



20 YEARS OF GENOMICS IN BRAZIL

MARCO ANTONIO ZAGO
PRESIDENT FAPESP

GENOMICS IS BORN IN BRAZIL



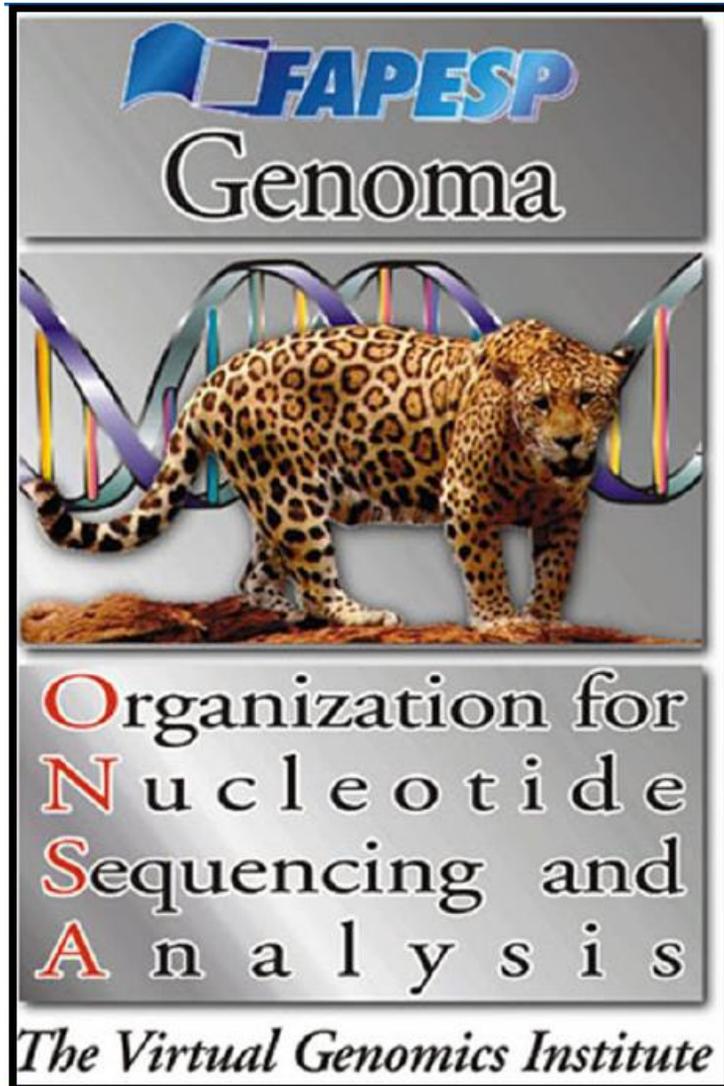
**13
JULY
2000**

FAPESP invested the equivalent of **US\$ 12 million**, largely dedicated to sequencers, computers and reagents, while the team brought together and trained researchers from a range of fields to develop a broad and long-lasting set of **skills and knowledge**

