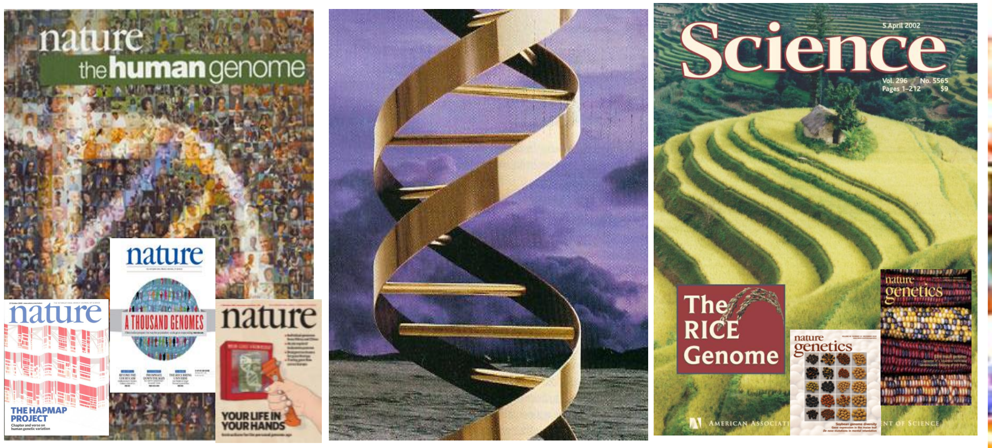
Needed by All, Owned by All, Done by All, Shared by All

The HGP, Genomics, & Future of Man



Huanming Yang Ph.D.

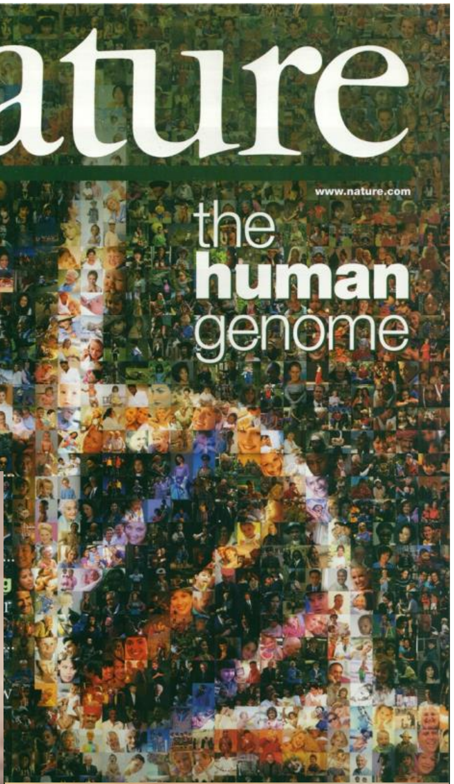
BGI – China, Shenzhen

A short story
about an old country
doing something new
by learning and collaborating.

The story began with …

Celebrating the 15th anniversary of completion of the human genome draft sequence.

June 26, 2000



White Hourse Science Event **10:19 am EST / June 26 , 2000**

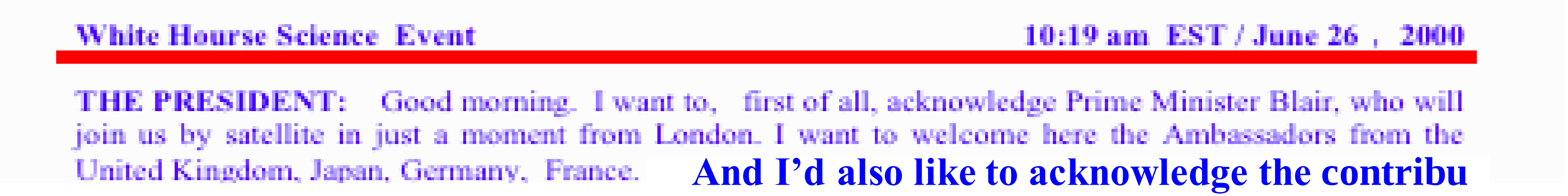
THE PRESIDENT: Good morning. I want to, first of all, acknowledge Prime Minister Blair, who will join us by satellite in just a moment from London. I want to welcome here the Ambassadors from the United Kingdom, Japan, Germany, France. **And I'd also like to acknowledge the contributions not only that their scientists, but also scientists from China, made to the vast international consortium that is the Human Genome Project.**

克林顿总统在“白宫科学庆典上的讲话（2000年6月26日，白宫东厅）：

“解读生命的天书，人类进步的里程碑”

……我还要感谢他们国家（美、日、德、法）的科学家，不仅是他们国家的，还有中国的科学家，对广泛国际合作的人类基因组计划所做的贡献！

> **“Scientists from Japan and Germany, France, *China*, and around the world have been involved, as well as the United Kingdom and the United States. And this undertaking, therefore, has brought together the public, private and non-profit sectors in an unprecedented international partnership.**
>
> **Tonny BLAIR (PM, UK)**



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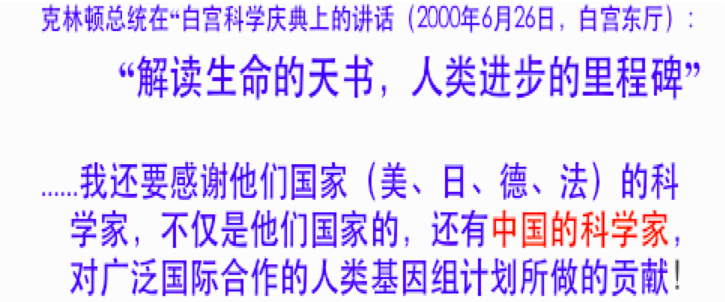

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Tonny BLAIR (PM, UK)

China’s participation in the HGP

In 1999, China's scientific leaders overcame skepticism from some members of the HGP — and from many of their own researchers — to become the only developing country to take a role in sequencing the human genome.

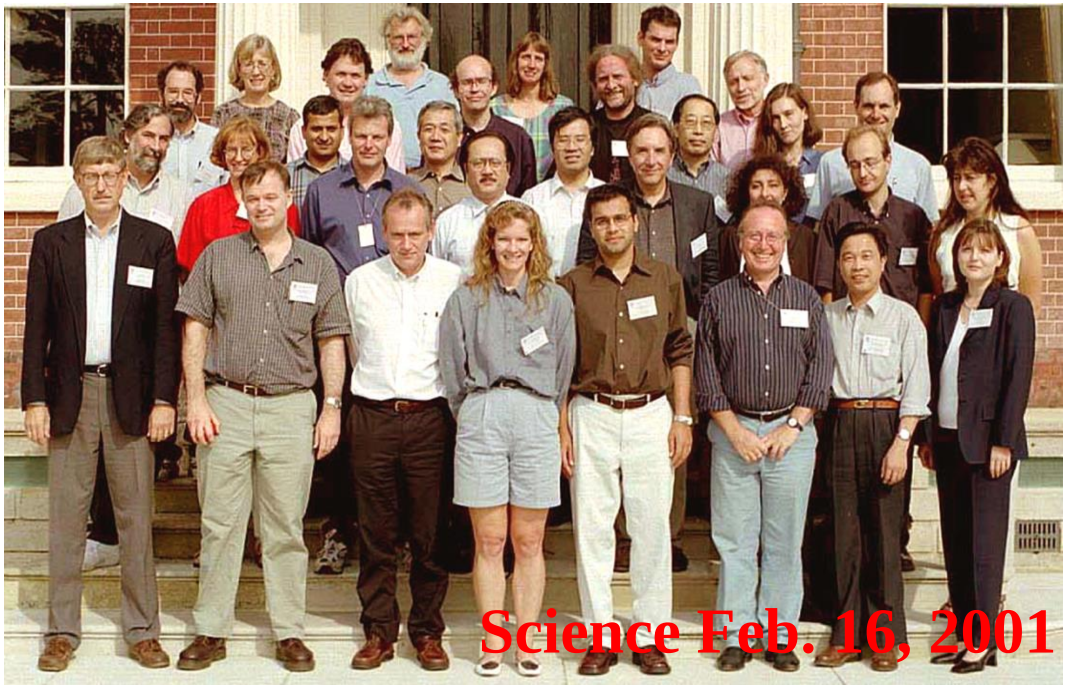
Nature, March 1, 2001

“中国成为其中唯一的发展中国家”

"China has become the latest contributor to the worldwide sequencing effort alongside France, Germany, Japan, UK and USA."

--- *International Human Genome Sequencing Consortium*

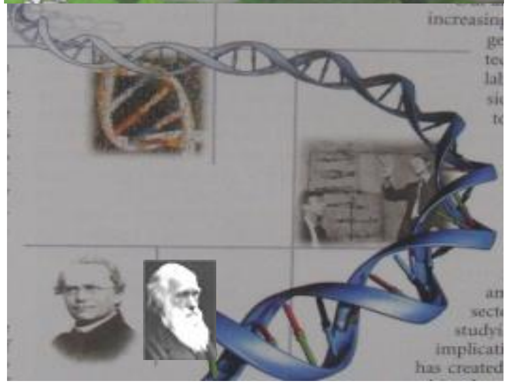
1 Sept. 1999

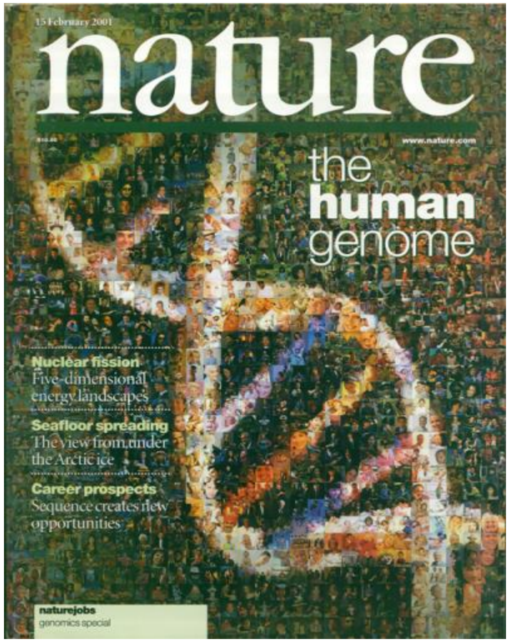


Science Feb. 16, 2001

The HGP contributes to reshaping the future of Man

Three Impacts of the HGP

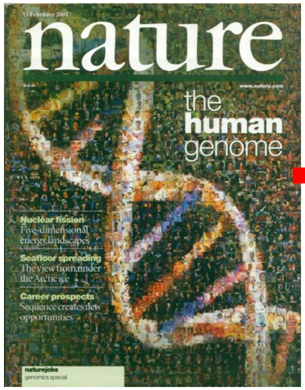




1. **A Culture of Collaboration** 合作的文化
2. **A New Field of Science & Industry**
3. **A New Tool for Biomedicine**

A Culture of Collaboration.

To Share Responsibility & Opportunities



nature

the human genome

Nuclear fission
Five-dimensional energy landscapes

Seafloor spreading
The view from under the Arctic ice

Career prospects
Sequence creates new opportunities

naturejobs
genomics special

27 October 2005 www.nature.com/nature

THE INTERNATIONAL WEEKLY JOURNAL OF SCIENCE

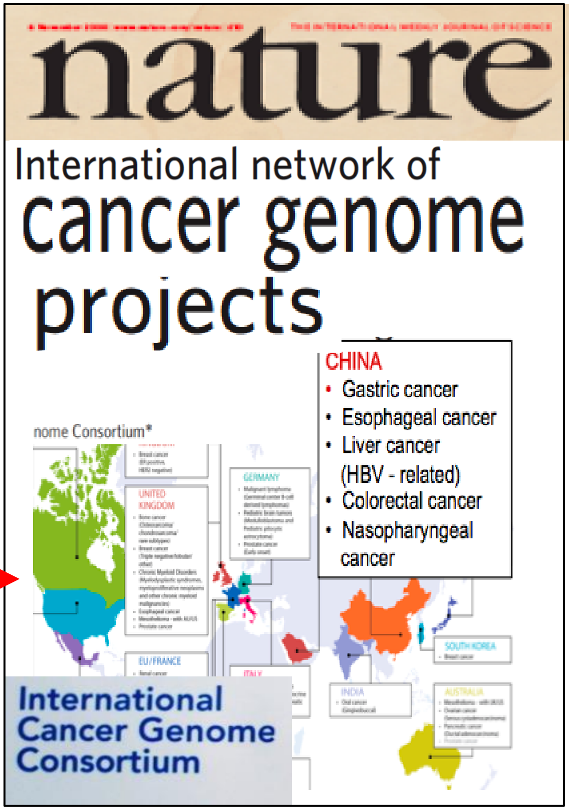
nature

THE HAPMAP PROJECT

Chapter and verse on human genetic variation

nature

A THOUSAND GENOMES



nature

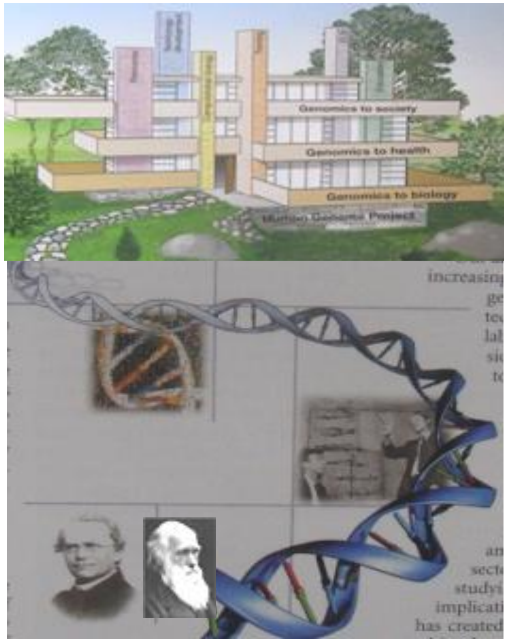
International network of cancer genome projects

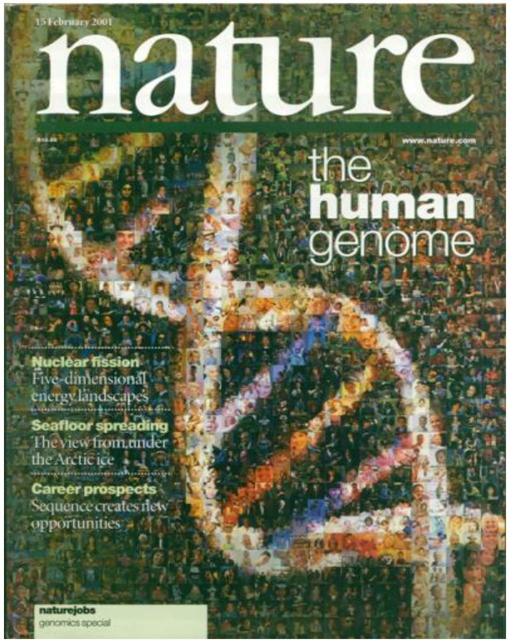
CHINA
- Gastric cancer
- Esophageal cancer
- Liver cancer (HBV - related)
- Colorectal cancer
- Nasopharyngeal cancer

International Cancer Genome Consortium

"Needed by all, done by all, shared by all!"

