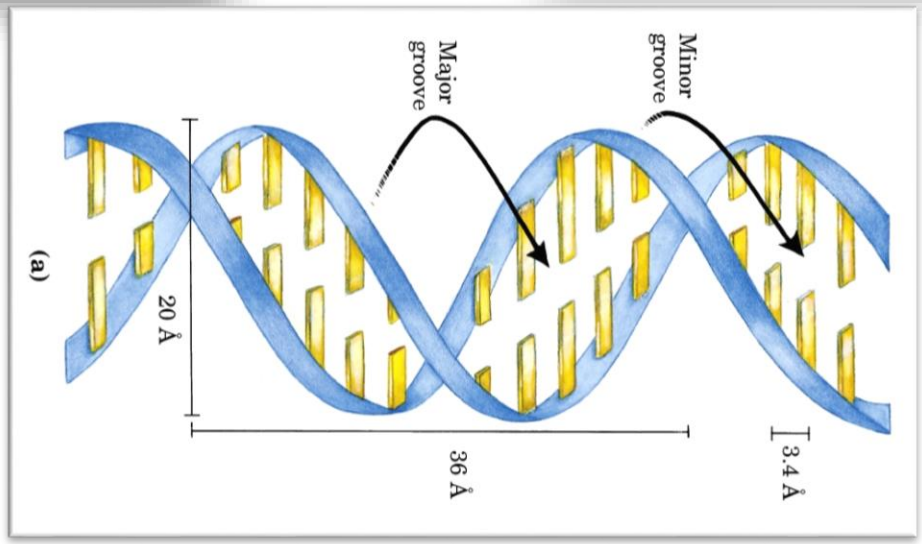
# ΑΠΟ ΤΗ ΓΕΝΕΤΙΚΗ ΣΤΗ ΓΟΝΙΔΙΩΜΑΤΙΚΗ, ΤΗΝ ΕΠΙ-ΜΕΤΑ ΚΑΙ ΠΑΝ-ΓΟΝΙΔΙΩΜΑΤΙΚΗ ΚΑΙ ΤΙΣ ΕΦΑΡΜΟΓΕΣ ΤΟΥΣ ΣΤΗΝ ΓΕΩΡΓΙΑ, ΤΗΝ ΔΙΑΤΡΟΦΗ ΚΑΙ ΤΗΝ ΠΡΟΣΤΑΣΙΑ ΤΗΣ ΥΓΕΙΑΣ

**Αθανάσιος Τσαυτάρης**

# ΓΕΝΕΤΙΚΗ



# Γενετική → Γονιδιωματική

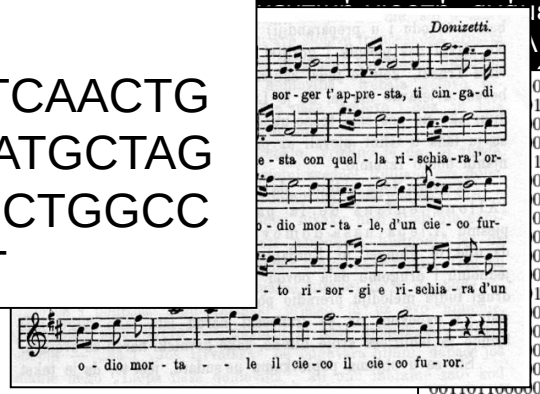
**Αυτόματη αλληλούχιση**

**λογισμικό**

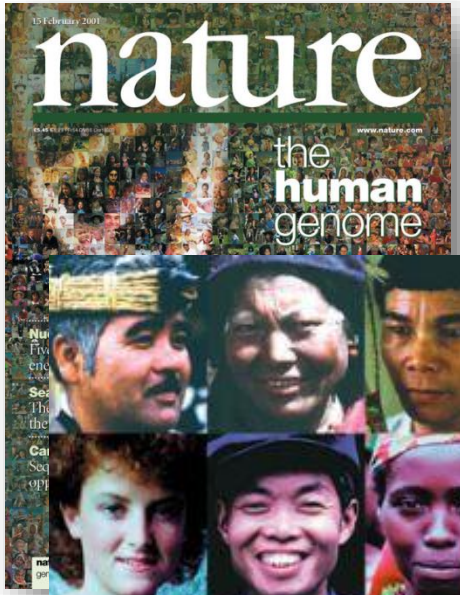
Αναγνώριση βάσης
Ποιότητα αλληλουχίας
Απομάκρυνση φορέα
Σύνδεση αλληλουχιών

