dorja-Rose NA⁴, Karimanzira O¹, Schramm CA⁵, Khoza T¹, Kitchin D¹, Bothe G³, Gorman J⁴, Garrett NJ⁶, Abdool Karim SS⁶, Shapiro L^{4,5}, Williamson C^{3,6,7}, Kwong PD⁴, Mascola JR⁴, Morris L^{1,2,6}, Moore PL^{1,2,6}.

Author information

Abstract

The elicitation of broadly neutralizing antibodies (bNAbs) is likely to be essential for a preventative HIV-1 vaccine, but this has not yet been achieved by immunization. In contrast, some HIV-1-infected individuals naturally mount bNAb responses during chronic infection, suggesting that years of maturation may be required for neutralization breadth. Recent studies have shown that viral diversification precedes the emergence of bNAbs, but the significance of this observation is unknown. Here we delineate the key viral events that drove neutralization breadth within the CAP256-VRC26 family of 33 monoclonal antibodies (mAbs) isolated from a superinfected individual. First, we identified minority viral variants, termed bNAb-initiating envelopes, that were distinct from both of the transmitted/founder (T/F) viruses and that efficiently engaged the bNAb precursor. Second, deep sequencing revealed a pool of diverse epitope variants (immunotypes) that were preferentially neutralized by broader members of the antibody lineage. In contrast, a 'dead-end' antibody sublineage unable to neutralize these immunotypes showed limited evolution and failed to develop breadth. Thus, early viral escape at key antibody-virus contact sites selects for antibody sublineages that can tolerate these changes, thereby providing a mechanism for the generation of neutralization breadth within a developing antibody lineage.

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Abstract

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Bhiman JN^{1,2}, Anthony C³, Dorja-Rose NA⁴, Karimanzira O¹, Schramm CA⁵, Khoza Garrett N⁶, Abdool Karim SS⁶, Shapiro L^{4,5}, Williamson C^{3,6,7}, Kwong PD⁴, Masco

Author information

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E Domingo, C Escarmis, N Sevilla, A Moya, SF Elena... - The FASEB Journal, 1996 - FASEB
Abstract A hallmark of RNA genomes is the error-prone nature of their replication and
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M Yamashita, M Krystal, WM Fitch, P Palese - Virology, 1988 - Elsevier
Abstract Sequence analyses and comparison of the genes coding for the nonstructural (NS)
and hemagglutinin (HA) proteins of different influenza B viruses isolated between 1940 and
1987 reveal that the number of substitutions is not always proportional to the time between ...
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Mechanisms of plant virus evolution
MJ Roossinck - Annual review of phytopathology, 1997 - annualreviews.org
Abstract Plant viruses utilize several mechanisms to generate the large amount of genetic
diversity found both within and between species. Plant RNA viruses and pararetroviruses
probably have highly error prone replication mechanisms, that result in numerous ...
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Virus evolution and genetic diversity of hantaviruses and their rodent hosts
A Plyusnin, SP Morzunov - Hantaviruses, 2001 - Springer
Abstract Unlike other members of the Bunyaviridae family, which must be regarded as
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maintained in the populations of their specific rodent hosts. Thus, the prefix "Robo"(from ...
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avirulent strains
T Toyoda, T Sakaguchi, H Hirota, B Gotoh, K Kuma... - Virology, 1989 - Elsevier
Abstract Sequence analysis and comparison of the fusion glycoprotein genes of 11 Newcastle disease **virus** (NDV) isolates indicated a high degree of functional and structural constraint exerted on the change of the glycoprotein. However, synonymous nucleotide ...
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Rearrangements in the 5' nontranslated region and phylogenetic analyses of cucumber mosaic **virus** RNA 3 indicate radial **evolution** of three subgroups asm.org (HTML)
MJ Roossinck, L Zhang, KH Hellwald - Journal of virology, 1999 - Am Soc Microbiol
ABSTRACT Cucumber mosaic **virus** (CMV) has been divided into two subgroups based on serological data, peptide mapping of the coat protein, nucleic acid hybridization, and nucleotide sequence similarity. Analyses of a number of recently isolated strains suggest ...
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Newcastle disease **virus evolution**: I. Multiple lineages defined by sequence variability of the hemagglutinin-neuraminidase gene
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Abstract We compared the hemagglutinin-neuraminidase gene sequence among 13 strains of Newcastle disease **virus** (NDV) isolated over the last 50 years. Although overall homology was remarkably high, the sequence variability demonstrated the existence of at least three ...
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What does structure tell us about virus evolution?
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The screenshot shows a Google Scholar search result for the article "What does structure tell us about virus evolution?" by Bamford, DH, Grimes, JM, and Stuart, DI. A "Cite" dialog box is open, displaying citation formats for MLA, APA, and Chicago. The MLA format is highlighted in orange. Below the dialog box, the abstract of the article is visible.