Three Impacts of the HGP





15 February 2001

nature

www.nature.com

the human genome

Nuclear fission
Five-dimensional energy landscapes

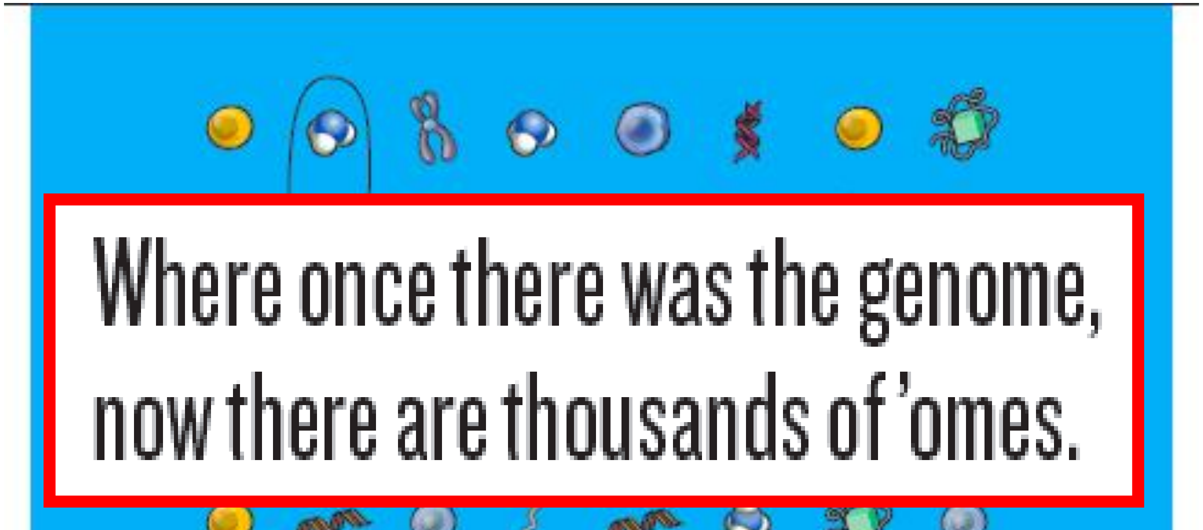
Seafloor spreading
The view from under the Arctic ice

Career prospects
Sequence creates new opportunities

naturejobs
genomics special

1. A Culture of Collaboration
2. **A New Field of Science & Industry**
3. A New Tool for Biomedicine

新的科学、产业



Where once there was the genome, now there are thousands of 'omes.

Nature 28 Feb., 2013

THE GOOD, THE BAD AND THE UGLY

Does your 'ome meet the criteria?

GOODOME

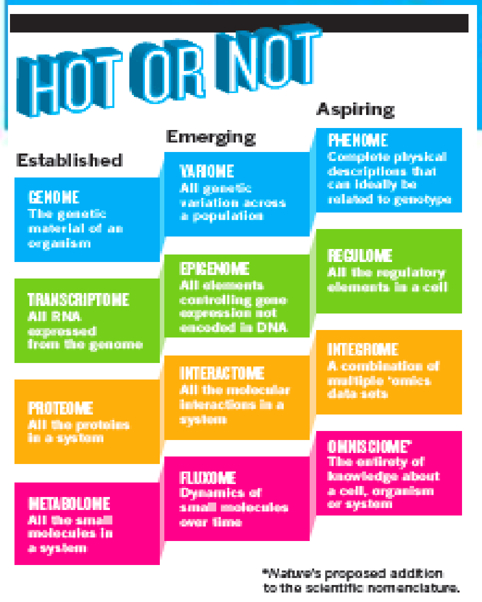
Encapsulates a new focus (Interactome: all interactions between biomolecules)

Refers to a comprehensive collection (Transcriptome: everything transcribed from DNA to RNA)

BADOME

Renames existing field (Nutriome: study of nutrients)

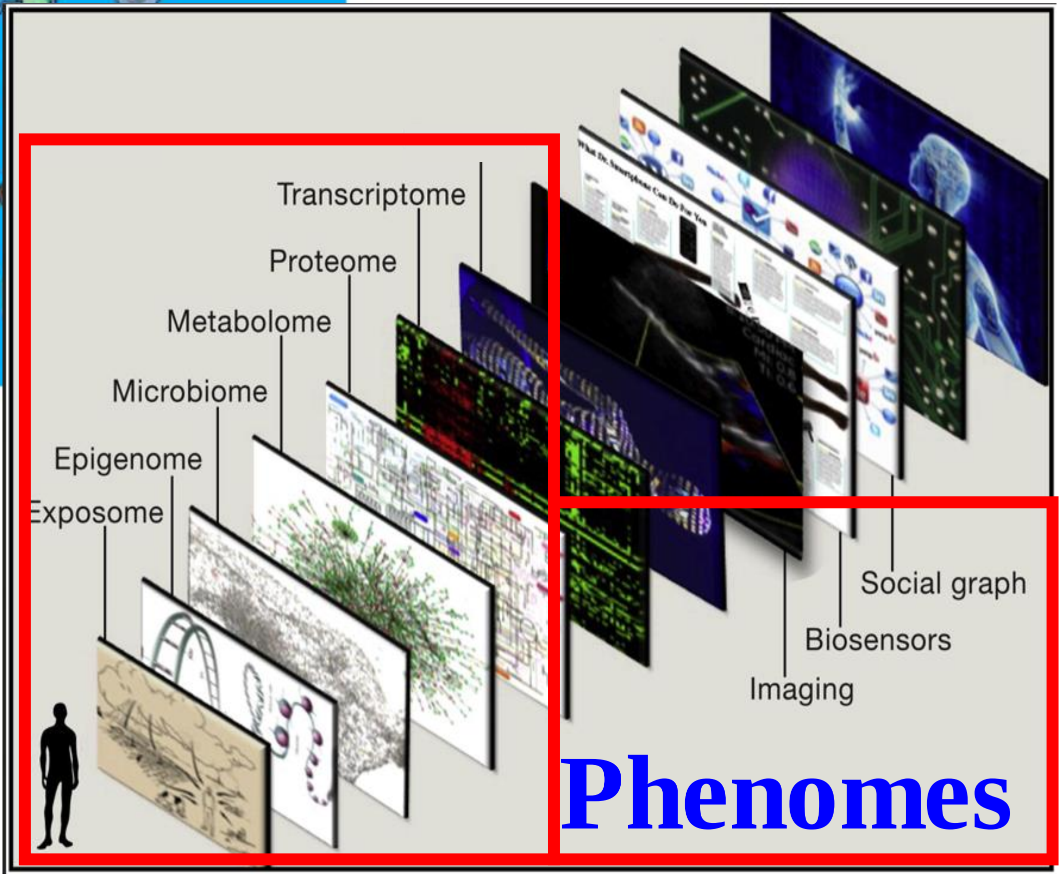
Limited in scope (Museome: sequenced DNA from objects in museum archives)



HOT OR NOT

Established	Emerging	Aspiring
GENOME The genetic material of an organism	**VARIOME** All genetic variation across a population	**PHENOME** Complete physical descriptions that can ideally be related to genotype
TRANSCRIPTOME All RNA expressed from the genome	**EPIGENOME** All elements controlling gene expression not encoded in DNA	**REGULOME** All the regulatory elements in a cell
PROTEOME All the proteins in a system	**INTERACTOME** All the molecular interactions in a system	**INTEGROME** A combination of multiple 'omics data sets
METABOLOME All the small molecules in a system	**FLUXOME** Dynamics of small molecules over time	**OMNISCIOME*** The entirety of knowledge about a cell, organism or system

*Nature's proposed addition to the scientific nomenclature.



Phenomes

“-omicsization” – HGP’s Impacts

“-Ome” & “-Omics”

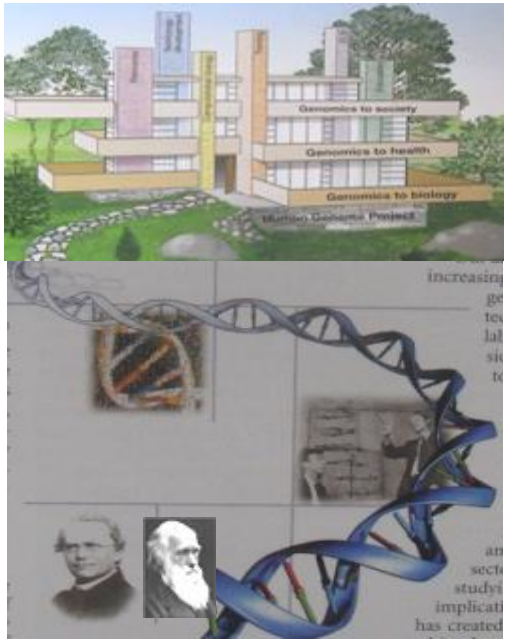
“- 组”、“- 组学” 和 “组学化”

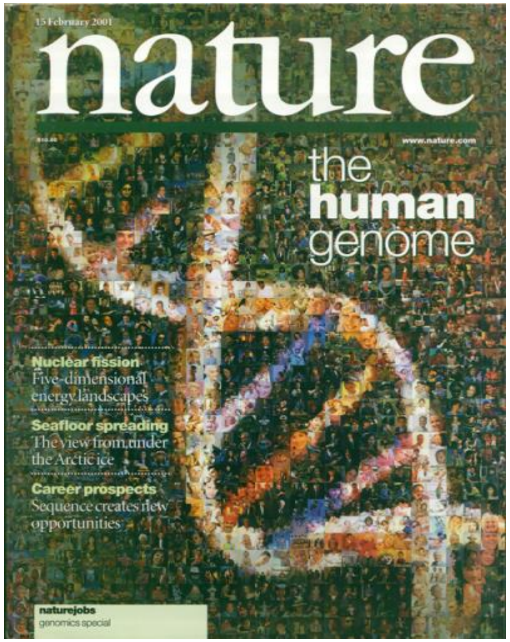
Transcriptome – Transcriptomics
Proteome – Proteomics
Methylome – Methylomics
Metabolome – Metabolomics
Phenome - Phenomics

Cancerome – Canceromics

> **“Today, we’ve gotten to the point where almost no biological phenomenon can escape “omicsization,” and within the next 25 years, omics will be the biggest, if not the only, game in town.”**
>
> Stephen Friend Oct. 1, 2011, The Scientist

Three Impacts of the HGP





1. A Culture of Collaboration
2. A New Field of Science & Industry
3. **A New Tool for Biomedicine** 新的技术

“Sequencing, sequencing, and sequencing!”

“测序，测序，再测序! ”

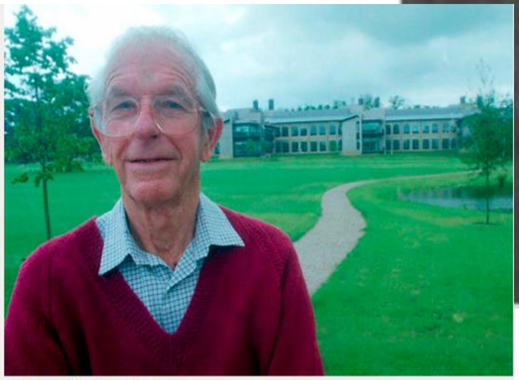
Ann. Rev. Biochem. 1988. 57:1–28
Copyright © 1988 by Annual Reviews Inc. All rights reserved

SEQUENCES, SEQUENCES, AND SEQUENCES

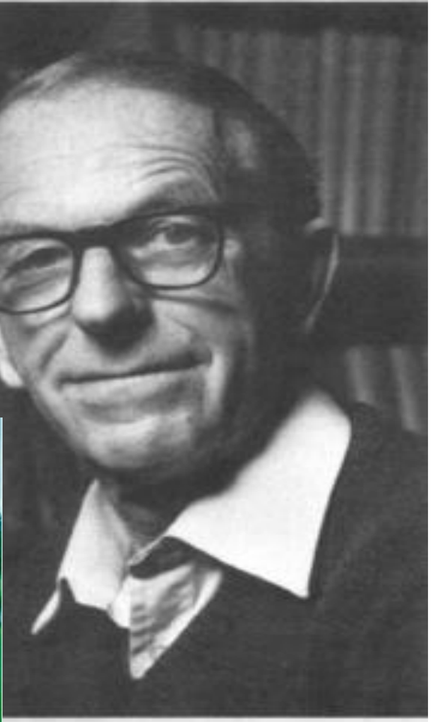
"序列，序列，还是序列!"

Frederick Sanger

"Father of Genomics"



Fred Sanger at the Sanger Centre



His contribution to DNA sequencing technology has transformed our understanding of life on earth by *making life digital*

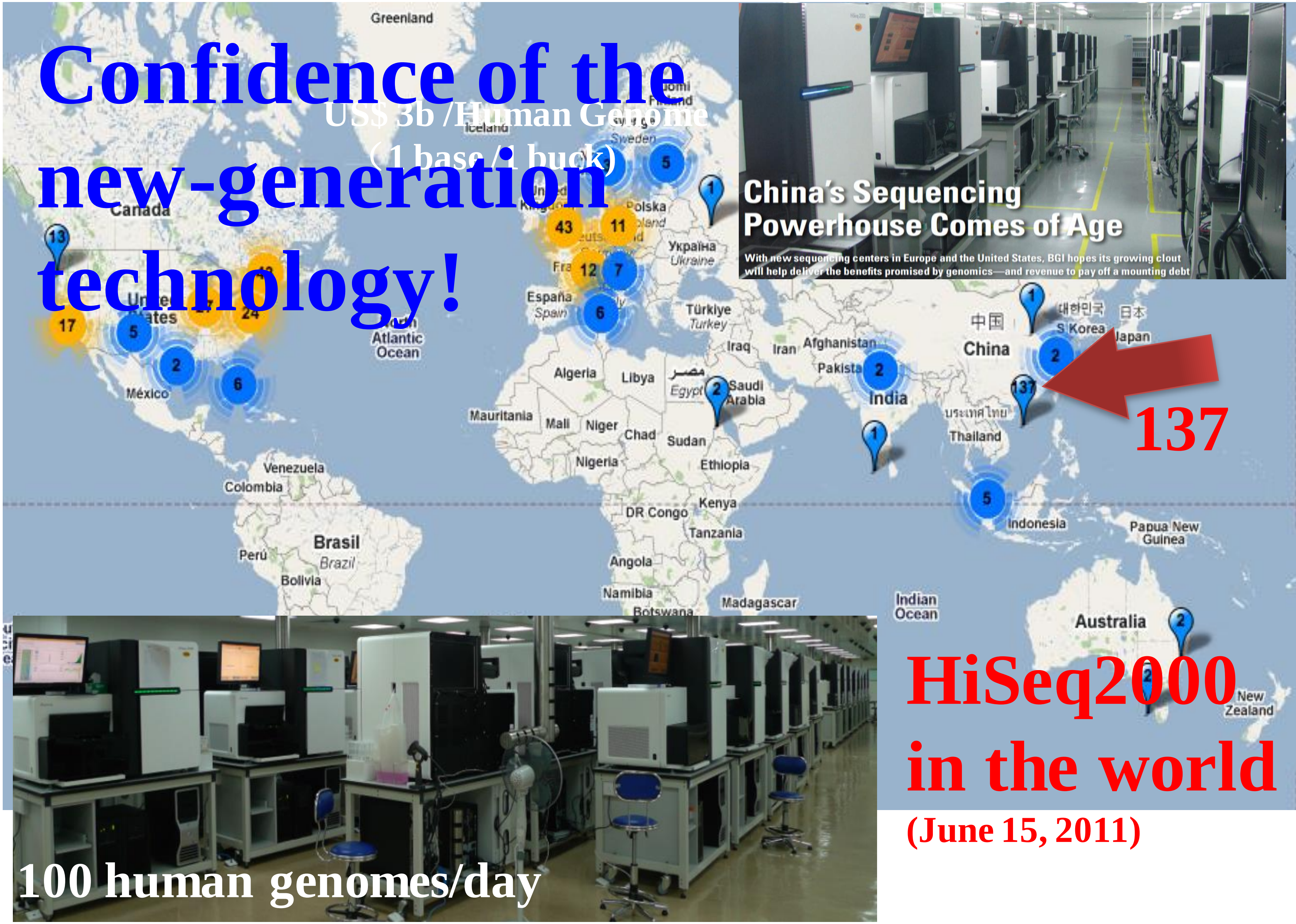
"Sequencing, sequencing, and sequencing!"