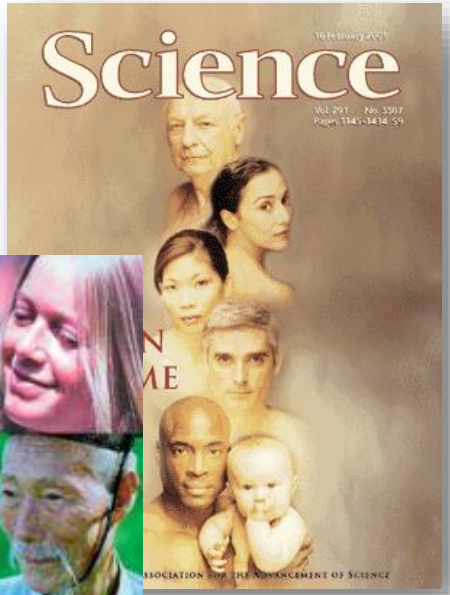
>Gene

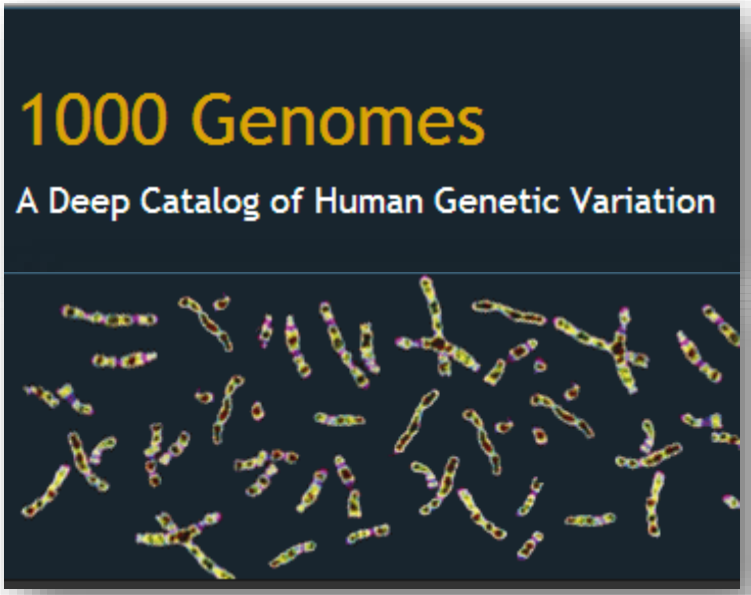
ACCTGTCAGTGTCAACTG
CTTCAATAGCTAATGCTAG
GCTCGATAATCGCTGGCC
TCAGCTCAGTCT



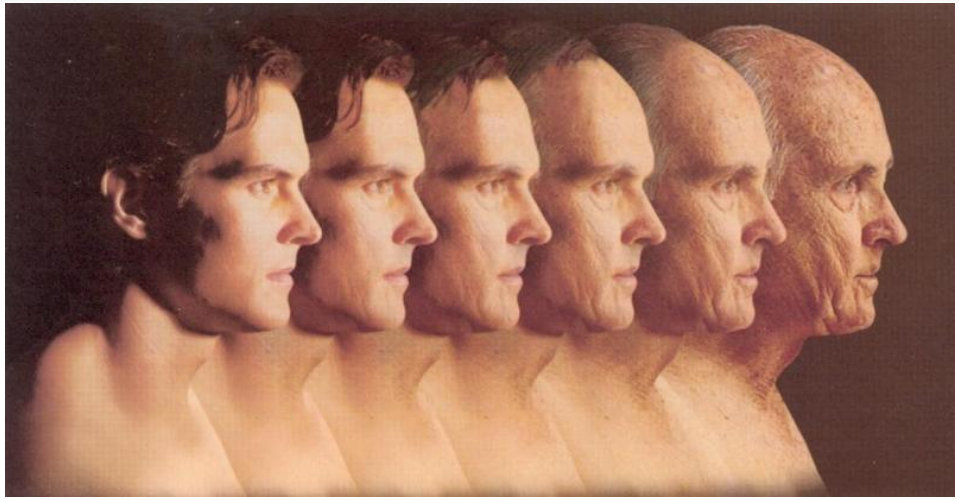
# ΤΟ ΑΝΘΡΩΠΙΝΟ ΓΟΝΙΔΙΩΜΑ

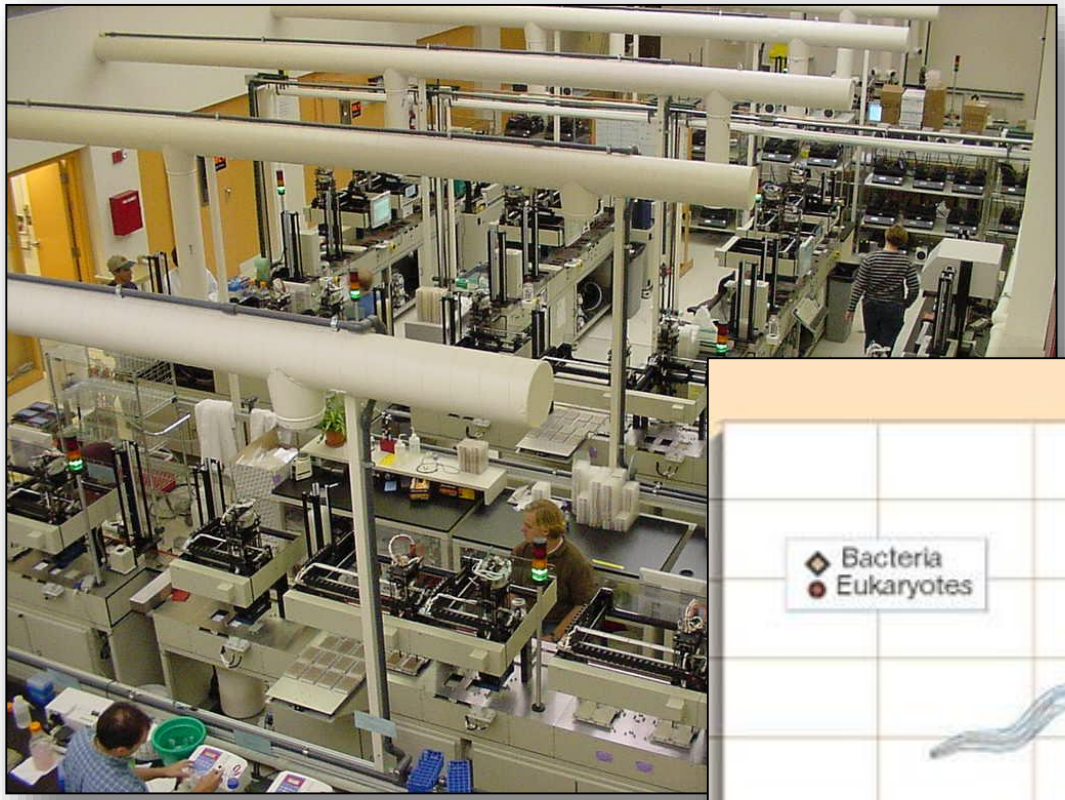