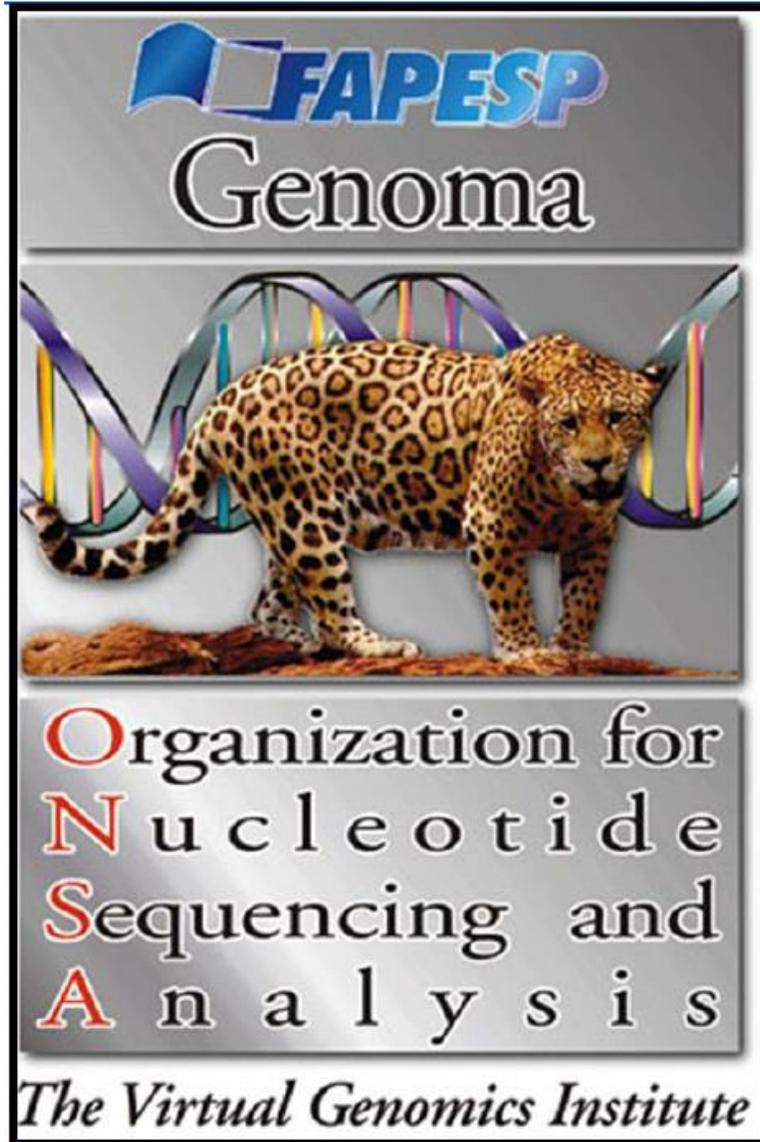


Xylella demonstrated the benefits of aiming high

AIMS



1. Complete sequencing of a bacterial genome in the range of 2 million bases (2Mb)
2. Analysis of the genome structure, coding and non-coding sequences and other features
3. Large scale identification of genes and expressed genes



Xylella fastidiosa

SugarCane

Human Cancer

Agronomical & Environmental

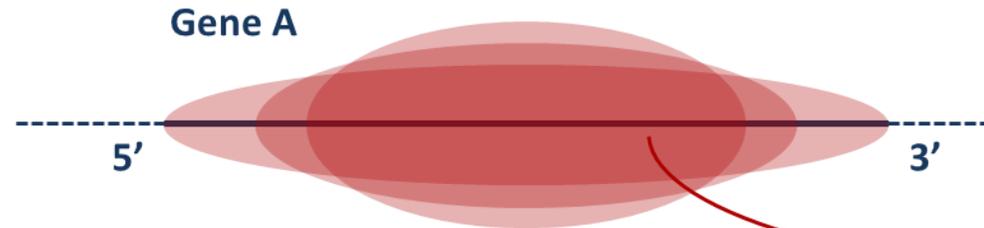
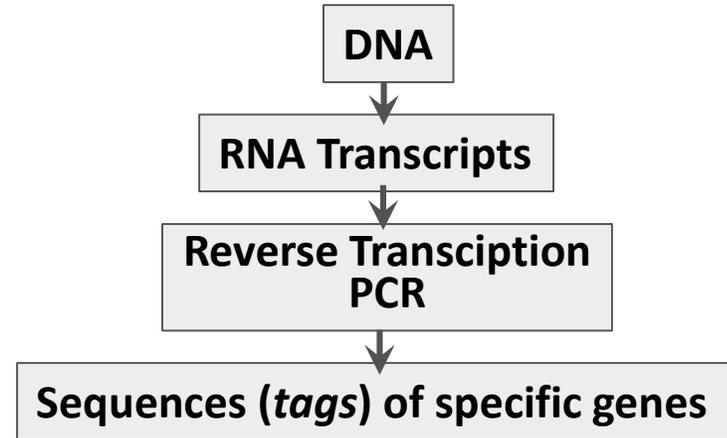
Xanthomonas citri

ANALYSIS OF TRANSCRIPTOME

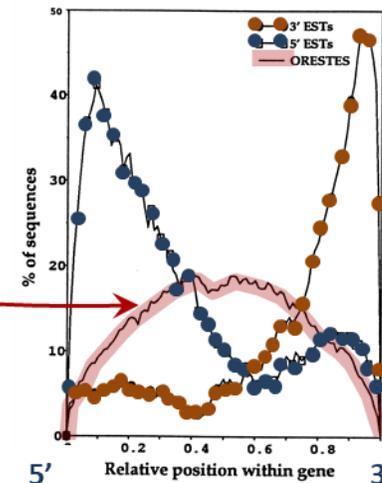
EST: expressed sequence tags

ORESTES: Open Reading (Frame) Expressed Sequence Tags

Manoel Dias-Neto
Andrew J Simpson



ESTs originated predominantly from the central region, usually a region coding for cDNA