"测序，测序，再测序! "

Confidence of the new-generation technology!

US$ 3b /Human Genome

（1 base /1 buck)



China's Sequencing Powerhouse Comes of Age

With new sequencing centers in Europe and the United States, BGI hopes its growing clout will help deliver the benefits promised by genomics—and revenue to pay off a mounting debt

137

HiSeq2000 in the world

(June 15, 2011)

100 human genomes/day

by Nick Loman (University of Birmingham). http://pathogenomics.bham.ac.uk

Dec. 13, 2009

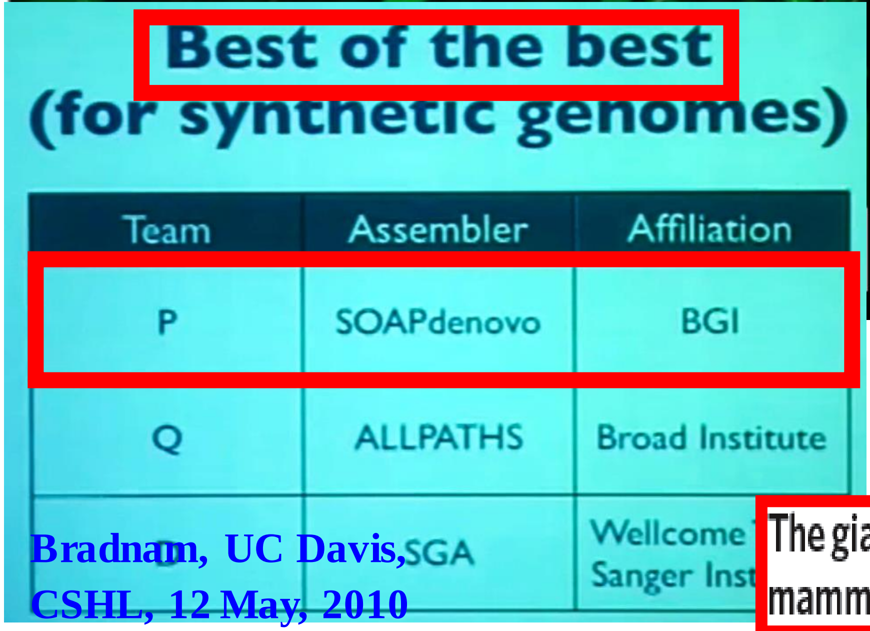
Must Read
F1000 Factor 6.0

The sequence and *de novo* assembly of the giant panda genome

No "genetic map"
No "physical map"
No prior knowledge of repeats

Making the wide applications of the new-generation sequencing Technology a reality.

NEWS & VIE



Best of the best
(for synthetic genomes)

Team	Assembler	Affiliation
P	SOAPdenovo	BGI
Q	ALLPATHS	Broad Institute
D	SGA	Wellcome Sanger Inst

Bradnam, UC Davis,
CSHL, 12 May, 2010

The giant-panda genome is the first reported *de novo* assembly of a large mammalian genome achieved using next-generation sequencing methods.

3 Feb. 2012

335: 516-519, 2012

中国已经成为测序的超级大国

Science

China's Sequencing Powerhouse Comes of Age

by Dennis Normile

BGI-Shenzhen has emerged as a genomics superpower.

Since its inception in 1999, BGI has focused on developing its sequencing and bioinformatics capabilities while turning to outside teams in crop science, human disease, and microbiology to help define its research objectives.

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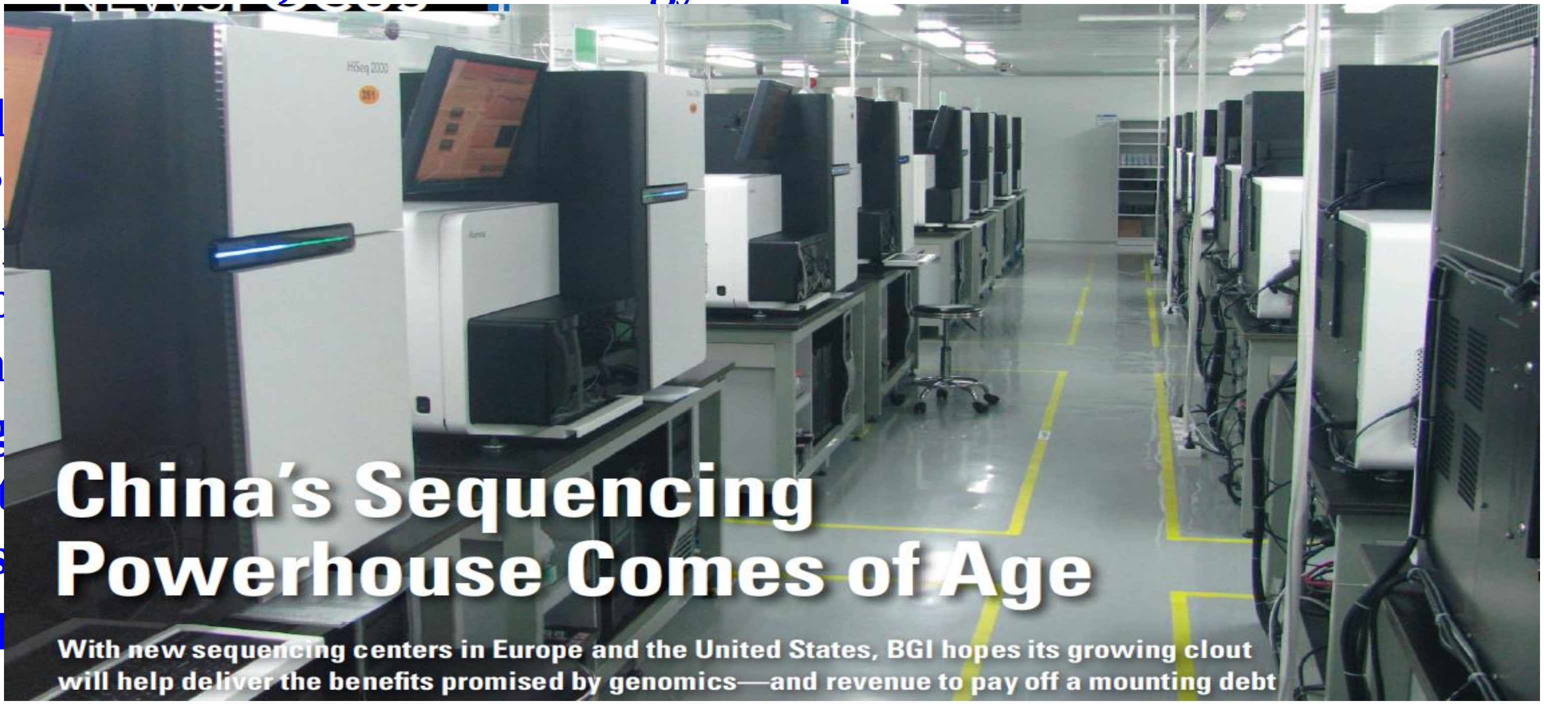


China's Sequencing Powerhouse Comes of Age

With new sequencing centers in Europe and the United States, BGI hopes its growing clout will help deliver the benefits promised by genomics—and revenue to pay off a mounting debt

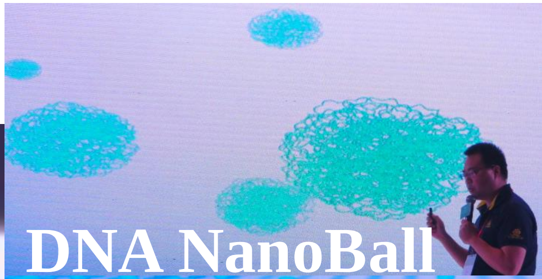
Sequencer, Made in China

BGISEQ-500

接受预定
2015年12月25日
Available for order Dec 25, 2015

启动交付
2016年 2 月15日
Shipping since Feb 15, 2016

首发地 中国
Available Now in China



DNA NanoBall

Pattern Array

DNB + PA

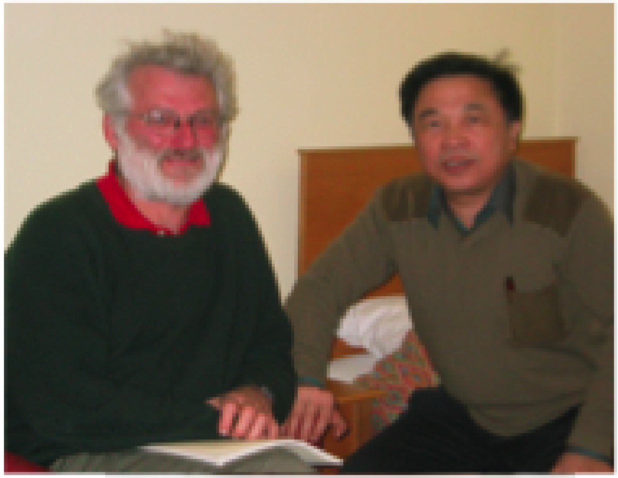
精准 Accuracy
简易 Simplicity
快速 Speed
灵活 Flexibility
经济 Affordable

Shenzhen All Rights Reserved

通量 Throughput	16-96个样本，3万样本/年 16-96 samples/run, 30,000 sample
操作 Operations	自动化文库构建和一键测序 Automated platform for sample prep one-touch sequencing
分析 Analysis	内嵌信息分析软件，全自 Integrated bioinformatics analysis
时间 TAT	最快24小时完成全检测 Completed within 24 hrs

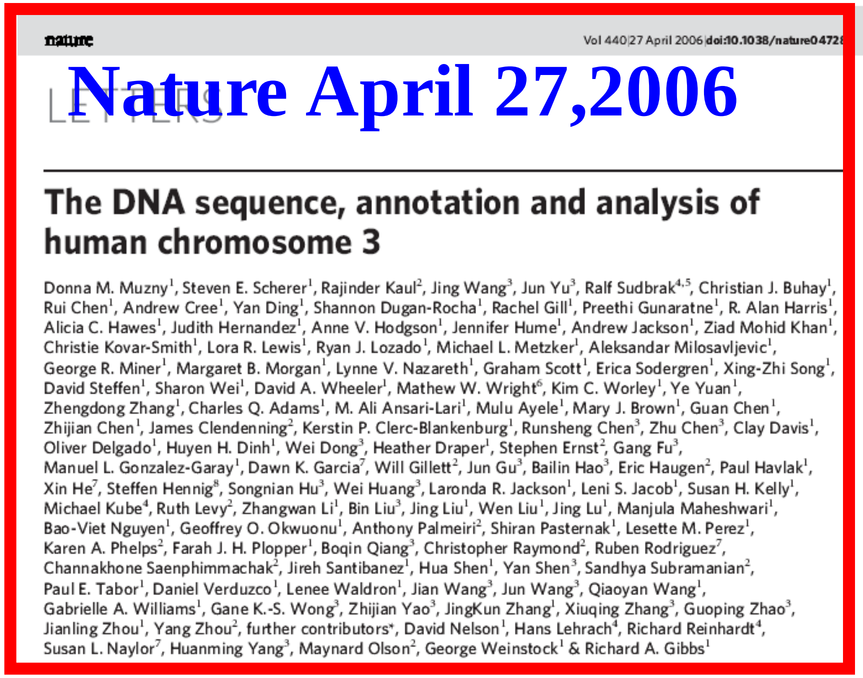
"Owned by All, Done by All, Shared by All"

"I especially salute the Chinese colleagues, who have contributed so much to the international genome effort… and affirmed its common ownership by all humankind."



感谢中国对"保证基因组属于全人类"的贡献

Nature April 27,2006



nature Vol 440|27 April 2006|doi:10.1038/nature0472

LETTERS

The DNA sequence, annotation and analysis of human chromosome 3

Donna M. Muzny[1], Steven E. Scherer[1], Rajinder Kaul[2], Jing Wang[3], Jun Yu[3], Ralf Sudbrak[4,5], Christian J. Buhay[1], Rui Chen[1], Andrew Cree[1], Yan Ding[1], Shannon Dugan-Rocha[1], Rachel Gill[1], Preethi Gunaratne[1], R. Alan Harris[1], Alicia C. Hawes[1], Judith Hernandez[1], Anne V. Hodgson[1], Jennifer Hume[1], Andrew Jackson[1], Ziad Mohid Khan[1], Christie Kovar-Smith[1], Lora R. Lewis[1], Ryan J. Lozado[1], Michael L. Metzker[1], Aleksandar Milosavljevic[1], George R. Miner[1], Margaret B. Morgan[1], Lynne V. Nazareth[1], Graham Scott[1], Erica Sodergren[1], Xing-Zhi Song[1], David Steffen[1], Sharon Wei[1], David A. Wheeler[1], Mathew W. Wright[6], Kim C. Worley[1], Ye Yuan[1], Zhengdong Zhang[1], Charles Q. Adams[1], M. Ali Ansari-Lari[1], Mulu Ayele[1], Mary J. Brown[1], Guan Chen[1], Zhijian Chen[1], James Clendenning[2], Kerstin P. Clerc-Blankenburg[1], Runsheng Chen[3], Zhu Chen[3], Clay Davis[1], Oliver Delgado[1], Huyen H. Dinh[1], Wei Dong[3], Heather Draper[1], Stephen Ernst[2], Gang Fu[3], Manuel L. Gonzalez-Garay[1], Dawn K. Garcia[7], Will Gillett[2], Jun Gu[3], Bailin Hao[3], Eric Haugen[2], Paul Havlak[1], Xin He[7], Steffen Hennig[8], Songnian Hu[3], Wei Huang[3], Laronda R. Jackson[1], Leni S. Jacob[1], Susan H. Kelly[1], Michael Kube[4], Ruth Levy[2], Zhangwan Li[1], Bin Liu[3], Jing Liu[1], Wen Liu[1], Jing Lu[1], Manjula Maheshwari[1], Bao-Viet Nguyen[1], Geoffrey O. Okwuonu[1], Anthony Palmeiri[2], Shiran Pasternak[1], Lesette M. Perez[1], Karen A. Phelps[2], Farah J. H. Plopper[1], Boqin Qiang[3], Christopher Raymond[2], Ruben Rodriguez[7], Channakhone Saenphimmachak[2], Jireh Santibanez[1], Hua Shen[1], Yan Shen[3], Sandhya Subramanian[2], Paul E. Tabor[1], Daniel Verduzco[1], Lenee Waldron[1], Jian Wang[3], Jun Wang[3], Qiaoyan Wang[1], Gabrielle A. Williams[1], Gane K.-S. Wong[3], Zhijian Yao[3], JingKun Zhang[1], Xiuqing Zhang[3], Guoping Zhao[3], Jianling Zhou[1], Yang Zhou[2], further contributors*, David Nelson[1], Hans Lehrach[4], Richard Reinhardt[4], Susan L. Naylor[7], Huanming Yang[3], Maynard Olson[2], George Weinstock[1] & Richard A. Gibbs[1]

News Release for Completion of Chromosome 3

"I salute all our friends and colleagues for their support of free data-sharing under the spirit of the Human Genome Project that is '*owned by all, done by all and shared by all*'", said Yang.