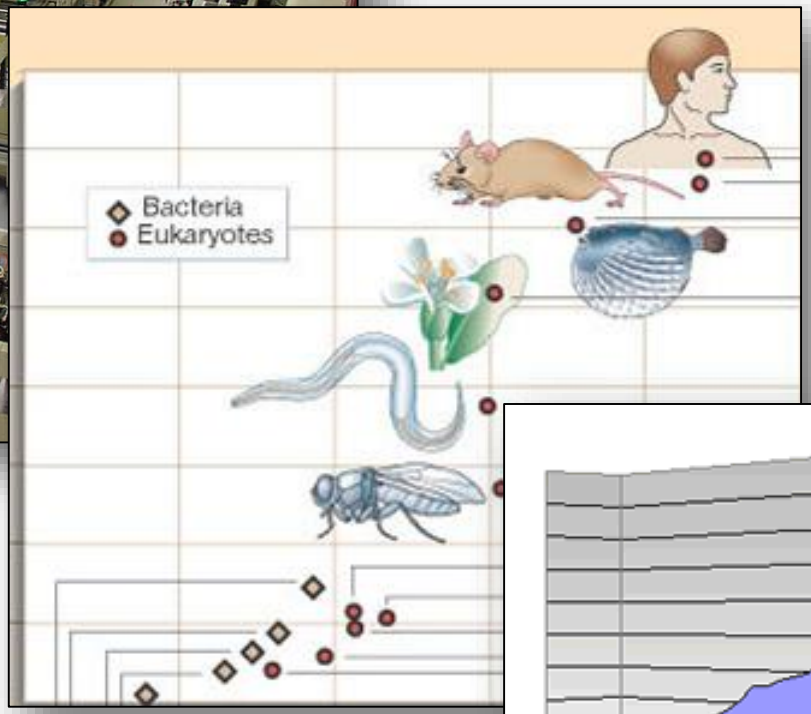



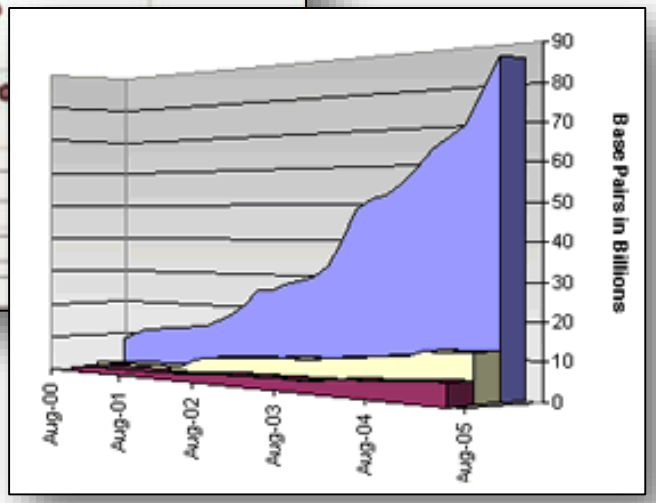








Bacteria
Eukaryotes


Base Pairs in Billions
90
80
70
60
50
40
30
20
10
0
Aug-00
Aug-01
Aug-02
Aug-03
Aug-04
Aug-05