2002 letters to nature

Comparison of the genomes of two *Xanthomonas* pathogens with differing host specificities

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(*Xcc*) causes black rot, which affects crucifers such as *Brassica* and *Arabidopsis*. Symptoms include marginal leaf chlorosis and darkening of vascular tissue, accompanied by extensive wilting and necrosis². *Xanthomonas campestris* pv. *campestris* is grown commercially to produce the exopolysaccharide xanthan gum, which is used as a viscosifying and stabilizing agent in many industries³. Here we report and compare the complete genome sequences of *Xac* and *Xcc*. Their distinct disease phenotypes and host ranges belie a high degree of similarity at the genomic level. More than 80% of genes are shared, and gene order is conserved along most of their respective chromosomes. We identified several groups of strain-specific genes, and on the basis of these groups we propose mechanisms that may explain the differing host specificities and pathogenic processes.

Xanthomonas axonopodis pv. *citri* (strain 306) has one circular chromosome comprising 5,175,554 base pairs (bp), and two plasmids: pXAC33 (33,699 bp) and pXAC64 (64,920 bp). *Xanthomonas campestris* pv. *campestris* (strain ATCC33913) has a single circular chromosome comprising 5,076,187 bp, and no plasmids (Table 1). The chromosomes of the two organisms have a high degree of collinearity (Fig. 1). The alignment shown in Fig. 1 suggests that just three major rearrangement events have occurred. One is an inver-

XANTHOMONAS TAENIA

Parasites & Vectors 2009



Open Access

Research

Transcriptome analysis of *Taenia solium* cysticerci using Open Reading Frame ESTs (ORESTES)

Carolina R Almeida¹, Patricia H Stoco², Glauber Wagner^{2,3}, Thaís CM Sincero², Gianinna Rotava², Ethel Bayer-Santos², Juliana B Rodrigues², Maísa M Sperandio², Antônio AM Maia⁴, Elida PB Ojopi¹, Arnaldo Zaha⁵, Henrique B Ferreira⁵, Kevin M Tyler⁶, Alberto MR Dávila⁷, Edmundo C Grisard^{*2,6} and Emmanuel Dias-Neto^{1,8}

DNA Research 2018

DNA Research, 2018, 25(5), 499–510
doi: 10.1093/dnares/dsy020
Advance Access Publication Date: 25 June 2018
Full Paper

Full Paper

The genome of tapeworm *Taenia multiceps* sheds light on understanding parasitic mechanism and control of coenurosis disease

Wenhui Li^{1,†}, Bo Liu^{2,†}, Yang Yang^{1,†}, Yuwei Ren^{2,†}, Shuai Wang^{1,†}, Conghui Liu^{2,†}, Nianzhang Zhang¹, Zigang Qu¹, Wanxu Yang², Yan Zhang², Hongbing Yan¹, Fan Jiang², Li Li¹, Shuqu Li², Wanzhong Jia^{1,3}, Hong Yin^{1,3}, Xuepeng Cai¹, Tao Liu⁴, Donald P. McManus^{5,*}, Wei Fan^{2,*}, and Baoquan Fu^{1,3,*}



ELSEVIER

Available online at www.sciencedirect.com



Biochemical and Biophysical Research Communications 333 (2005) 230–240

BBRC

www.elsevier.com/locate/ybbrc

2005

Identification of 18 new transcribed retrotransposons in *Schistosoma mansoni*

Ricardo DeMarco^a, Abimael A. Machado^b, Alexandre W. Bisson-Filho^a,

**XANTHOMONAS
TAENIA
SCHISTOSOMA**

2013

**nature
genetics**

Transcriptome analysis of the acoelomate human parasite *Schistosoma mansoni*

Sergio Verjovski-Almeida¹, Ricardo DeMarco¹, Elizabeth A L Martins², Pedro E M Guimarães³, Elida P B Ojopi³, Apuã C M Paquola⁴, João P Piazza⁵, Milton Y Nishiyama Jr.⁴, João P Kitajima^{5,15}, Rachel E Adamson⁶, Peter D Ashton⁶, Maria F Bonaldo⁷, Patricia S Coulson⁶, Gary P Dillon⁶, Leonardo P Farias², Sheila P Gregorio^{1,3}, Paulo L Ho², Ricardo A Leite⁸, L Cosme C Malaquias⁹, Regina C P Marques⁸, Patricia A Miyasato¹⁰, Ana L T O Nascimento², Fernanda P Ohlweiler¹⁰, Eduardo M Reis^{1,4}, Marcela A Ribeiro¹¹, Renata G Sá¹², Gaëlle C Stukart³, M Bento Soares^{7,13}, Cybele Gargioni¹⁴, Toshie Kawano¹⁰, Vanderlei Rodrigues¹²,