Chromosome 3 Consortium

“The HGP Spirit”

“Needed by All (共需),

Owned by All (共有),

Done by All (共为),

Shared by All (共享)!”

“The HGP Spirit”

“Needed by All (共需),

Owned by All (共有),

Done by All (共为),

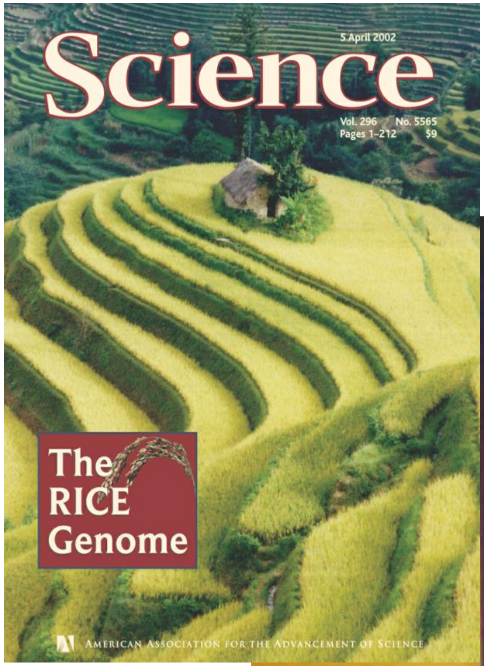
Shared by All (共享)!”

The story continued with the rice genome data

Now it is China's *turn*

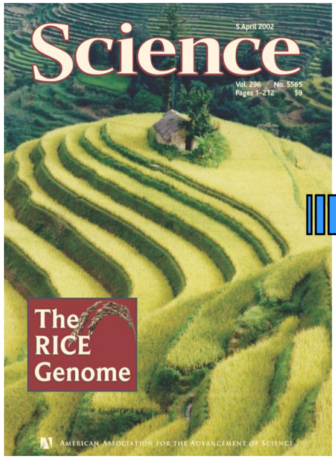
or *in return* to the world

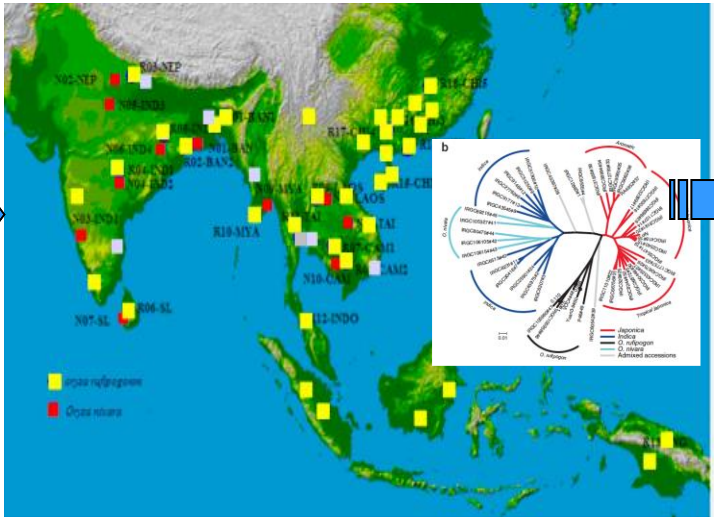
5 April, 2002, Beijing



nature biotechnology 30:105-1011, 2012

Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes





3000 strains sequenced

IRG Traditional Germplasm

100,000 cultivated accessions

3000 Rice Genome Sequences Made Publicly Available on World Hunger Day

3000株水稻基因组序列于“世界饥饿日”公开发布

（2014-05-28）

The open-access, open-data journal *GigaScience* (published by BGI) announces today the publication of the genome sequences of 3000 rice strains along with the release of this entire dataset. The publication and release of this enormous data set (which quadruples the current amount of publicly available rice sequence data) coincides with World Hunger Day to highlight one of the primary goals of this project— to develop resources that will aid in improving global food security, especially in the poorest areas of the world.

This work is the completion of stage one of the 3000 Rice Genomes Project, a collaborative effort made up of the Chinese Academy of Agricultural Sciences (CAAS), the International Rice Research Institute (IRRI), and BGI, and is funded by the Bill and Melinda Gates Foundation and the Chinese Ministry of Science and Technology.

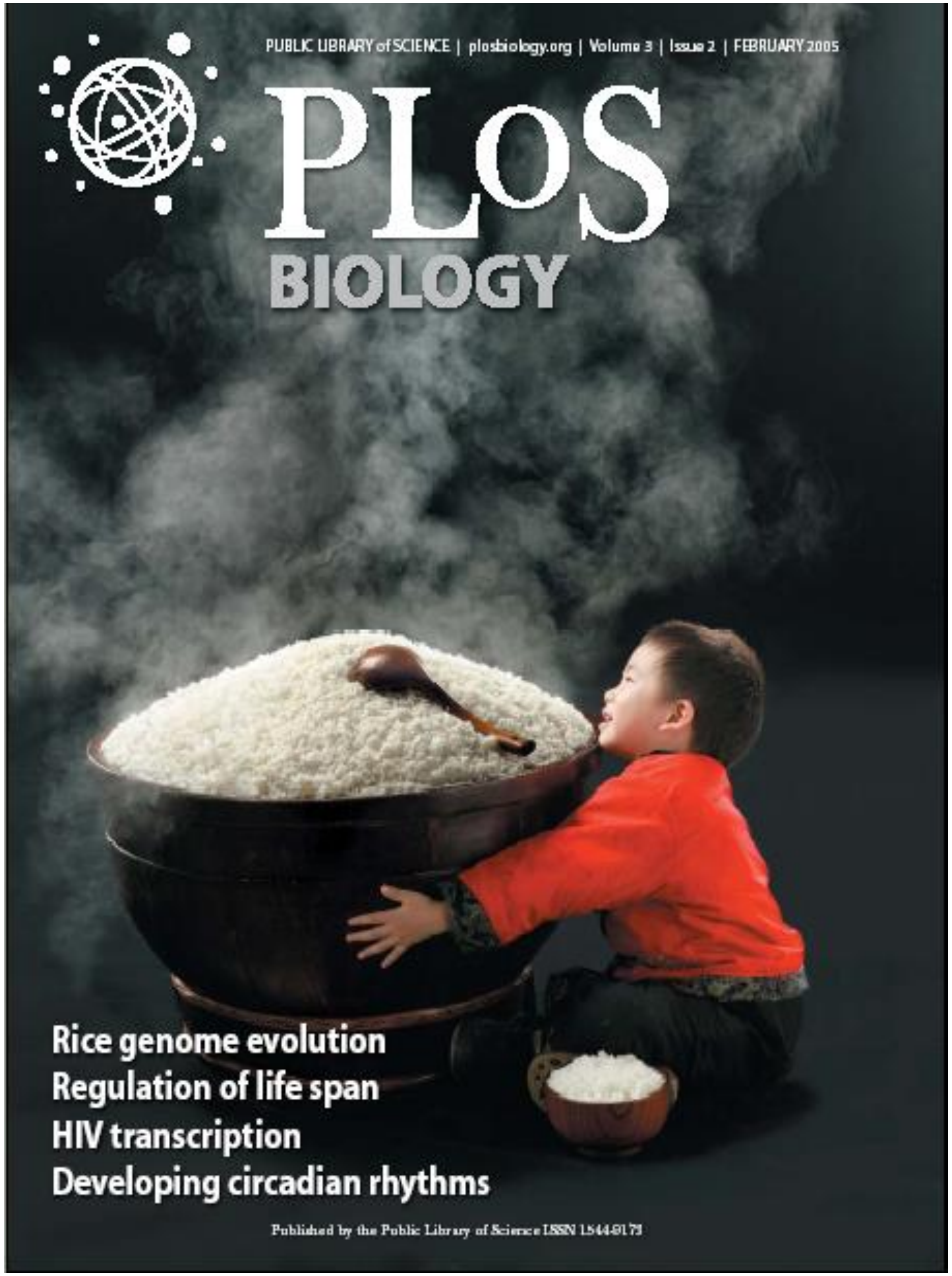
The Sciensts (June, 2014)

Members of the 3,000 Rice Genomes Project last month (May 28) delivered on their promise to make public thegenomic sequences of 3,000 rice varieties from 89 countries. Their initial analysis of the monumental dataset was published in*GigaScience.*

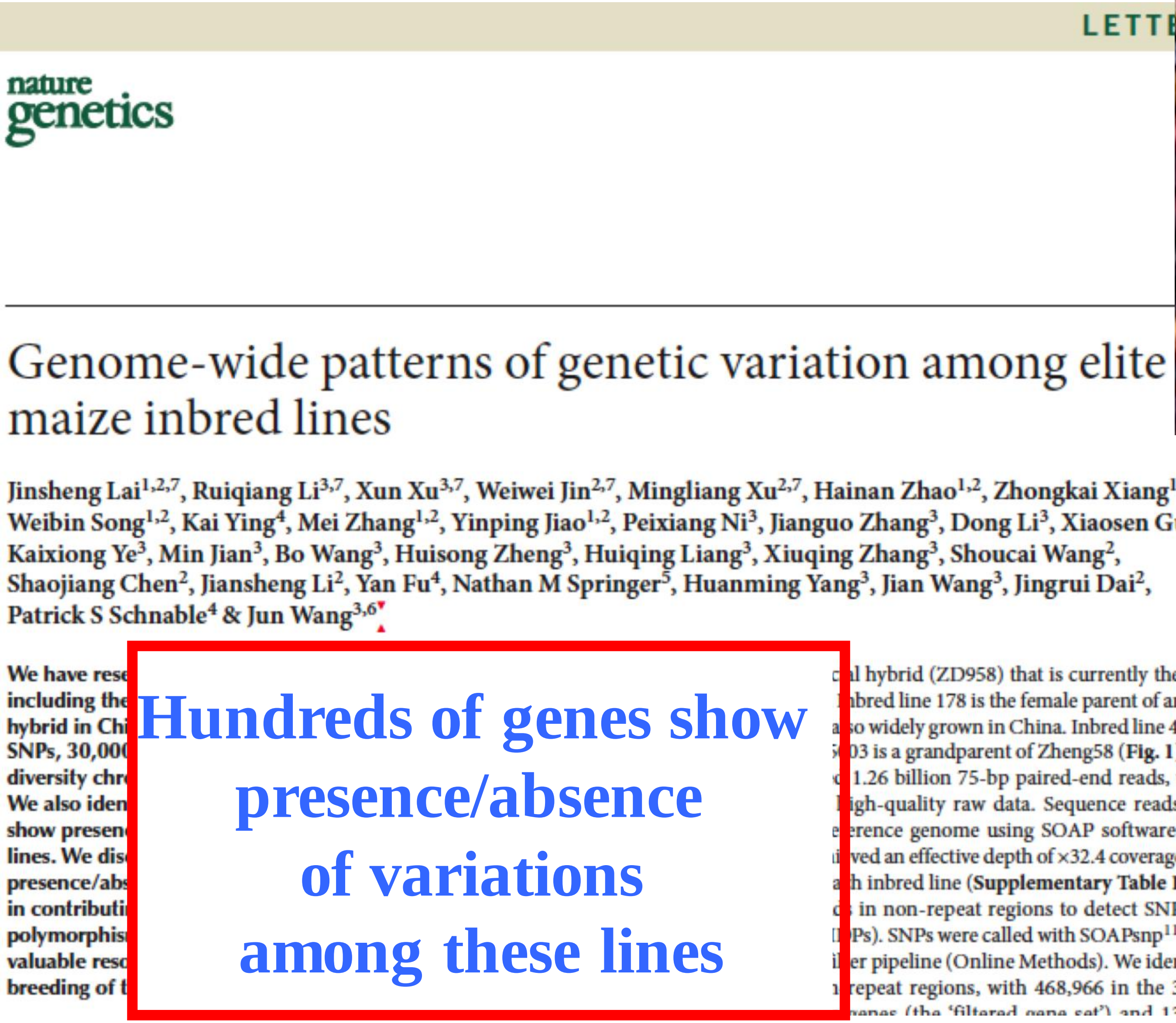
2014年5月28日，中国农业科学院、国际水稻研究所、华大基因联合开展的“3000株水稻基因组项目”在 GigaScience 上正式发表 3000株水稻基因组序列，所有数据以可引用形式在该杂志的数据库 GigaDB 中公开。该项目产生的数据是目前已公开水稻序列数据量的四倍。在“世界饥饿日”这天发布并公开这庞大的数据集，是为了体现该项目的最主要目标之一，为全球研究人员提供海量的水稻基因序列资源，为改善全球尤其是最穷困地区的粮食安全提供育种资源。

Not only for ourselves

“It is cooked for all who need.”



42: 1027-1030, 2010



LETTE

nature
genetics

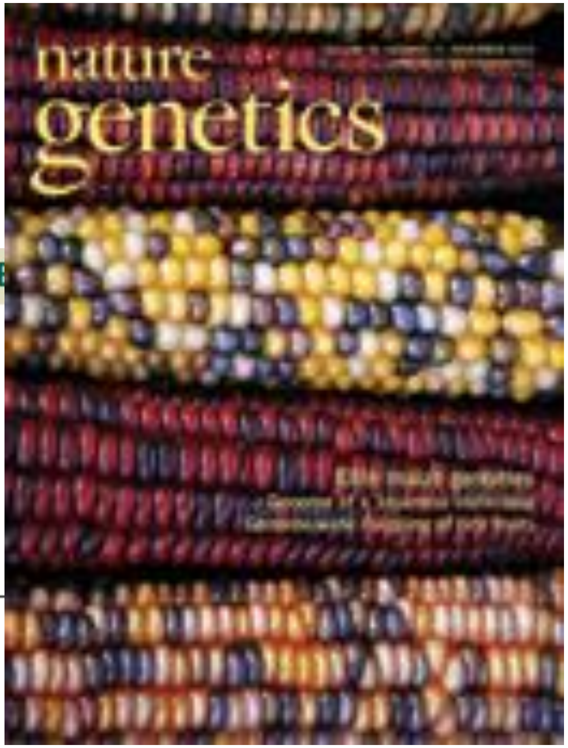
Genome-wide patterns of genetic variation among elite maize inbred lines

Jinsheng Lai[1,2,7], Ruiqiang Li[3,7], Xun Xu[3,7], Weiwei Jin[2,7], Mingliang Xu[2,7], Hainan Zhao[1,2], Zhongkai Xiang[1,2], Weibin Song[1,2], Kai Ying[4], Mei Zhang[1,2], Yinping Jiao[1,2], Peixiang Ni[3], Jianguo Zhang[3], Dong Li[3], Xiaosen Guo[3], Kaixiong Ye[3], Min Jian[3], Bo Wang[3], Huisong Zheng[3], Huiqing Liang[3], Xiuqing Zhang[3], Shoucai Wang[2], Shaojiang Chen[2], Jiansheng Li[2], Yan Fu[4], Nathan M Springer[5], Huanming Yang[3], Jian Wang[3], Jingrui Dai[2], Patrick S Schnable[4] & Jun Wang[3,6]

We have rese
including the
hybrid in Chi
SNPs, 30,000
diversity chr
We also iden
show presen
lines. We dis
presence/abs
in contributi
polymorphis
valuable reso
breeding of t