HiSeqX
Welcome
illumina

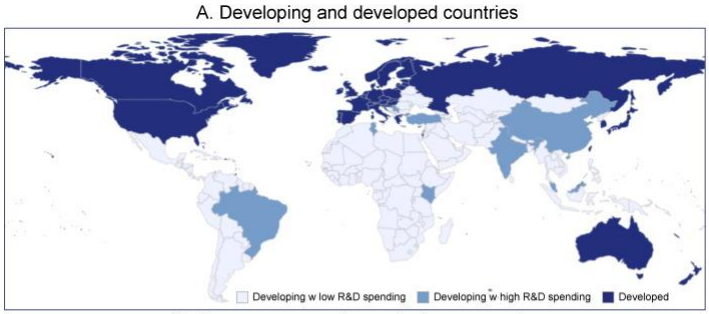
**NGS**

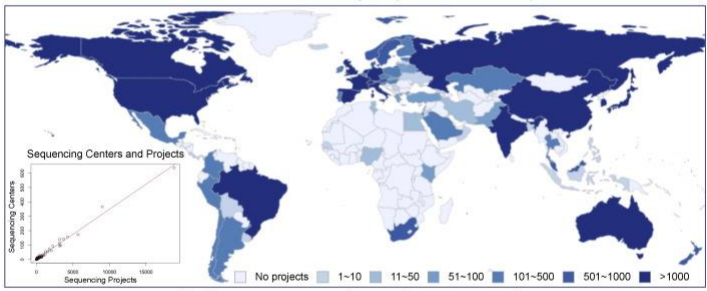
By Jeremy Hsu (/author/jeremy-hsu)
Posted 25 Mar 2015 | 15:47 GMT

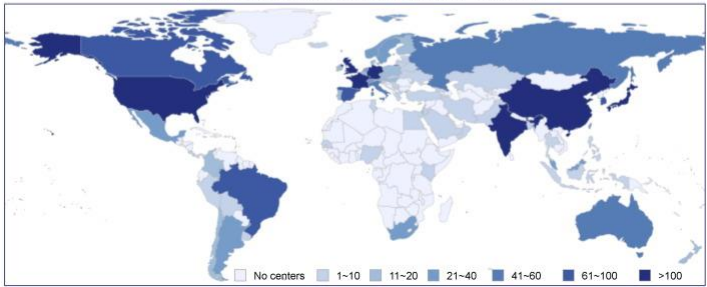
When the first Viking explorers began settling Iceland, none could have imagined that

Photo: Chris Lund

The blood of a thousand Icelanders.