www.nature.com/naturegenetics

SCIENTIFIC REPORTS

OPEN

2017 The *Schistosoma mansoni* genome encodes thousands of long non-coding RNAs predicted to be functional at different parasite life-cycle stages

Received: 9 June 2017
Accepted: 15 August 2017
Published online: 05 September 2017

Elton J. R. Vasconcelos^{1,2,3}, Lucas F. daSilva^{1,2}, David S. Pires¹, Guilherme M. Lavezzo^{1,2}, Adriana S. A. Pereira^{1,2}, Murilo S. Amaral¹ & Sergio Verjovski-Almeida^{1,2}

nature

Vol 460 | 16 July 2009 | doi:10.1038/nature08180

ARTICLES

2012

The genome of the blood fluke *Schistosoma mansoni*

Matthew Berriman¹, Brian J. Haas^{3†}, Philip T. LoVerde⁴, R. Alan Wilson⁵, Gary P. Dillon⁵, Gustavo C. Cerqueira^{6,7,8}, Susan T. Mashiyama^{9,10}, Bissan Al-Lazikani¹¹, Luiza F. Andrade¹², Peter D. Ashton¹, Martin A. Aslett¹, Daniella C. Bartholomeu^{3†}, Gaëlle Blandin³, Conor R. Caffrey³, Avril Coghlan¹³, Richard Coulson², Tim A. Day¹⁴, Art Delcher⁷, Ricardo DeMarco^{5,15,16}, Appolinaire Djikeng³, Tina Eyre¹, John A. Gamble¹, Elodie Ghedin^{3†}, Yong Gu¹, Christiane Hertz-Fowler¹, Hirohisa Hirai¹⁷, Yuriko Hirai¹⁷, Robin Houston¹, Alasdair Ivns^{1†}, David A. Johnston^{18†}, Daniela Lacerda^{3†}, Camila D. Macedo^{6,9}, Paul McVeigh¹⁴, Zemin Ning¹, Guilherme Oliveira¹², John P. Overington³, Julian Parkhill¹, Mihaela Pertea⁷, Raymond J. Pierce¹⁹, Anna V. Protasio¹, Michael A. Quail¹, Marie-Adèle Rajandream¹, Jane Rogers^{1†}, Mohammed Sajid^{3†}, Steven L. Salzberg^{7,8}, Mario Stanke²⁰, Adrian R. Tivey¹, Owen White^{1†}, David L. Williams^{21†}, Jennifer Wortman^{3†}, Wenjie Wu^{1†}, Mostafa Zamanian¹⁴, Adhemar Zerlotini¹¹, Claire M. Fraser-Liggett^{3†}, Barclay G. Barrell¹ & Najib M. El-Sayed^{13,6,7,8}

COFFEE GENOME

ESTs 2002



Programa Agronomical and Environmental Genome (AEG) (FAPESP)
Centro Nacional de Recursos Genéticos (CENARGEN) (Embrapa)