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MLA Bamford, Dennis H., Jonathan M. Grimes, and David I. Stuart. "What does structure tell us about virus evolution?." *Current opinion in structural biology* 15.6 (2005): 655-663.

APA Bamford, D. H., Grimes, J. M., & Stuart, D. I. (2005). What does structure tell us about virus evolution?. *Current opinion in structural biology*, 15(6), 655-663.

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São vários os tipos de trabalhos acadêmicos e suas denominações e não há consenso sobre os significados dos diversos termos empregados. Por isso, adotamos, neste trabalho, o entendimento que é dado pela ABNT ou, quando inexistente, o mais aceito, tendo por base a literatura sobre o assunto.

Esta obra não contempla todos os tipos de trabalhos acadêmicos ou científicos. O interesse está voltado para aqueles típicos de disciplinas, conclusão de cursos de graduação e pós-graduação, projeto de pesquisa, além de redação e formatação de artigo.

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BASIC GENETIC MECHANISMS

DNA, Chromosomes, and Genomes

CHAPTER 4

IN THIS CHAPTER

THE STRUCTURE AND FUNCTION OF DNA

CHROMOSOMAL DNA AND ITS PACKAGING IN THE CHROMATIN FIBER

CHROMATIN STRUCTURE AND FUNCTION

THE GLOBAL STRUCTURE OF CHROMOSOMES

Life depends on the ability of cells to store, retrieve, and translate the genetic instructions required to make and maintain a living organism. This hereditary information is passed on from a cell to its daughter cells at cell division, and from one generation of an organism to the next through the organism's reproductive cells. The instructions are stored within every living cell as its genes, the information-containing elements that determine the characteristics of a species as a whole and of the individuals within it.

As soon as genetics emerged as a science at the beginning of the twentieth century, scientists became intrigued by the chemical structure of genes. The information in genes is copied and transmitted from cell to daughter cell millions of times during the life of a multicellular organism, and it survives the process essentially unchanged. What form of molecule could be capable of such accurate and almost unlimited replication and also be able to exert precise control, directing multicellular development as well as the daily life of every cell? What kind of instructions does the genetic information contain? And how can the enormous amount

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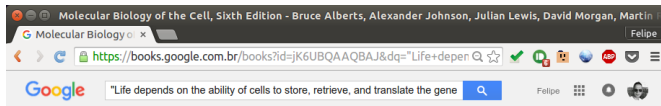
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In a previous study (Kellgren and Bier, 1956), three sets of x rays of the hands were used to assess inter- and intra-observer differences in interpreting changes of rheumatoid arthritis. Wide disagreement between observers was found, and it was concluded that, to ensure ...

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Osteo-arthrosis. Prevalence in the population and relationship between symptoms and x-ray changes.

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This study of osteo-arthrosis, or degenerative joint disease, is based on the same survey material as the corresponding paper on rheumatoid arthritis (Kellgren and Lawrence, 1956). A one-in-ten random sample of the population aged 55-64 years in the Lancashire town of ...

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The WOMAC (Western Ontario and McMaster Universities) Osteoarthritis Index is a tested questionnaire to assess symptoms and physical functional disability. We adapted the WOMAC for the German language and tested its metric properties, test-retest reliability ...