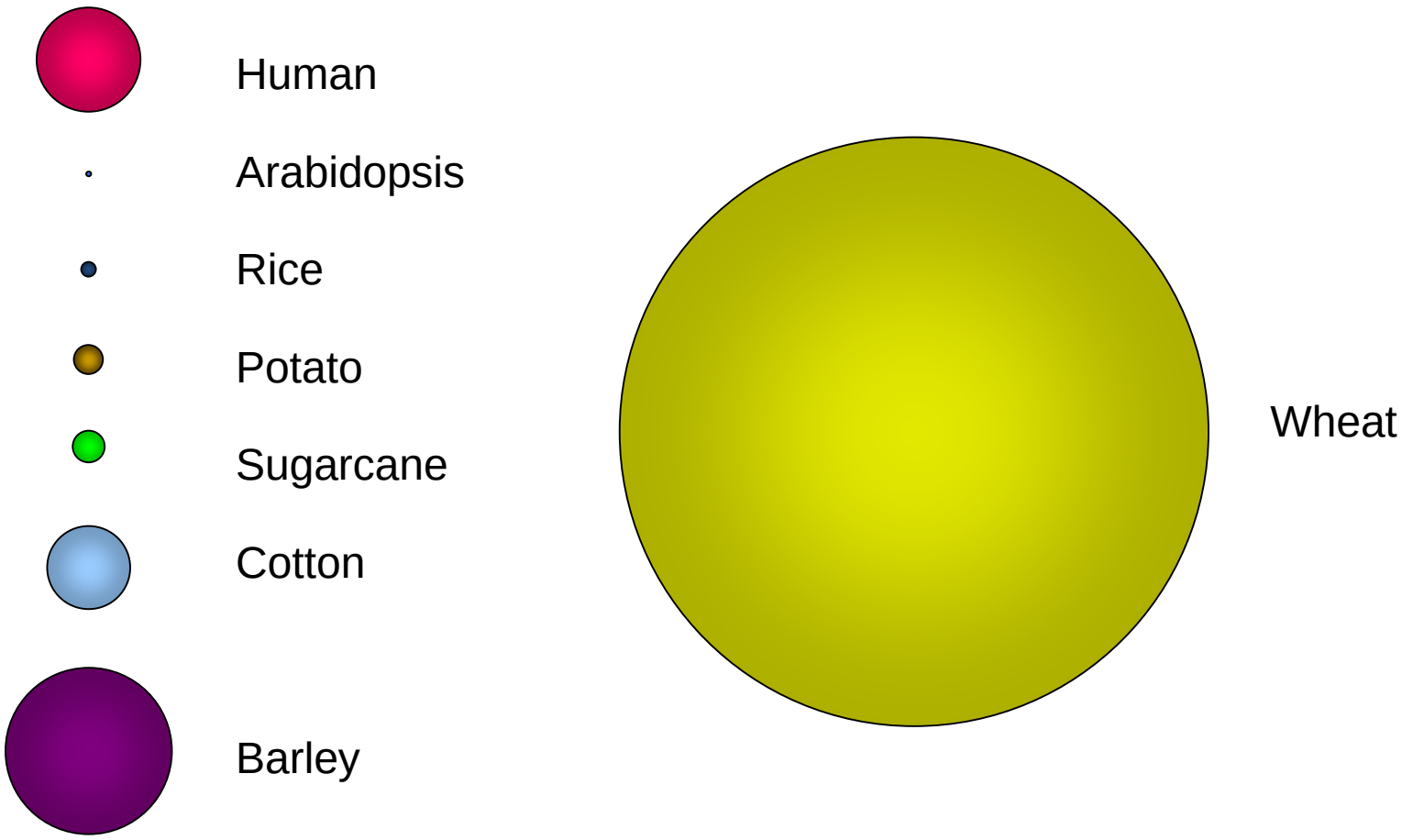




## Large-scale whole-genome sequencing of the Icelandic population

**Daniel F Gudbjartsson, Hannes Helgason, Sigurjon A Gudjonsson, Florian Zink, Asmundur Oddson, Arnaldur Gylfason, Soren Besenbacher, Gisli Magnusson, Bjarni V Halldorsson, Eirikur Hjartarson, Gunnar Th Sigurdsson, Simon N Stacey, Michael L Frigge, Hilma Holm, Jona Saemundsdottir, Hafdis Th Helgadottir, Hrefna Johannsdottir, Gunnlaugur Sigfusson, Gudmundur Thorgeirsson, Jon Th Sverrisson, Solveig Gretarsdottir, G Bragi Walters, Thorunn Rafnar, Bjarni Thjodleifsson, Einar S Bjornsson *et al.***

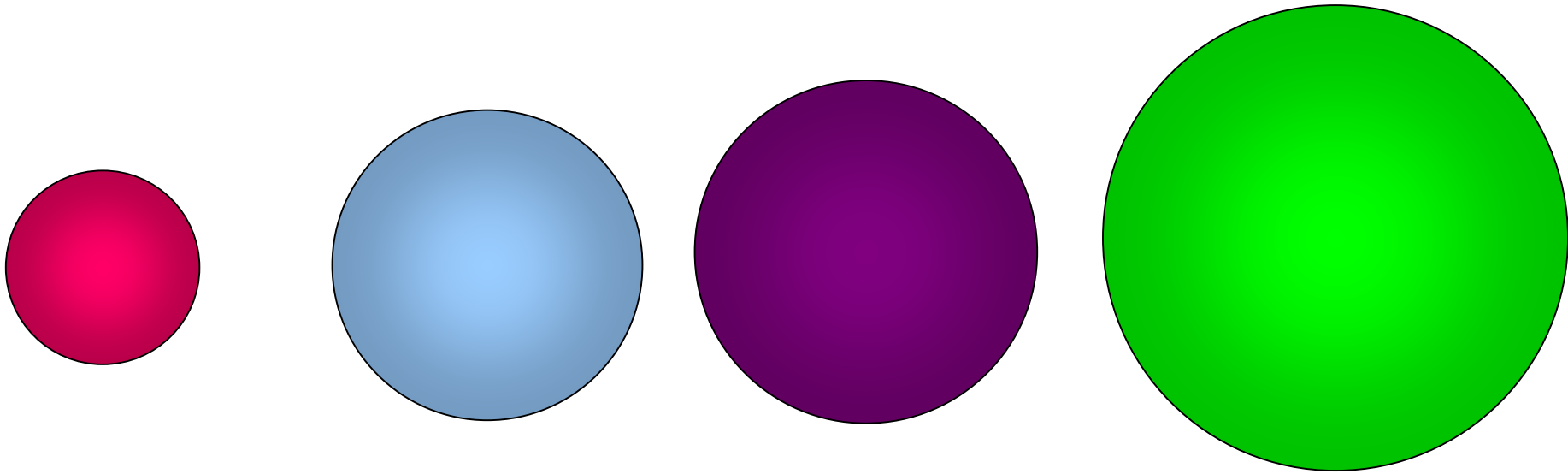
*Nature Genetics* **47**, 435–444 (2015) doi:10.1038/ng.3247