Braz. J. Plant Physiology 2006

MINIREVIEW

Brazilian coffee genome project: an EST-based genomic resource

Luiz Gonzaga Esteves Vieira^{1*5}, Alan Carvalho Andrade^{2*}, Carlos Augusto Colombo^{3*}, Ana Heloneida de Araújo Moraes², Ângela Metha², Angélica Carvalho de Oliveira², Carlos Alberto Labate⁴, Celso Luis Marino⁸, Cláudia de Barros Monteiro-Vitorello^{6a}, Damares de Castro Monte², Éder Giglioti⁹, Edna Teruko Kimura¹⁰, Eduardo Romano², Eiko Eurya Kuramae¹¹, Eliana Gertrudes Macedo Lemos¹², Elionor Rita Pereira de Almeida², Érika C. Jorge⁵, Érika V. S. Albuquerque², Felipe Rodrigues da Silva², Felipe Vinecky², Haiko Enok Sawazaki³, Hamza Fahmi A. Dorry¹⁴, Helaine Carrer⁷, Ilka Nacif Abreu¹⁵, João A. N. Batista², João Batista Teixeira², João Paulo Kitajima^{17a}, Karem Guimarães Xavier⁴, Liziane Maria de Lima², Luis Eduardo Aranha de Camargo⁶, Luiz Filipe Protasio Pereira¹⁸, Luiz Lehmann Coutinho⁵, Manoel Victor Franco Lemos¹³, Marcelo Ribeiro Romano^{4a}, Marcos Antonio Machado¹⁹, Marcos Mota do Carmo Costa², Maria Fátima Grossi de Sá², Maria Helena S. Goldman²⁰, Maria Inês T. Ferro¹², Maria Laine Penha Tinoco², Mariana C. Oliveira²¹, Marie-Anne Van Sluys²¹, Milton Massao Shimizu¹⁵, Mirian Perez Maluf²², Mirian Therezinha Souza da Eira²³, Oliveira Guerreiro Filho³, Paulo Arruda²⁴, Paulo Mazzafera¹⁵, Pilar Drummond Sampaio Correa Mariani¹⁶, Regina L.B.C. de Oliveira²⁵, Ricardo Harakava²⁶, Silvia Filippi Balbao¹⁵, Siu Mui Tsai²⁷, Sonia Marli Zingaretti di Mauro¹², Suzana Neiva Santos², Walter José Siqueira³, Gustavo Gilson Lacerda Costa²⁸, Eduardo Fernandes Formighieri²⁸, Marcelo Falsarella Carazzolle^{28*}, Gonçalo Amarante Guimarães Pereira^{28*}.

**These authors contributed equally to this work.*



Analysis and Functional Annotation of an Expressed Sequence Tag Collection for Tropical Crop Sugarcane

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de Setta et al. *BMC Genomics* 2014, 15:540
<http://www.biomedcentral.com/1471-2164/15/540>

2014



RESEARCH ARTICLE

Open Access

Building the sugarcane genome for biotechnology and identifying evolutionary trends

Nathalia de Setta^{1,2}, Cláudia Barros Monteiro-Vitorello³, Cushla Jane Metcalfe¹, Guilherme Marcelo Queiroga Cruz¹, Luiz Eduardo Del Bem⁴, Renato Vicentini⁴, Fábio Tebaldi Silveira Nogueira⁵, Roberta Alvares Campos⁶, Sideny Lima Nunes⁶, Paula Cristina Gasperazzo Turrini¹, Andreia Prata Vieira¹, Edgar Andrés Ochoa Cruz¹, Tatiana Caroline Silveira Corrêa¹, Carlos Takeshi Hotta⁶, Alessandro de Mello Varani³, Sonia Vautrin⁷, Adilson Silva da Trindade⁸, Mariane de Mendonça Vilela⁴, Carolina Gimiliani Lembke⁶, Paloma Mieko Sato⁶, Rodrigo Fandino de Andrade⁶, Milton Yutaka Nishiyama Jr⁶, Claudio Benicio Cardoso-Silva⁴, Katia Castanho Scortecci⁸, Antônio Augusto Franco Garcia³, Monalisa Sampaio Carneiro⁹, Changsoo Kim¹⁰, Andrew H Paterson¹⁰, Hélène Bergès⁷, Angélique D'Hont¹¹, Anete Pereira de Souza⁴, Gláucia Mendes Souza⁶, Michel Vincentz⁴, João Paulo Kitajima¹² and Marie-Anne Van Sluys^{1*}

SUGAR CANE



nature
genetics

2018

ARTICLES

<https://doi.org/10.1038/s41588-018-0237-2>

Corrected: Publisher Correction

OPEN

Allele-defined genome of the autopolyploid sugarcane *Saccharum spontaneum* L.