Hundreds of genes show presence/absence of variations among these lines

al hybrid (ZD958) that is currently the most
nbred line 178 is the female parent of another
so widely grown in China. Inbred line 478 is a
03 is a grandparent of Zheng58 (**Fig. 1**).
1.26 billion 75-bp paired-end reads, which
igh-quality raw data. Sequence reads were
erence genome using SOAP software v2.18
ved an effective depth of ×32.4 coverage, with
h inbred line (**Supplementary Table 1**).
in non-repeat regions to detect SNPs and
Ps). SNPs were called with SOAPsnp[11] using
er pipeline (Online Methods). We identified
repeat regions, with 468,966 in the 32,540



Potato Genome Project

Science Daily, Sept. 29, 2009

OUTLOOK
Alzheimer's disease

nature

THE INTERNATIONAL WEEKLY JOURNAL OF SCIENCE

The DNA sequence of the South American tuber eaten around the world PAGE 189

THE POTATO GENOME

July, 2011

Thanks to a new computer program developed by the Beijing Genomics Institute, the potato genome assembly, which is publicly available on the PGSC website (http://www.potatogenome.net/), covers 95 percent of potato genes.

nature biotechnology

online 15 May 2012

Genome sequence of foxtail millet (*Setaria italica*) provides insights into grass evolution and biofuel potential

Gengyun Zhang[1,2,6], Xin Liu[1,6], Zhiwu Quan[1,2,6], Shifeng Cheng[1,6], Xun Xu[1–3,6], Shengkai Pan[1,6], Min Xie[1], Peng Zeng[1], Zhen Yue[1], Wenliang Wang[1], Ye Tao[1], Chao Bian[1], Changlei Han[1], Qiuju Xia[1,2], Xiaohua Peng[1,2], Rui Cao[1], Xinhua Yang[1], Dongliang Zhan[1], Jingchu Hu[1], Yinxin Zhang[1,2], Henan Li[1,2], Hua Li[1,2], Ning Li[1,2], Junyi Wang[1], Chanchan Wang[1,2], Renyi Wang[1,2], Tao Guo[1,2], Yanjie Cai[1,2], Chengzhang Liu[1,2], Haitao Xiang[1], Qiuxiang Shi[1,2], Ping Huang[1,2], Qingchun Chen[1,2], Yingrui Li[1], Jun Wang[1,4], Zhihai Zhao[5] & Jian Wang[1,2]

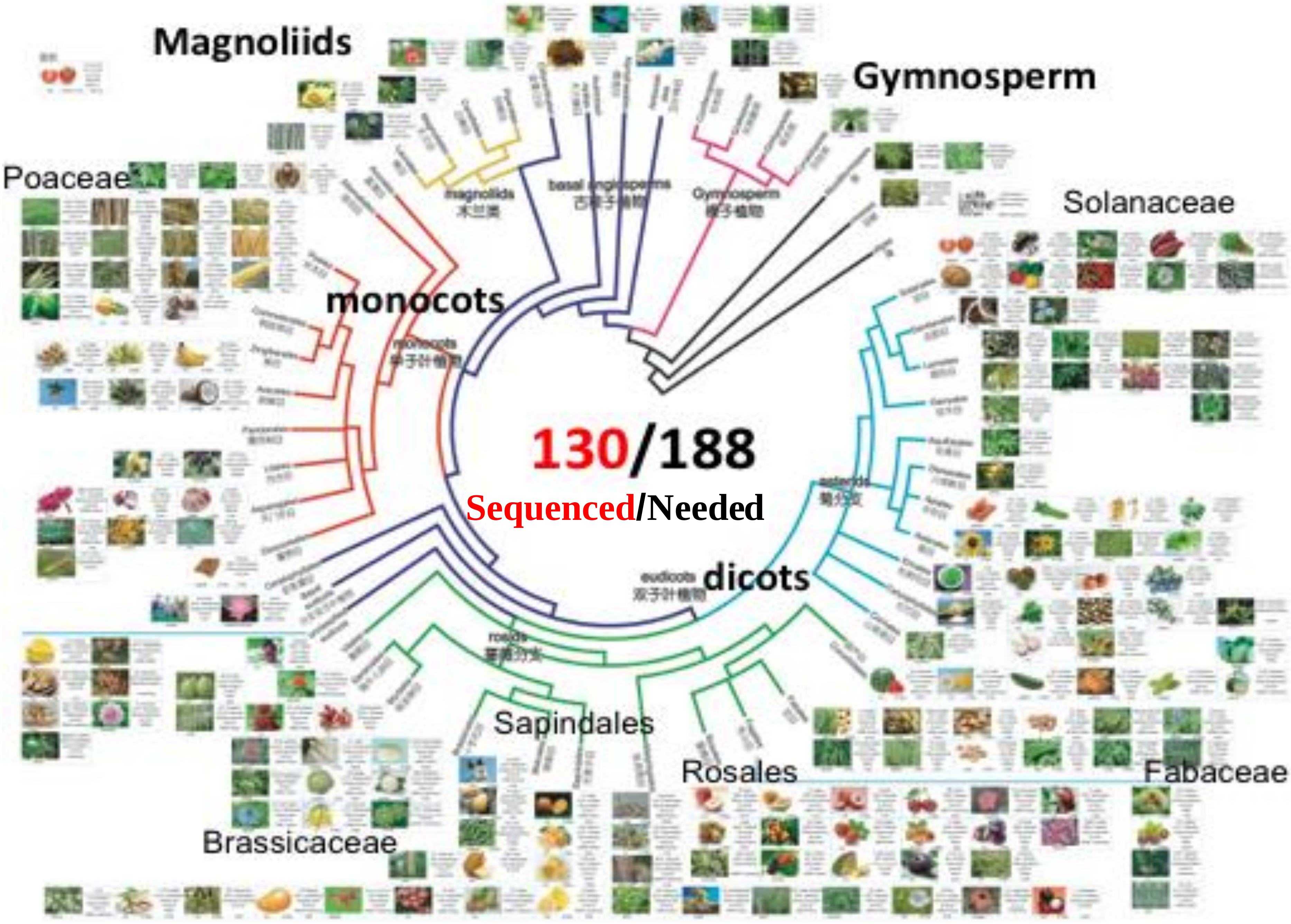
常规谷：600斤/亩

Normal Millet : 4500kg/hectare

杂交谷：1600斤/亩

Hybrid Millet : 12000kg/hectare

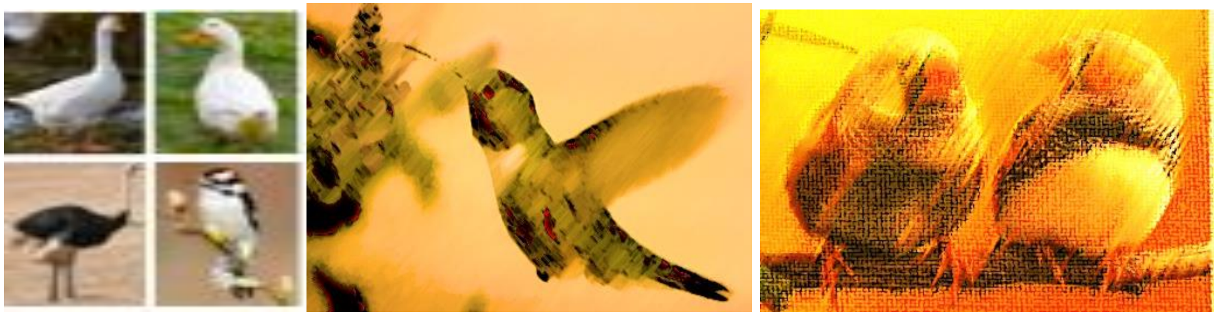
Sept. 13, 2015



130/188

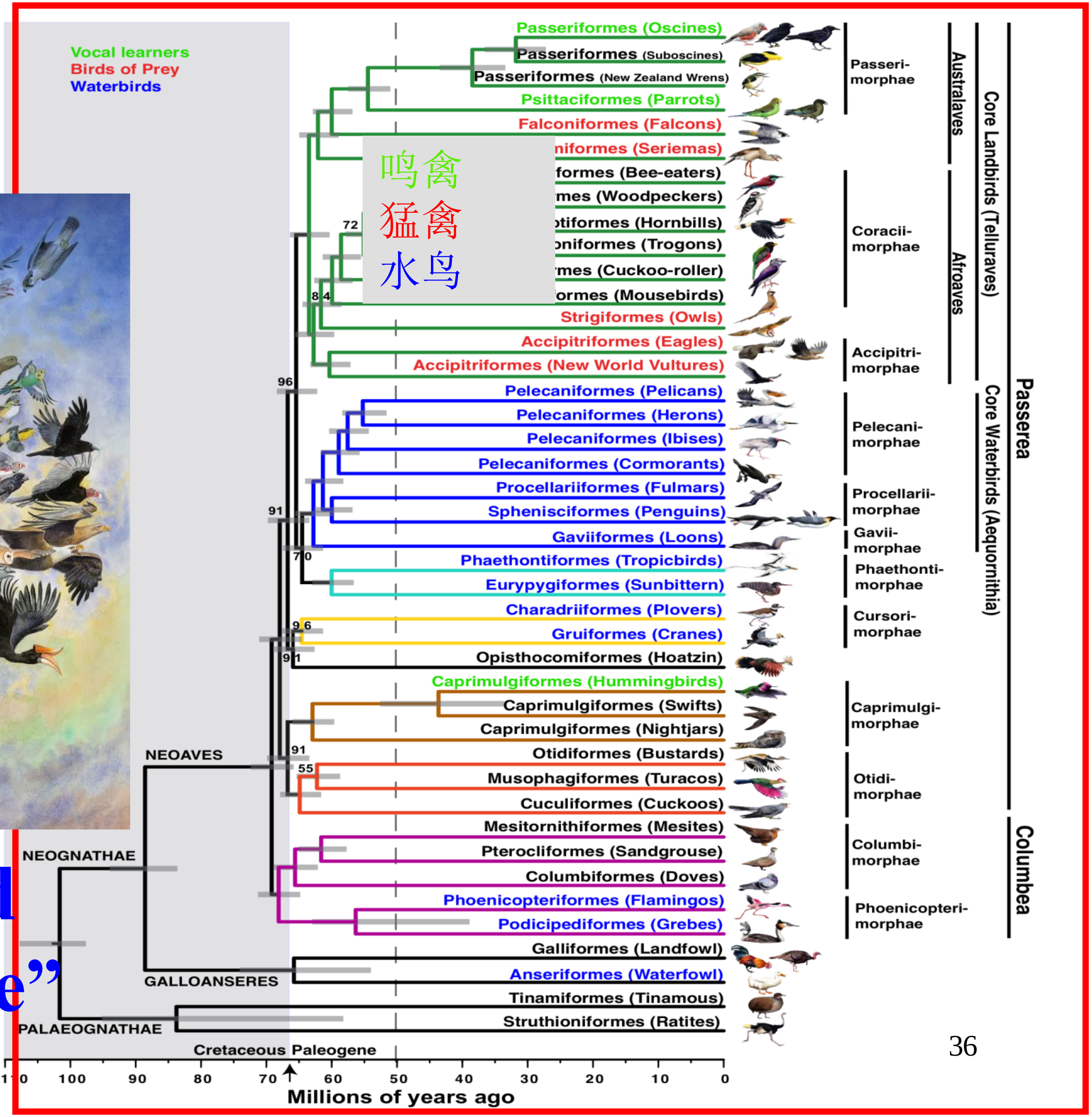
Sequenced/Needed

48 Representative Classes of Birds



To turn all samples into data.

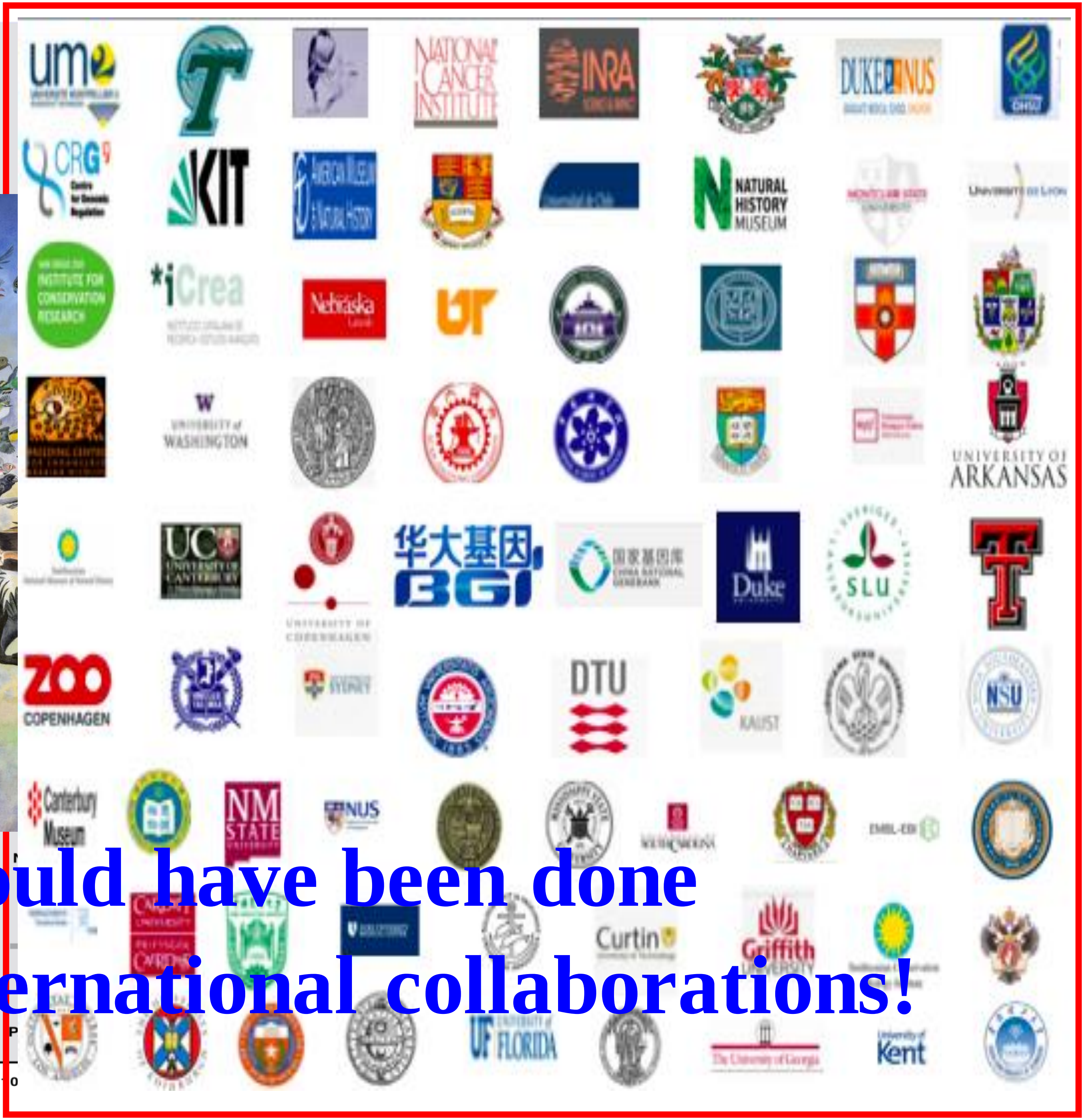
鸟类"生命之树"