# Plant Genomes – Haploid Size

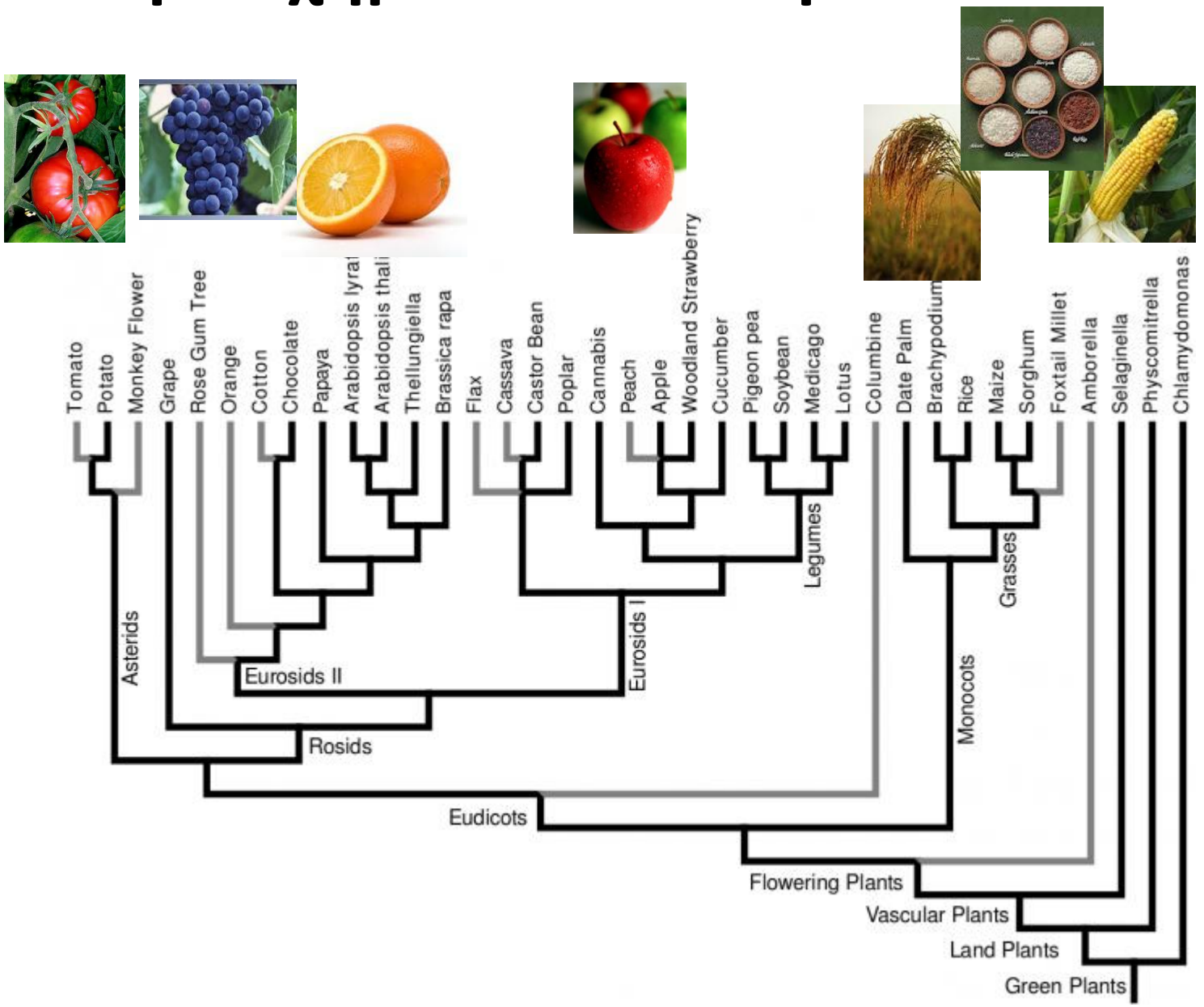



Diameter proportional to genome haploid genome size

# Plant Genomes – Total Size



# Αλληλουχημένα Γονιδιώματα Φυτών



nature genetics
OPEN

The draft genome of watermelon (*Citrullus lanatus*) and resequencing of 20 diverse accessions