Jisen Zhang^{1,20*}, Xingtian Zhang^{1,20}, Haibao Tang^{1,20}, Qing Zhang^{1,20}, Xiuting Hua¹, Xiaokai Ma¹, Fan Zhu², Tyler Jones³, Xinguang Zhu⁴, John Bowers⁵, Ching Man Wai⁶, Chunfang Zheng⁷, Yan Shi¹, Shuai Chen¹, Xiuming Xu¹, Jingjing Yue¹, David R. Nelson⁸, Lixian Huang¹, Zhen Li¹, Huimin Xu¹, Dong Zhou¹, Yongjun Wang¹, Weichang Hu¹, Jishan Lin¹, Youjin Deng¹, Neha Pandey², Melina Mancini², Dessirée Zerpa², Julie K. Nguyen², Liming Wang¹, Liang Yu², Yinghui Xin², Liangfa Ge², Jie Arro², Jennifer O. Han², Setu Chakrabarty², Marija Pushko², Wenping Zhang¹, Yanhong Ma¹, Panpan Ma¹, Mingju Lv⁴, Faming Chen⁹, Guangyong Zheng⁹, Jingsheng Xu¹, Zhenhui Yang¹, Fang Deng¹, Xuequn Chen¹, Zhenyang Liao¹, Xunxiao Zhang¹, Zhicong Lin¹, Hai Lin¹, Hansong Yan¹, Zheng Kuang¹, Weimin Zhong¹, Pingping Liang¹, Guofeng Wang¹, Yuan Yuan¹, Jiaxian Shi¹, Jinxiang Hou¹, Jingxian Lin¹, Jingjing Jin¹⁰, Peijian Cao¹⁰, Qiaochu Shen¹, Qing Jiang¹, Ping Zhou¹, Yaying Ma¹, Xiaodan Zhang¹, Rongrong Xu¹, Juan Liu¹, Yongmei Zhou¹, Haifeng Jia¹, Qing Ma¹, Rui Qi¹, Zhiliang Zhang¹, Jingping Fang¹, Hongkun Fang¹, Jinjin Song¹, Mengjuan Wang¹, Guangrui Dong¹, Gang Wang¹, Zheng Chen¹, Teng Ma¹, Hong Liu¹, Singha R. Dhungana¹¹, Sarah E. Huss², Xiping Yang¹², Anupma Sharma¹³, Jhon H. Trujillo¹⁴, Maria C. Martinez¹⁴, Matthew Hudson¹⁵, John J. Riascos¹⁴, Mary Schuler², Li-Qing Chen², David M. Braun¹¹, Lei Li¹, Qingyi Yu¹³, Jianping Wang^{11,12}, Kai Wang¹, Michael C. Schatz¹⁶, David Heckerman¹⁷, Marie-Anne Van Sluys¹⁸, Gláucia Mendes Souza¹⁹, Paul H. Moore³, David Sankoff⁷, Robert VanBuren⁶, Andrew H. Paterson⁵, Chifumi Nagai^{3*} and Ray Ming^{1,2*}

GENES AND LONG LIFE



bioRxiv

THE PREPRINT SERVER FOR BIOLOGY

Whole-genome sequencing of 1,171 elderly admixed individuals from the largest Latin American metropolis (São Paulo, Brazil)

 Michel S. Naslavsky,
  Marília O. Scliar,
  Guilherme L. Yamamoto,
 Jaqueline Yu Ting Wang,
 Stepanka Zverinova,
 Tatiana Karp,
 Kelly Nunes,
  José Ricardo Magliocco Ceroni,
 Diego Lima de Carvalho,
 Carlos Eduardo da Silva Simões,
 Daniel Bozoklian,
 Ricardo Nonaka,
 Nayane dos Santos Brito Silva,
 Andreia da Silva Souza,
 Heloísa de Souza Andrade,
 Marília Rodrigues Silva Passos,
 Camila Ferreira Bannwart Castro,
  Celso T. Mendes-Junior,
 Rafael L. V. Mercuri,
 Thiago L. A. Miller,
 Jose Leonel Buzzo,
 Fernanda O. Rego,
 Nathalia M Araújo,
 Wagner CS Magalhães,
  Regina Célia Mingroni-Netto,
  Victor Borda,
  Heinner Guio,
 Mauricio L Barreto,
  Maria Fernanda Lima-Costa,
  Bernardo L Horta,
  Eduardo Tarazona-Santos,
  Diogo Meyer,
  Pedro A. F. Galante,
 Victor Guryev,
  Erick C. Castelli,
  Yeda A. O. Duarte,
  Maria Rita Passos-Bueno,
  Mayana Zatz

doi: <https://doi.org/10.1101/2020.09.15.298026>

**COMPLETE SEQUENCING OF GENOMES
 1.171 ELDERLY FROM SÃO PAULO**

**Individual ancestry of each genome
 in relation to reference populations
 Average of ancestral variations**

EUROPEAN	72,6±2,6
AFRICAN	17,8±2,1
ASIAN	2,8
NATIVE AMERICAN	6,7

Cientistas do Brasil sequenciam genoma do novo coronavírus em apenas 48 horas

Brazilian scientists sequence the genome of the new coronavirus in just 48 hours



***Brazil sequenced in 2 days, whereas others
countries take an average of 15 days***

Brasil já identificou ao menos 25 sublinhagens da variante Delta: quais são os riscos para o País?