鸣禽
猛禽
水鸟

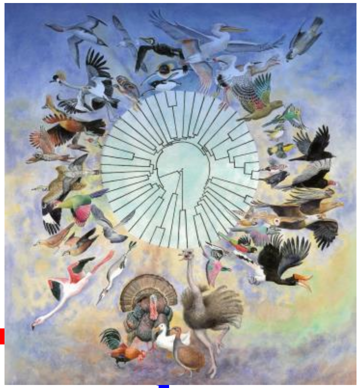
A digitalized "Tree of Life"

鸟类"生命之树"

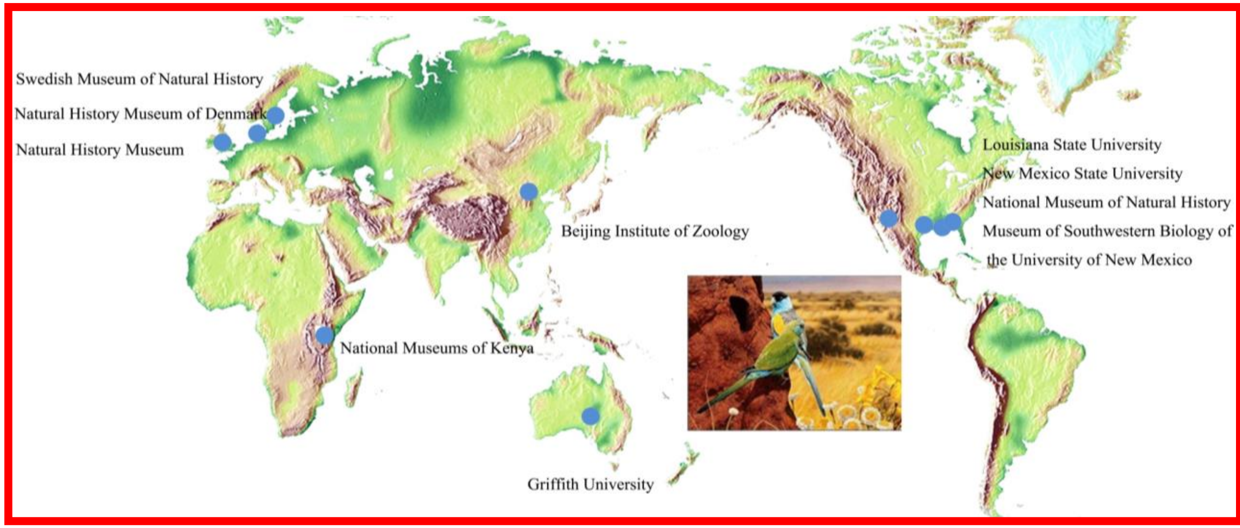


Nothing would have been done without international collaborations!

B10K - Toward decoding all bird genomes



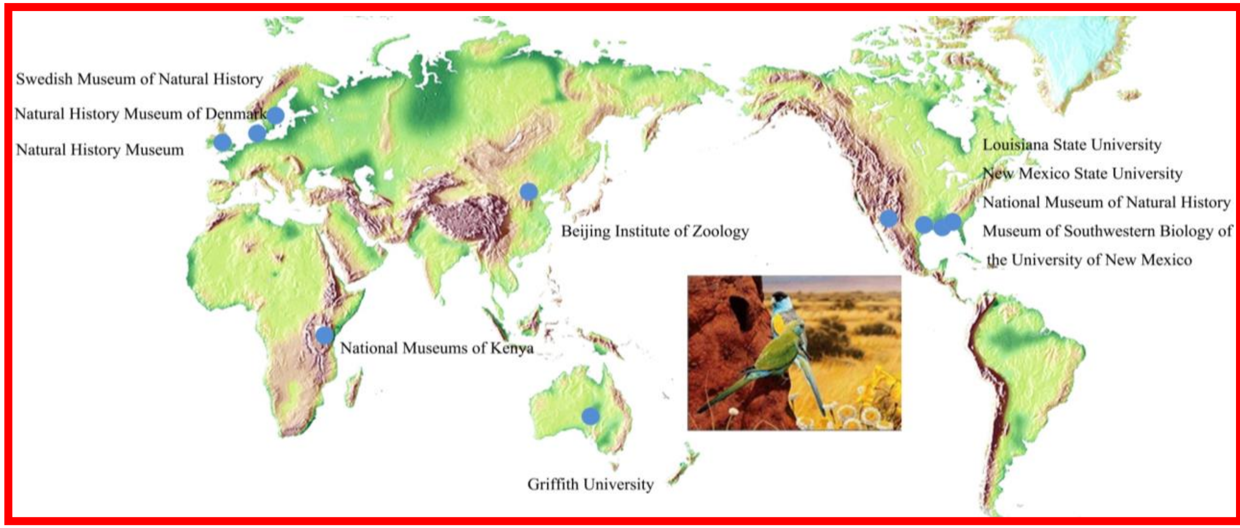
(3rd June, 2015) Today we formally announce the launch of the Bird 10,000 genomes (B10K) project (http://b10k.genomics.cn/), an initiative to generate representative draft genome sequences from all extant bird species within the next five years. …The announcement of the B10K project is published online today in Nature.



V10K - Toward “sequencing every(living)thing on the planet

(23rd Oct, 2015) Today, G10K consortium and BGI announced a new collaboration plan to do the genome sequencing for 10,000 vertebrates.

The project will also include a few hundred marine invertebrate species to be organized by Global Invertebrate Genome Alliance (GIGA).



Toward "sequencing everybody in the world"

"人人基因组"

The 10-100K British Genomes Project
The 1% Danes' Genomes Project

Obama Announces Efforts To Analyze DNA From 1 Million People

Reuters | By Toni Clarke and Sharon Begley

Posted: 01/30/2015 1:07 pm EST | Updated: 01/30/2015 1:59 pm EST

To sequence everybody in the world

“人人基因组”

The 1 M Chinese Genomes Project

G1B Project

A 10 years' proposal to sequence 1 billion people for all in the whole world

"人人基因组"

Human -Omes Sequencing (- Oct. 2015)

Whole Genomes: 41,000

Whole Exoms: 85,000

Gene Testing for deafness: 480,000

NIPT for Tri-21: 740,000

Publications by BGI and Its Partners

(related to new-generation sequencing technology)

(Nov. 2008 – June 2015)

Journal	Impact Factor (2013)	2008	2009	2010	2011	2012	2013	2014	2015	Total
Science	33.611		1	3	3	4	2	11	1	25
Science Translational Medicine	15.843						1			1
Nature	41.456	1	2	4	5	5	4	5	2	28
Nature Genetics	29.352		1	3	5	13	10	7	3	42
Nature Communications										43
Nature Biotechnology										19
Nature Reviews Drug Discovery										1
Nature Medicine										1
Nature Methods										4
Nature Reviews Genetics										1
Nature Reviews Microbiology										1
Cell	32.242							2		5
Cell Host Microbe	12.328								1	1
Cell Stem Cell	22.268							2		3
NEJM	55.873									1
Sum		1	6	12	21	32	36	50	18	176

Flowers of collaboration!

Never forget:

WE = All collaborators

They are ever our teachers & pioneers

ature
iotechnology

ANALYSIS

doi:10.1038/nature08696

ARTICLES

ARTICLES

Building the sequen
pan-genome

Ruiqiang Li[1,2,7], Yingrui Li[1,7], Hancheng Zheng[1,3,7], R
Yuanyuan Ren[1], Geng Tian[1], Jinxiang Li[1], Guangyu Z
Dongfang Li[1,6], Hongzhi Cao[1,6], Xueda Hu[1], H
Lars Bolund[1,5], Karsten Kristiansen[1,2], Huanmi

The sequence and *de novo* a
giant panda genome

Ruiqiang Li[1,2*], Wei Fan[1*], Geng Tian[1,3*], Hongmei Zhu[1*], Lin He[4,5*], Jing
Bo Li[1], Yinqi Bai[1], Zhihe Zhang[8], Yaping Zhang[6], Wen Wang[6], Jun Li[1], Fuwen

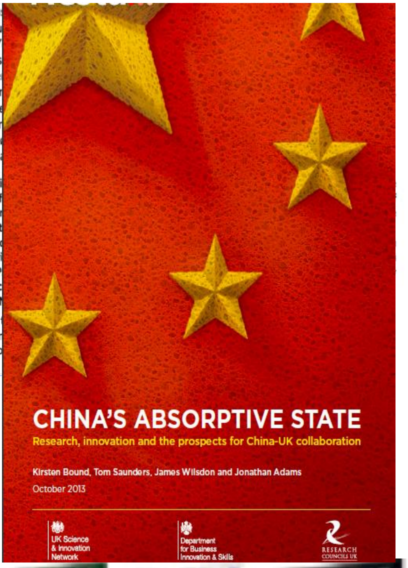
The diploid genome se
individual

Jun Wang[1,2,3,4*], Wei Wang[1,3*], Ruiqiang Li[1,3,4*], Yingrui Li
, Jun Li[1], Juanbin Zhang[1], Yiran Guo[1,7], Binx
Zhenglin Du[1], Dong Li[1], Yiqing Zhao[1,7], Yuji
Michael Inouye[8], John Pool[9], Xin Yi[1,7], Jing Z

Science express Report

Ancient human genome sequence of an
extinct Palaeo-Eskimo

Morten Rasmussen[1,2*], Yingrui Li[2,3*], Stinu
Ida Moltke[4], Mait Metspalu[5], Ene Metspalu
Kasper Nielsen[7], M. Thomas P. Gilbert[1,2], Y
Hanne Munkholm Kamp[1,4], Andrew S. Wils
Eline D. Lorenzen[1], Jonas Binladen[1], Xiaose
Minfeng Chen[2,3], Ludovic Orlando[13], Karsten



CHINA'S ABSORPTIVE STATE

Research, innovation and the prospects for China-UK collaboration

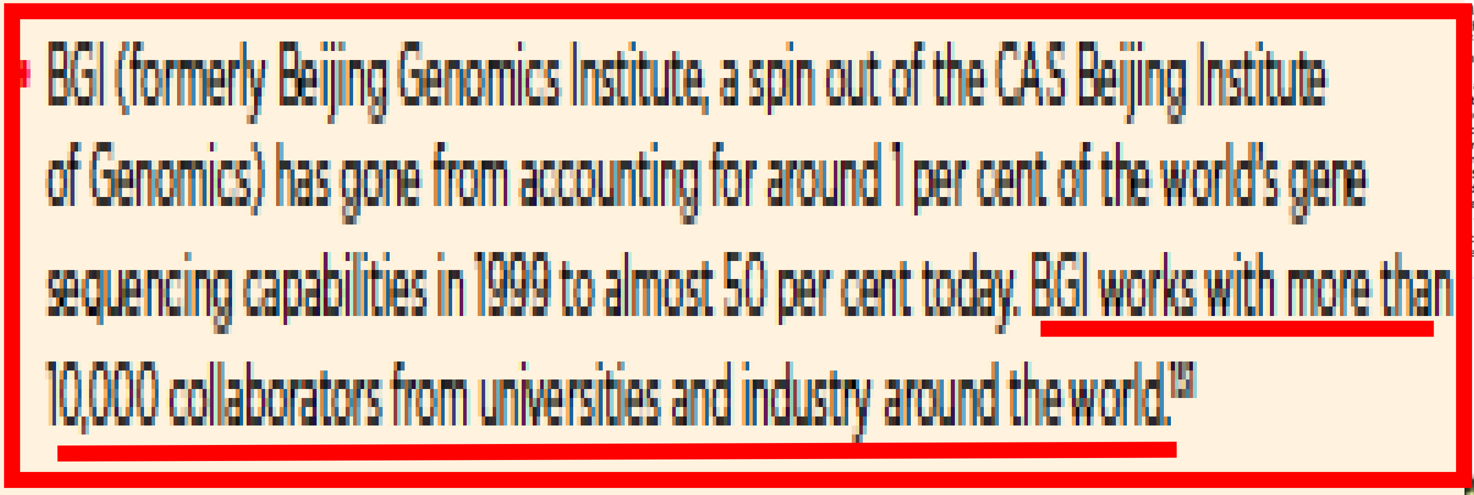
Kirsten Bound, Tom Saunders, James Wilsdon and Jonathan Adams

October 2013

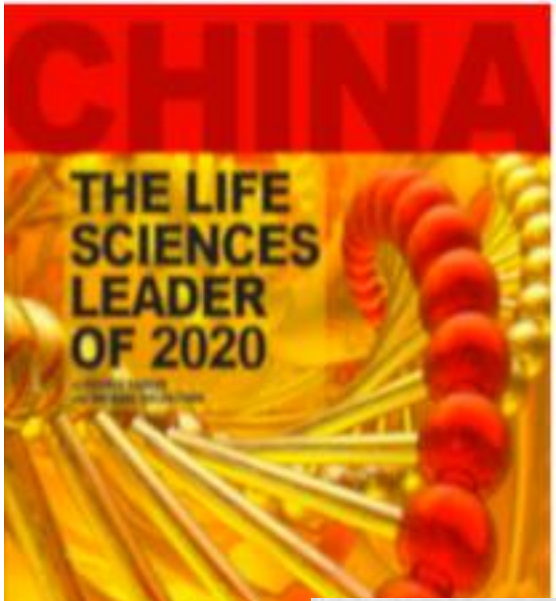
UK Science & Innovation Network

Department for Business Innovation & Skills

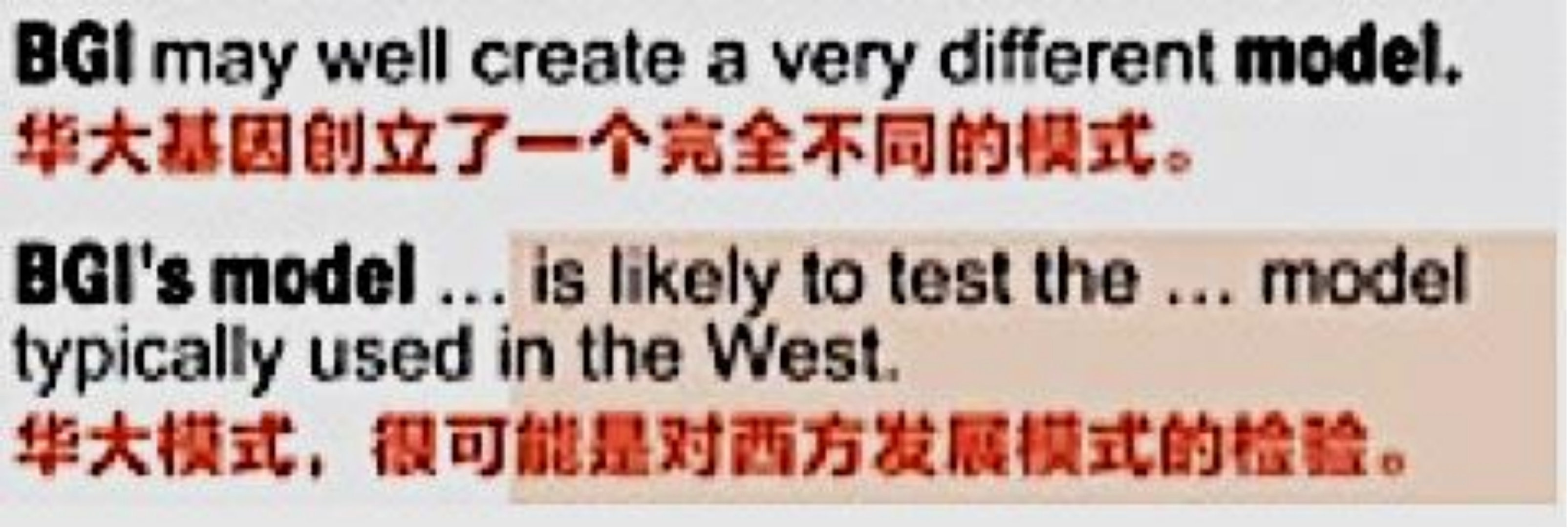
Research Councils UK



- BGI (formerly Beijing Genomics Institute, a spin out of the CAS Beijing Institute of Genomics) has gone from accounting for around 1 per cent of the world's gene sequencing capabilities in 1999 to almost 50 per cent today. BGI works with more than 10,000 collaborators from universities and industry around the world.[19]



Nothing would have been done without international collaborations!