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Resequencing of 31 wild and cultivated soybean genomes identifies patterns of genetic diversity and selection

nature genetics

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

The Plant Cell, Vol. 26: 121–135, January 2014, www.plantcell.org © 2014 American Society of Plant Biologists. All rights reserved.

nature biotechnology

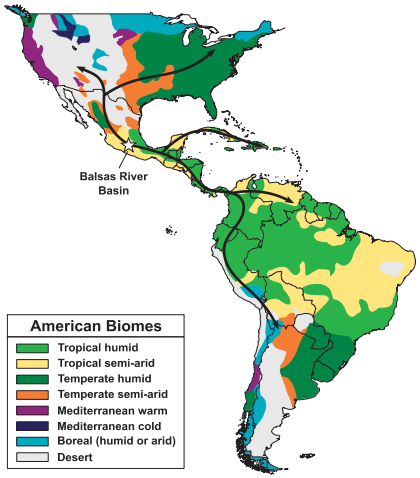
LARGE-SCALE BIOLOGY ARTICLE

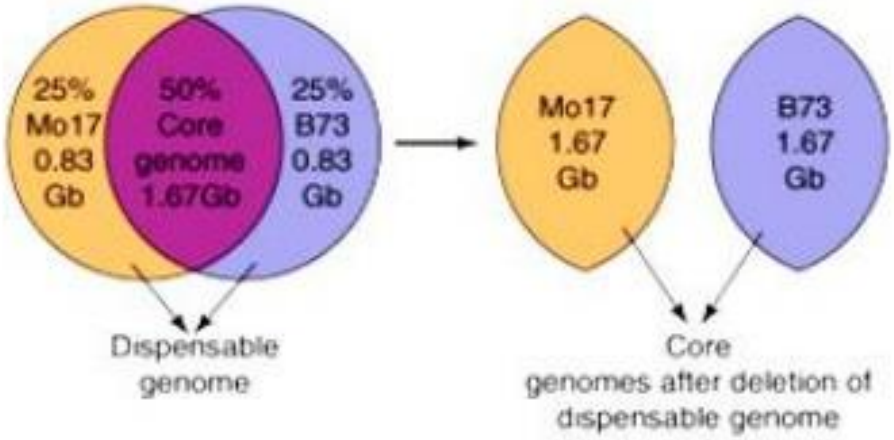
# Insights into the Maize Pan-Genome and Pan-Transcriptome[W][OPEN]

Candice N. Hirsch,[a,b,1] Jillian M. Foerster,[c,2] James M. Johnson,[c,3] Rajandeep S. Sekhon,[c,d] German Muttoni,[c,4] Brieanne Vaillancourt,[a,b] Francisco Peñagaricano,[e] Erika Lindquist,[f] Mary Ann Pedraza,[f] Kerrie Barry,[f] Natalia de Leon,[c,d] Shawn M. Kaeppler,[c,d] and C. Robin Buell[a,b,5]

*De novo* assembly of soybean wild relatives for pan-genome analysis of diversity and agronomic traits

- **Pan-genome:** The set of all genes present in the genomes of a group of organisms
  - **Core genome:** shared among individuals.
  - **Dispensable genome:** an individual-specific or partially-shared among individuals.




From: Morgante et al. Current Opinion in Plant Biology 10, 149-155 (2007)

ARTICLE

Received 10 Feb 2015 | Accepted 11 Mar 2015 | Published 16 Apr 2015

DOI: 10.1038/ncomms7914 OPEN

# High-resolution genetic mapping of maize pan-genome sequence anchors

Fei Lu[1], Maria C. Romay[1], Jeffrey C. Glaubitz[1], Peter J. Bradbury[2], Robert J. Elshire[1], Tianyu Wang[3], Yu Li[3], Yongxiang Li[3], Kassa Semagn[4], Xuecai Zhang[5], Alvaro G. Hernandez[6], Mark A. Mikel[6,7], Ilya Soifer[8], Omer Barad[8] & Edward S. Buckler[1,2]

In addition to single-nucleotide polymorphisms, structural variation is abundant in many plant genomes. The structural variation across a species can be represented by a 'pan-genome', which is essential to fully understand the genetic control of phenotypes. However, the pan-genome's complexity hinders its accurate assembly via sequence alignment. Here we demonstrate an approach to facilitate pan-genome construction in maize. By performing 18 trillion association tests we map 26 million tags generated by reduced representation sequencing of 14,129 maize inbred lines. Using machine-learning models we select 4.4 million accurately mapped tags as sequence anchors, 1.1 million of which are presence/absence variations. Structural variations exhibit enriched association with phenotypic traits, indicating that it is a significant source of adaptive variation in maize. The ability to efficiently map ultrahigh-density pan-genome sequence anchors enables fine characterization of structural variation and will advance both genetic research and breeding in many crops.