Reino Unido monitora nova mutação e Belém alerta sobre tipo de vírus não identificado pelos testes; orientações de especialistas são completar o esquema vacinal contra a covid, manter distanciamento social e usar máscara

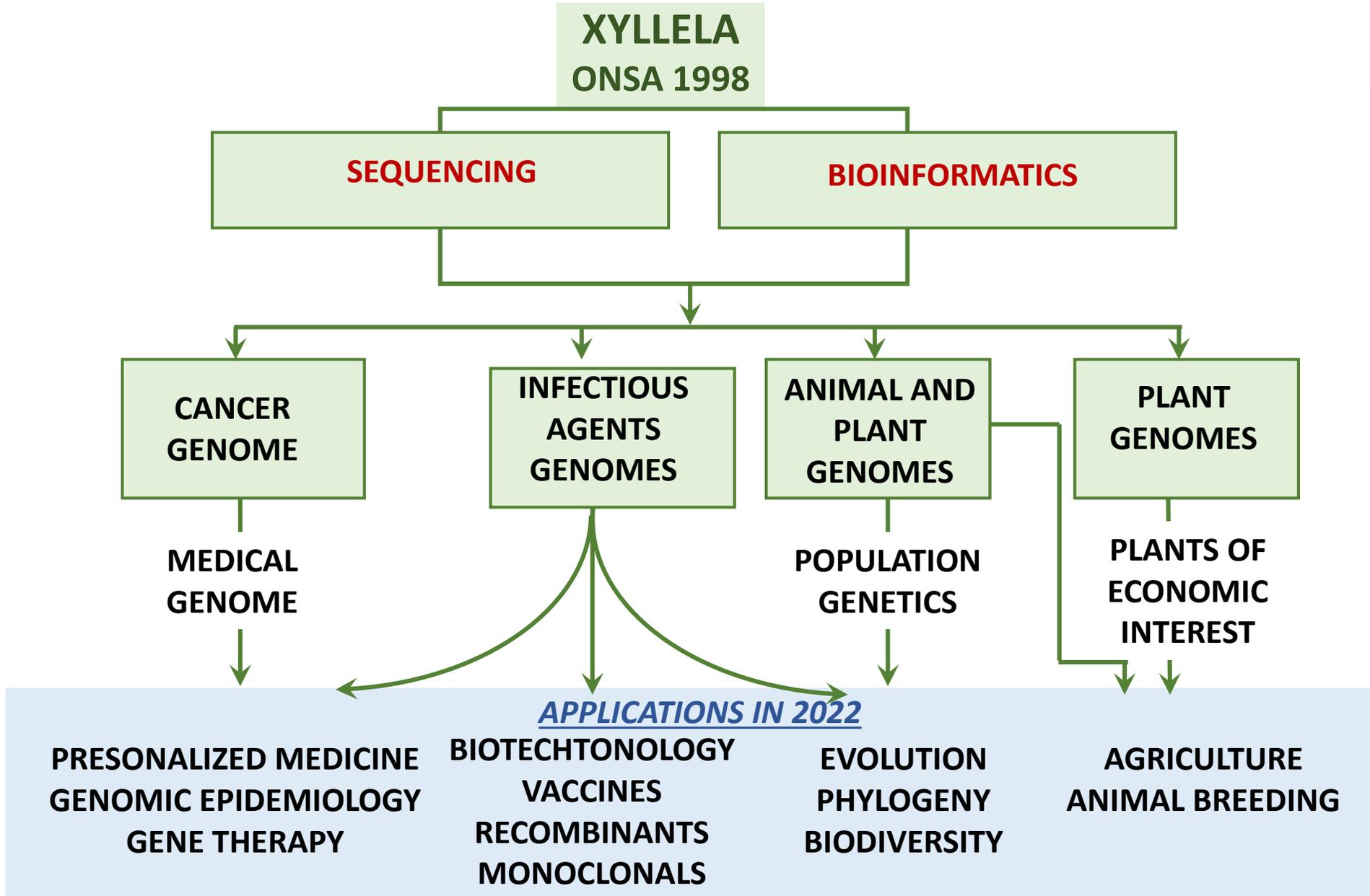
Ítalo Lo Re, O Estado de S.Paulo
26 de outubro de 2021 | 10h00