BGI may well create a very different **model.**
华大基因创立了一个完全不同的模式。

BGI's model ... is likely to test the ... model typically used in the West.
华大模式，很可能是对西方发展模式的检验。

15 Years Later

EAGLES: European Actions for Global Life Sciences

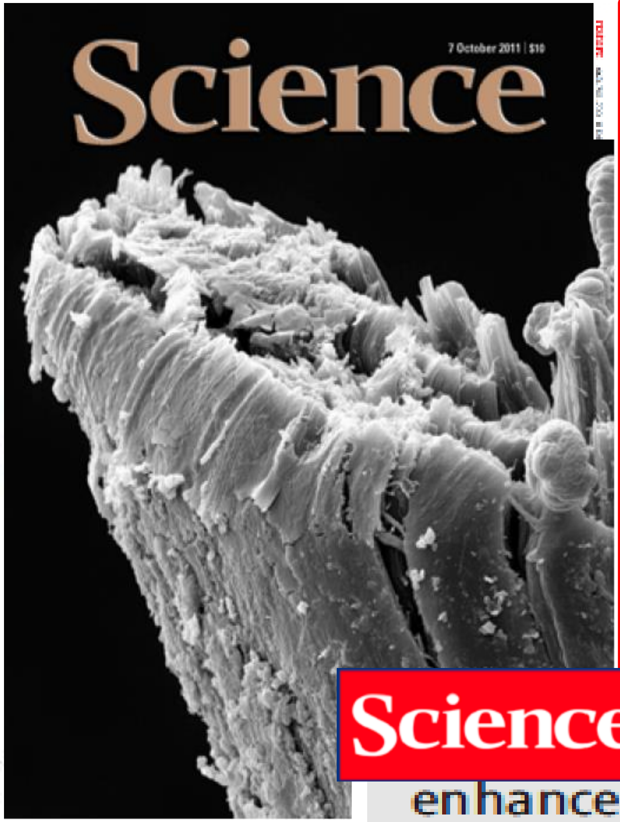
To raise the banner of

Science

and

Humanity!

Trace DNA Sequencing



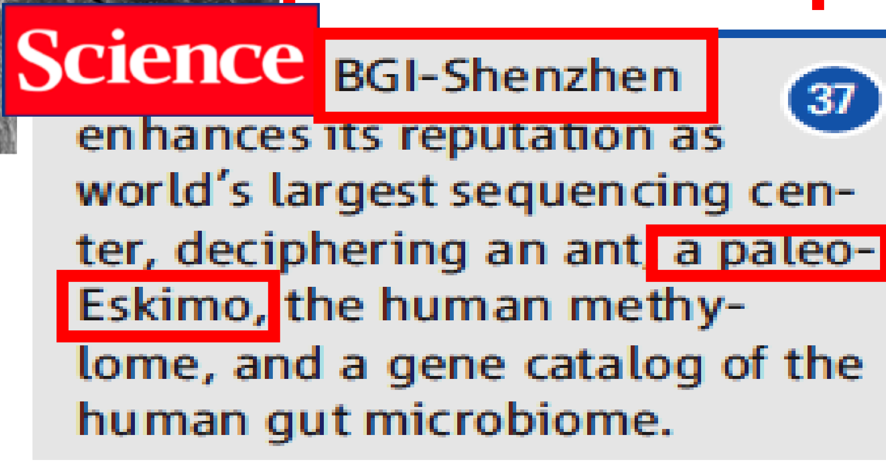
nature

online 26 June, 2013

An early Middle Pleistocene horse (560-780 kyr BP)

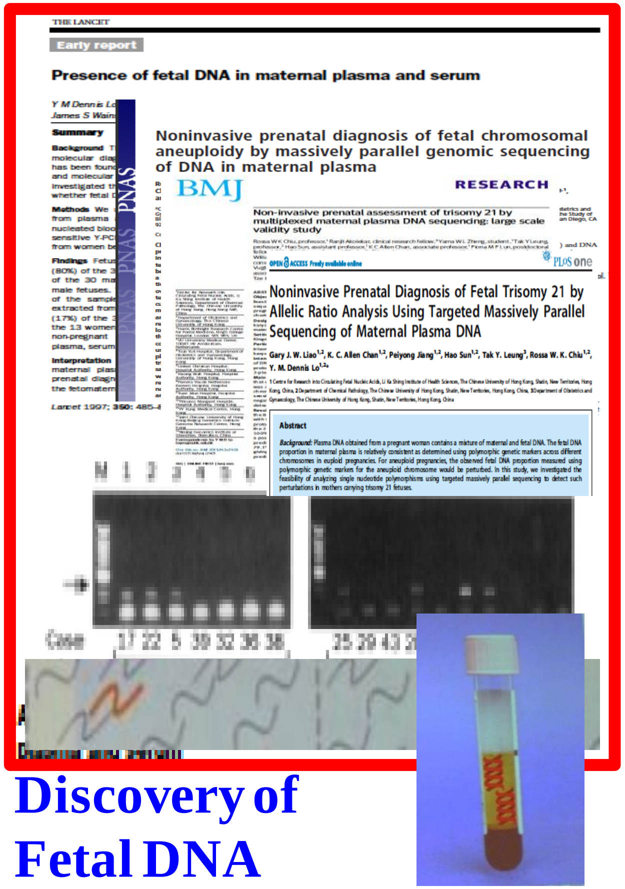
微量DNA基因组分析

(Ancient DNA Analysis)



Science BGI-Shenzhen 37

enhances its reputation as world's largest sequencing center, deciphering an ant, a paleo-Eskimo, the human methylome, and a gene catalog of the human gut microbiome.



THE LANCET

Early report

Presence of fetal DNA in maternal plasma and serum

Noninvasive prenatal diagnosis of fetal chromosomal aneuploidy by massively parallel genomic sequencing of DNA in maternal plasma

BMJ RESEARCH

Non-invasive prenatal assessment of trisomy 21 by multiplexed maternal plasma DNA sequencing: large scale validity study

OPEN ACCESS Freely available online PLoS one

Noninvasive Prenatal Diagnosis of Fetal Trisomy 21 by Allelic Ratio Analysis Using Targeted Massively Parallel Sequencing of Maternal Plasma DNA

Gary J. W. Liao[1,2], K. C. Allen Chan[1,2], Peiyong Jiang[1,2], Hao Sun[1,2], Tak Y. Leung[3], Rossa W. K. Chiu[1,2], Y. M. Dennis Lo[1,2*]

1 Centre for Research into Circulating Fetal Nucleic Acids, Li Ka Shing Institute of Health Sciences, The Chinese University of Hong Kong, Shatin, New Territories, Hong Kong, China, 2 Department of Chemical Pathology, The Chinese University of Hong Kong, Shatin, New Territories, Hong Kong, China, 3 Department of Obstetrics and Gynaecology, The Chinese University of Hong Kong, Shatin, New Territories, Hong Kong, China

Abstract

Background: Plasma DNA obtained from a pregnant woman contains a mixture of maternal and fetal DNA. The fetal DNA proportion in maternal plasma is relatively consistent as determined using polymorphic genetic markers across different chromosomes in euploid pregnancies. For aneuploid pregnancies, the observed fetal DNA proportion measured using polymorphic genetic markers for the aneuploid chromosome would be perturbed. In this study, we investigated the feasibility of analyzing single nucleotide polymorphisms using targeted massively parallel sequencing to detect such perturbations in mothers carrying trisomy 21 fetuses.

Discovery of
Fetal DNA
in Mother's Blood

+

nature

CLIMATE RESEARCH
'Next generation' scenarios

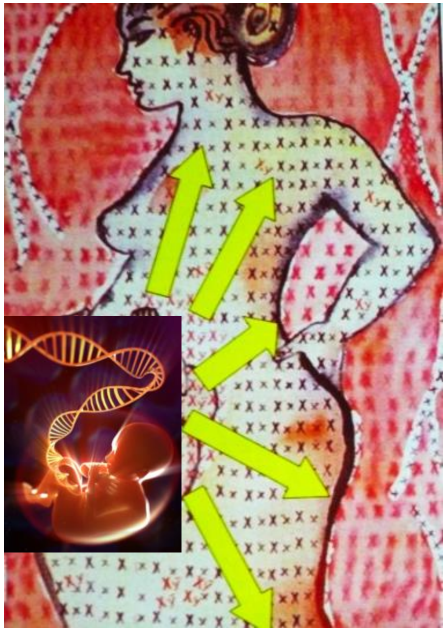
SOUTHERN AFRICA
Audit of post-apartheid science

BENZODIAZEPINES
Neural basis of addiction

THE ANCIENT HUMAN GENOME
Strand of hair yields 4,000-year-old DNA sequence

Science

Large Scale
High Throughout
Sequencing



NIPDT

(Non-Invasive
Prenatal DNA Testing)

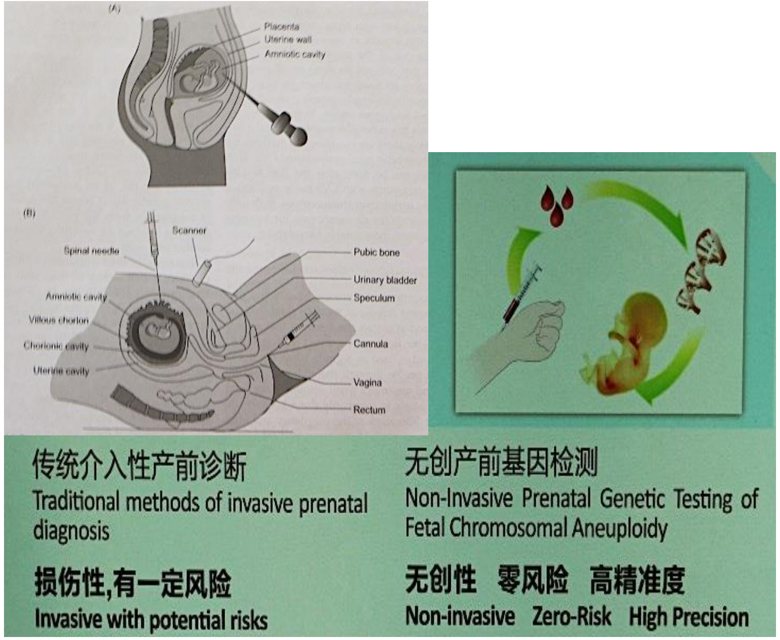
Non-Invasive Prenatal Testings

By sequencing

As of Oct., 2015:

Total cases: >700,000

Detected cases: >3,000

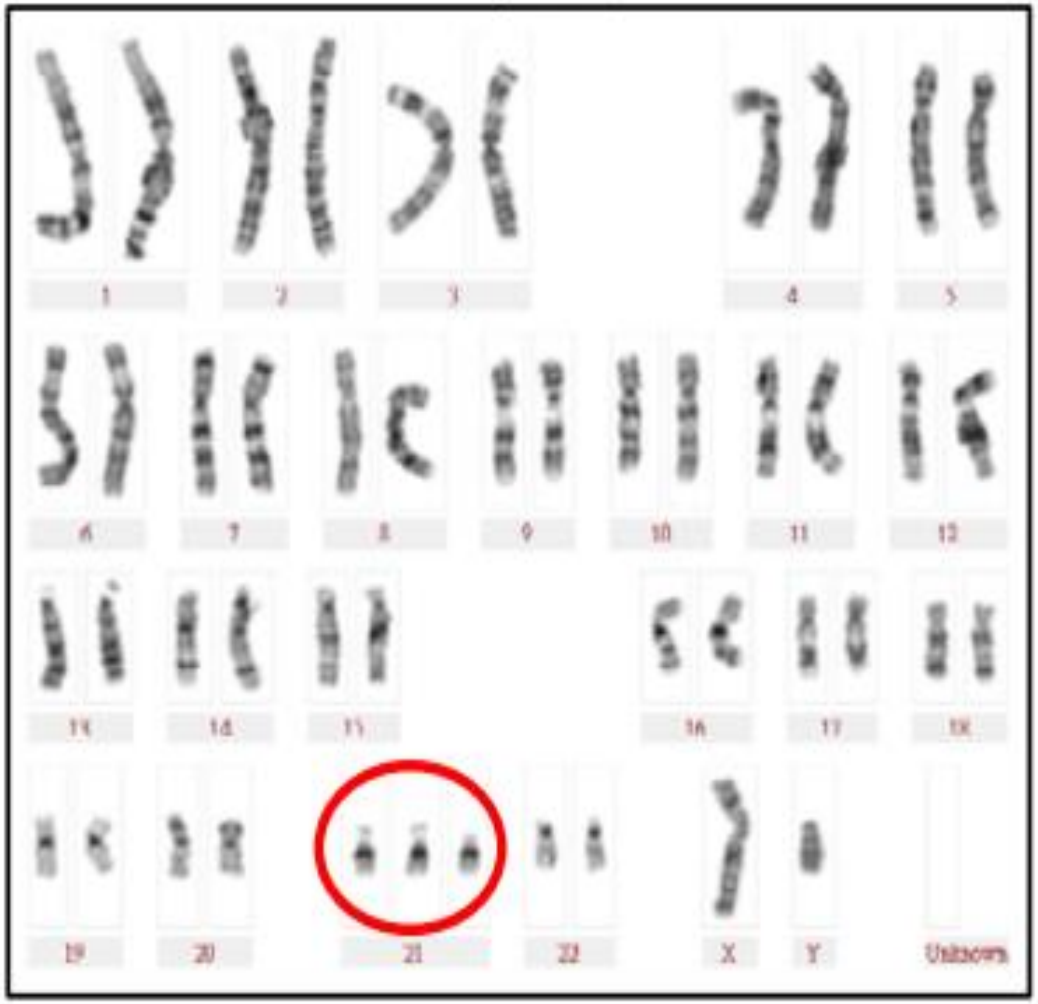


传统介入性产前诊断
Traditional methods of invasive prenatal diagnosis

损伤性,有一定风险
Invasive with potential risks

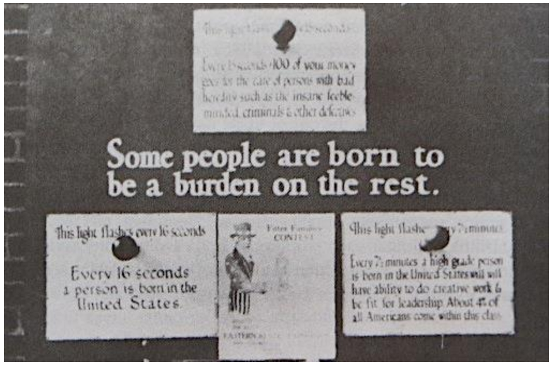
无创产前基因检测
Non-Invasive Prenatal Genetic Testing of Fetal Chromosomal Aneuploidy

无创性 零风险 高精准度
Non-invasive Zero-Risk High Precision



Down Syndrome

Raise the Banner of Science & Humanity!