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DT Felson, JJ Anderson, A Naimark... - *Annals of Internal Medicine* ..., 1988 - Am Coll Physicians
... cause. Design: Cohort study with weight and other important variables measured in 1948 to 1951 (mean age of subjects, 37 years) and **knee arthritis** evaluated in 1983 to 1985 (mean age of subjects, 73 years). Setting: Population ...
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... trial comparing aerobic exercise and resistance exercise with a health education program in older adults with **knee osteoarthritis: the Fitness Arthritis and Seniors Trial** ...
WH Ettinger, R Burns, SP Messier, W Applegate... - *Jama*, 1997 - jama.jamanetwork.com
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CJM Bachmeier, LM March, MJ Cross... - *Osteoarthritis and ...*, 2001 - Elsevier
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Osteotomy about the knee for degenerative and rheumatoid arthritis
MB COVENTRY - *The Journal of Bone & Joint Surgery*, 1973 - jbj.s.org
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Analysis of the discordance between radiographic changes and **knee** pain in osteoarthritis of the **knee**.

MT Hannan, DT Felson, T Pincus - The Journal of rheumatology, 2000 - europepmc.org

... radiographic **knee** OA and 34% reported **knee** pain. CONCLUSION: Substantial discordance exists in this population based study between radiographic OA of the **knee** versus **knee** pain, versus a diagnosis of **arthritis** by a physician. ...

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Radiological assessment of osteo-**arthrosis**

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Annalise B. Paaby^{1,2}, Alan O. Bergland³, Emily L. Behrman¹ and Paul S. Schmidt¹

Version of Record online: 20 NOV 2014
DOI: 10.1111/evo.12546
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- 104. Barrón, M.G., **Fiston-Lavier, A.-S.**, **Petrov, D.A.**, and González-Pérez, J. (2014). Population genomics of transposable elements in *Drosophila*. *Annual Review of Genetics*, **48**:561–81.
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- 101. **Zhu, Y.**, Siegal, M.L., Hall, D.W., and **Petrov, D.A.** (2014). Reply to Chen and Zhang: On interpreting genome-wide trends from yeast mutation accumulation data. *Proc. Natl. Acad. Sci.*, **111**, E4063.

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Trends in Ecology & Evolution Cell Press

Volume 22, Issue 3, March 2007, Pages 156–165

Review

Parasites: proxies for host genealogy and ecology?

Caroline M. Nieberding^{1,2}, Isabelle Olivieri³

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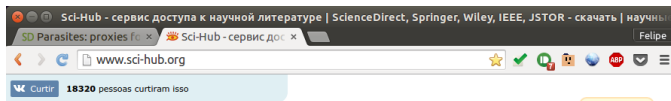
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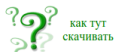


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Parasites: proxies for host genealogy and ecology?

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Genetic information is used extensively to reconstruct the evolutionary and demographic history of organisms. Recently, it has been suggested that genetic information from some parasites can complement genetic data from their hosts. This approach relies upon the hypothesis that such parasites share a common history with their host. In some cases, parasites provide an additional source of information because parasite data can better reconstruct the common history. Here, we discuss which parasite traits are important in determining their usefulness for analysing host history. The key is the matching of the traits of the parasite (e.g. effective population size, generation time, mutation rate and level of host specificity) with the timescales (phylogenetic, phylogeographic and demographic) that are relevant to the issues of concern in host history.

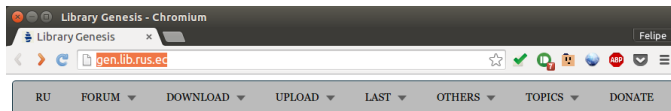
Whiteman and Parker [6] partly summarized the theoretical framework for using parasites as proxies for their host evolutionary history. Here, we further explain why parasites have become used as host 'proxies'. We emphasize that such 'proxy' parasites should share the host genealogical history and provide a better resolution of this common history than would the host itself. We argue that the choice of the most relevant parasite varies with the timescale of the analysis (phylogenetic, phylogeographic or demographic; see Glossary) and that parasites could be most useful at the phylogeographic and demographic scales. A better understanding of the relationship between parasites and their hosts is needed to address the questions that can be addressed.

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