ESPECIAL CORONAVÍRUS

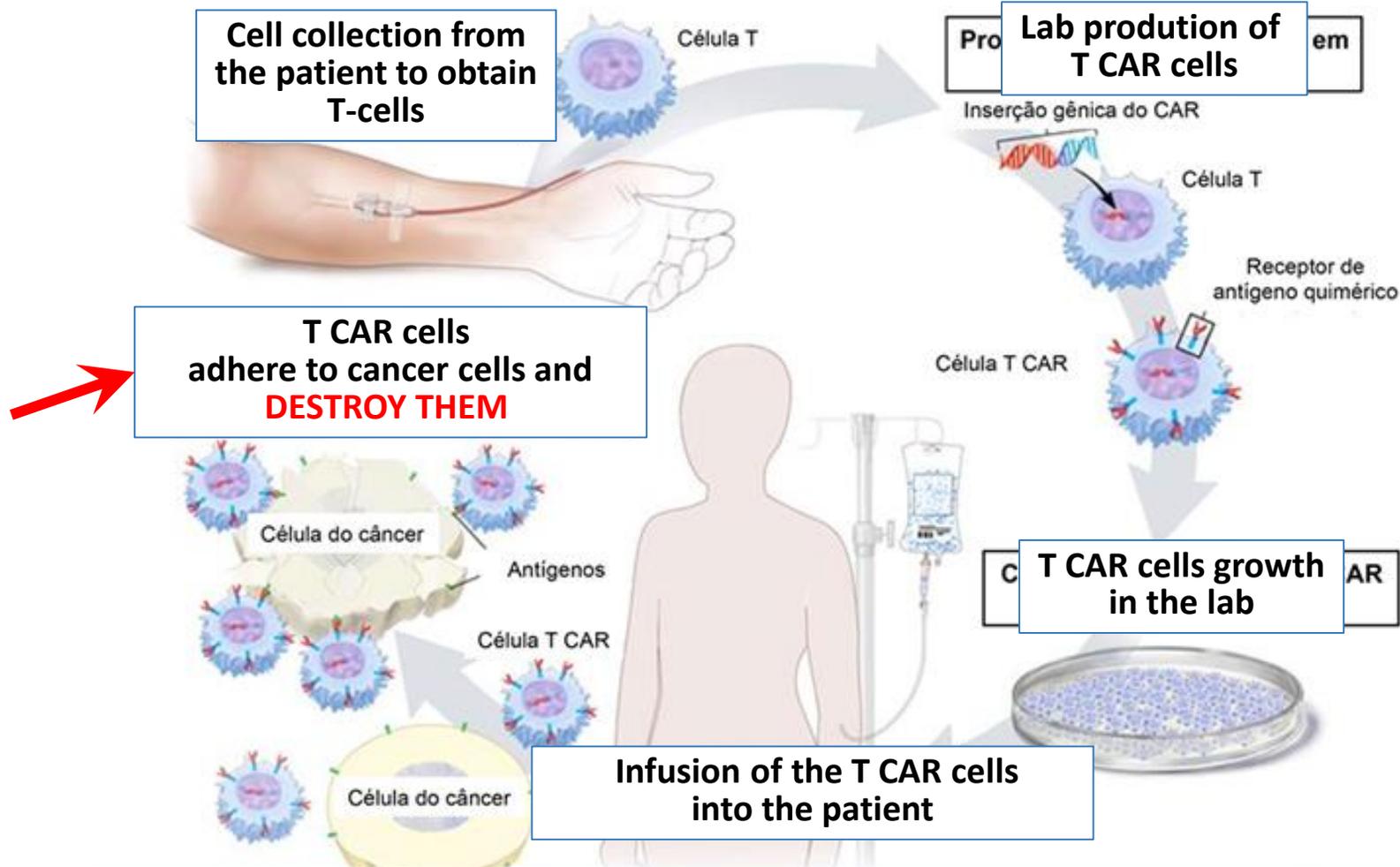
SAIBA MAIS

LEGACY OF THE FAPESP GENOME PROGRAM



INTERVENING IN THE GENOME

TREATMENT OF CANCER WITH T-CAR CELLS



ONLY EXAMPLE OF THIS FORM OF THERAPY IN LATIN AMERICA – FAPESP SUPPORTED CEPIDE IN RIBEIRÃO PRETO

GENOMICS AND BIOINFORMATICS IN BRAZIL WERE BORN IN FAPESP