This light flashes every 15 seconds

Every 15 seconds $100 of your money goes for the care of persons with bad heredity such as the insane feeble-minded, criminals & other defectives

Some people are born to be a burden on the rest.

This light flashes every 16 seconds

Every 16 seconds a person is born in the United States.

Fitter Families CONTEST

This light flashes every 7½ minutes

Every 7½ minutes a high grade person is born in the United States who will have ability to do creative work & be fit for leadership. About 4% of all Americans come within this class.

Genomics has never provided any evidences for Eugenics!

We are all equal!

“Life Sciences for All” in the 21st Century

Humanity
Ethics
Legal
Public Relationship/Policy Making
Culture
Economy/Education
Safety/Security
Society

HELPCESS Issues

(from ELSI to HELPCESS issues)

“Science & Humanity!”

Confidence of Science

is

Confidence of Humanity!

“… by All!”

“By All” is to share with all!

“Needed by All!”

We are faced with the same challenges!

“Needed/demanded by All!”

Global/Social demands
are the propellers of science,

and scientific innovations are the generators of new demands.

We have the same dreams for

a better future of all!

“Owned by All!”

We are living in the same world!

We own the same opportunities
to develop!

“Done by All!”

To share is to share the opportunities

to build confidence of science,

to learn how to do science,

to improve ourselves and

to develop ourselves!

“Done by All!”

To share is to share

the equal partnership and

the equal “rights to say”

together with the developing part

of the world!

“Done by All!”

To share is to share the opportunity and the future!

“Science & Future!”

Confidence of Science

is

Confidence of Future!

Confident of the brilliant

Future of Man

Needed by All,
Owned by All,
Done by All,
Shared by All!

BGI’s Missions

To share what we have with all others.

To work together with those to do something
they want but are unable to do.

and those who are better than us
to learn from them while collaborating

To work together with those to do something
bigger, faster, cheaper, and better.

To promote global genomics!

“Science & Humanity!”

Confidence of Science

is

Confidence of

the Younger Generations!

Give me!

"Give me those who are younger,

Give me those who are smarter,

Give me those who are more devoted!

I am responsible for taking care of
all the troubles you would make,

I am obligated to
find right teachers for you."

Confidence of Science!

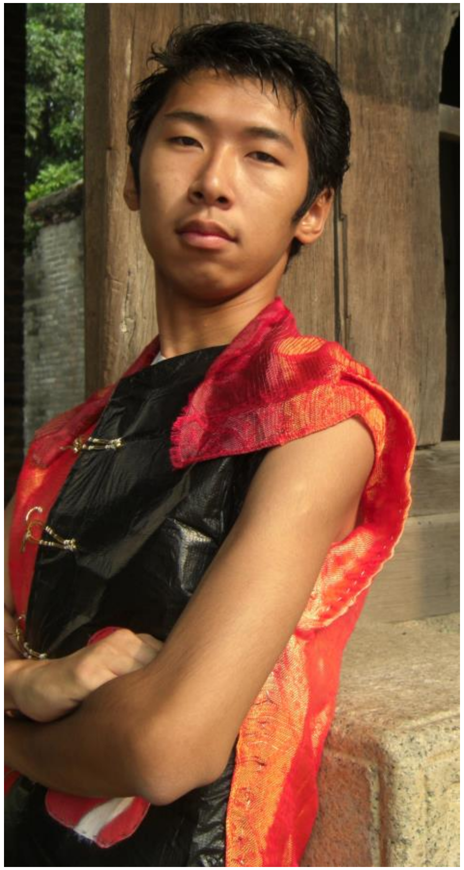
nature

www.nature.com/nature Vol 464 | Issue no. 7285 | 4 March 2010

" … these BGI researchers are smart, confident and, for their age, tremendously experienced."

If Nature's interviews are anything to go by, these BGI researchers are smart, confident and, for their age, tremendously experienced.

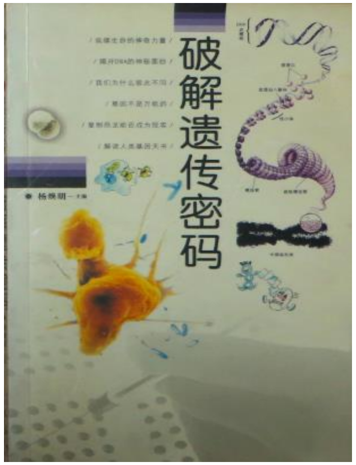
The 3rd/4th Generations



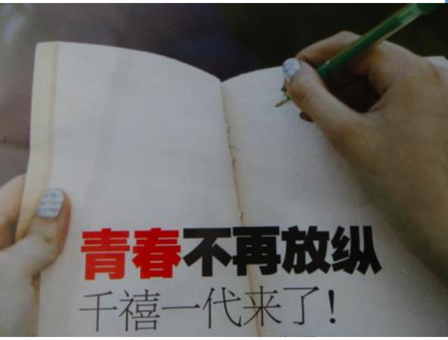
宋海华副省长给华工三学子罗锐邦 (右二)
等人颁发2009年度“广东十大新闻人物”奖

We are
very confident of
the “post-1980” & “post-1990”

Education is for the day after tomorrow!



"Gene should also be taught to the kids!"



I'm coming!

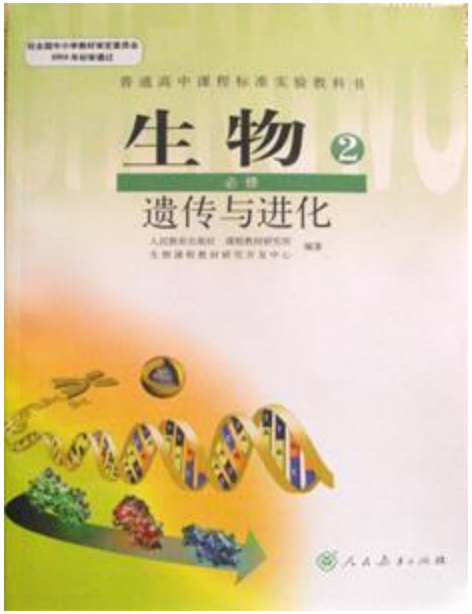
Genes in the textbooks for school kids

普通高中课程标准实验教科书

生物

选修3

现代生物科技专题

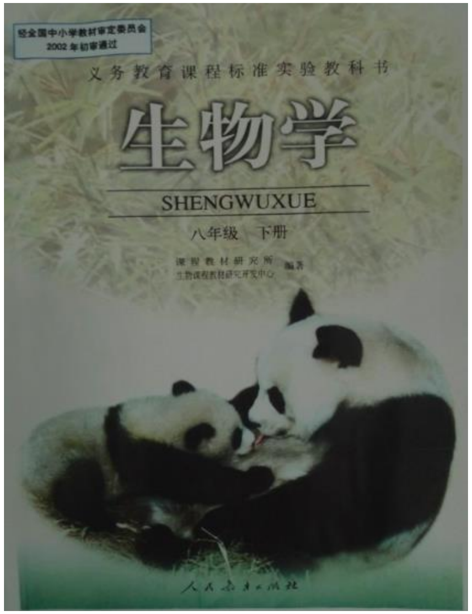


普通高中课程标准实验教科书

生物 ②

必修

遗传与进化



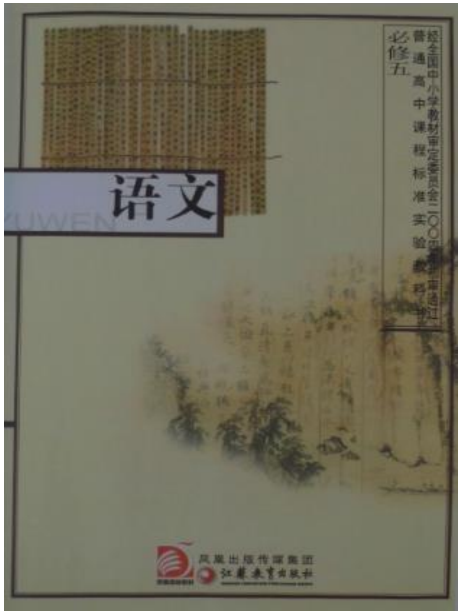
经全国中小学教材审定委员会
2002年初审通过

义务教育课程标准实验教科书

生物学

SHENGWUXUE

八年级 下册

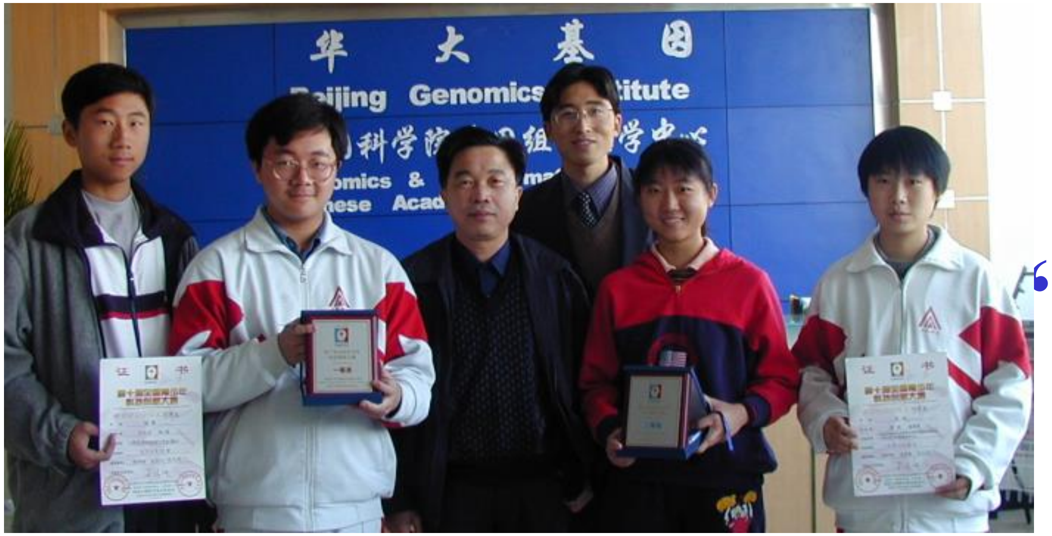


语文

YUWEN

必修五

普通高中课程标准实验教科书



"Gene should also be taught to the kids!"

基因组学 2015

Genomics 2015

杨焕明　主编

(征求意见版，仅供内部试用)
2015年9月9日

((***Textbook,*** 439 pages）

Scientific American: Research Leader of the Year, 2002

“When you drink
from the well,

don’t forget who
helped dig it!”

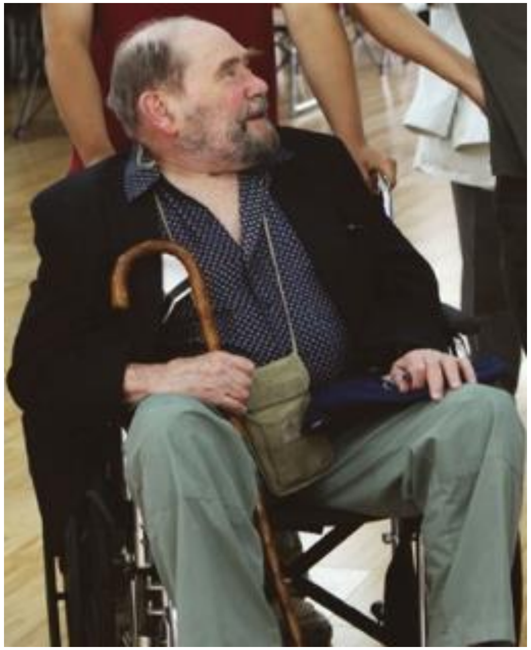
“饮水思源”

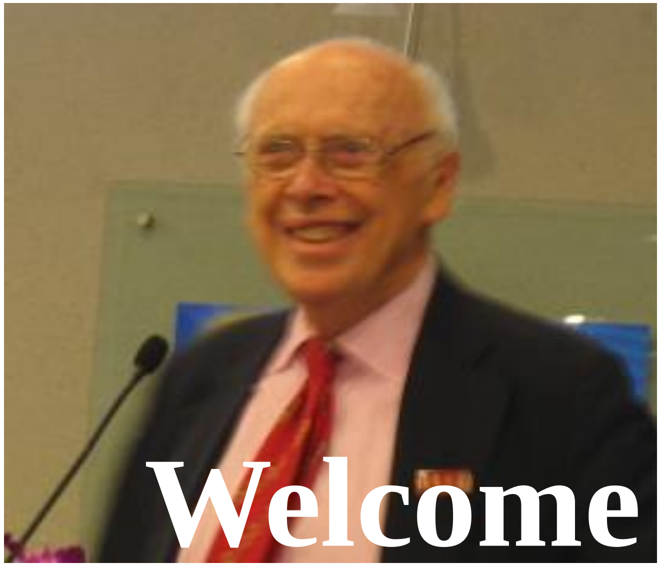
Gratitude speech at the reception by *Scientific American*

“One Day’s Teacher,
All Life’s Teacher”

欢迎做客华大！

Welcome to BGI!

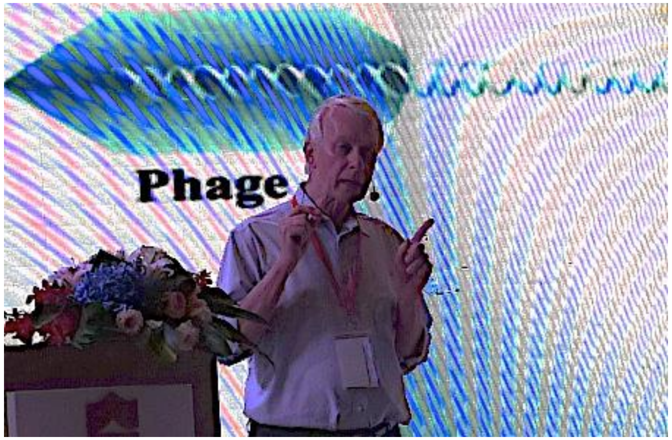




Welcome to

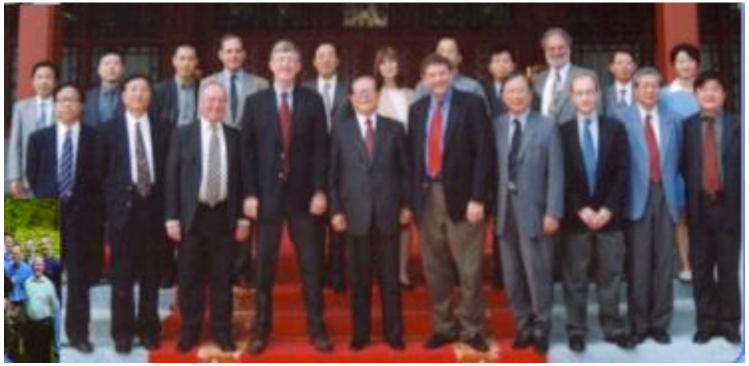
华大国际会议

International Conference on Genomics (ICG-11)



Oct., 2016, China

期盼与君合作
Let’s collaborate!



Acknowledgment

Sponsors

Chinese Academy of Sciences
Ministry of Science and Technology
National Natural Science Foundation
Beijing Municipal Government
Hangzhou Municipal Government
Shenzhen Municipal Government
All Other Local Governments

All our supporters, collaborators
international advisors
colleagues and friends
and all my young staff

Thanks!

yanghm@genomics.cn