# Μελέτη βιοποικιλότητας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PATHOGENS
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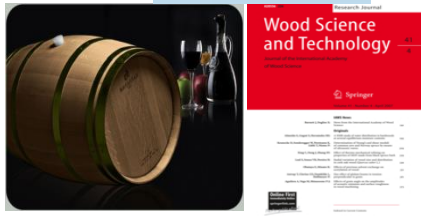
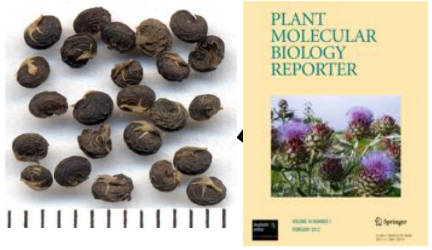
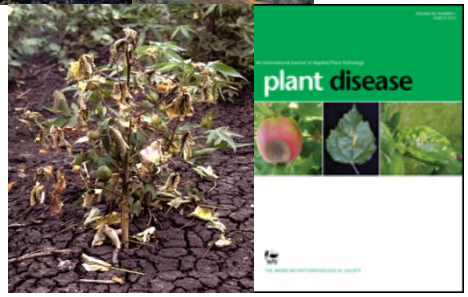
COMPUTATIONAL
BIOLOGY


FOOD RESEARCH
INTERNATIONAL

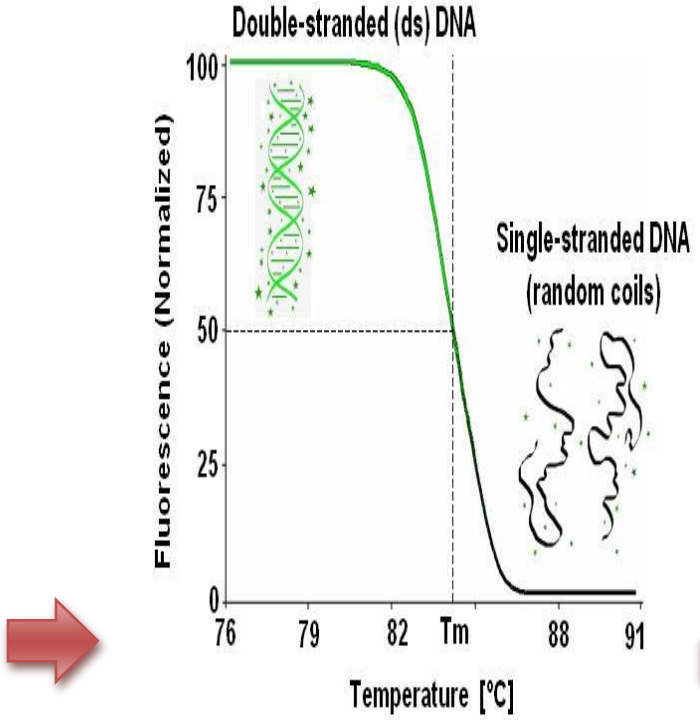

Wood Science
and Technology


Tree Genetics
& Genomes


PLANT
MOLECULAR
BIOLOGY
REPORTER


plant disease


WORK IN PROGRESS






**Ποικιλία /Είδος**

**HRM ανάλυση**

**Τελικό προϊόν**

CONTROL
CONTROL
FOOD CONTROL
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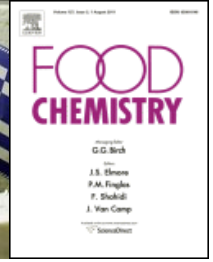
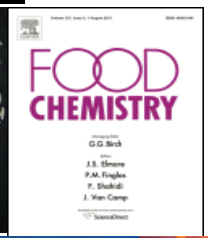
CONTROL
CONTROL
CONTROL



FOOD
CHEMISTRY



FOOD
CHEMISTRY



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FOOD CONTROL
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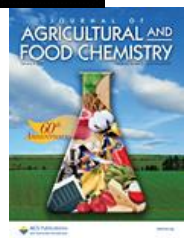
European
Food Research &
Technology



AGRICULTURAL AND
FOOD CHEMISTRY



FOOD RESEARCH
INTERNATIONAL



CONTROL
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FOOD CONTROL
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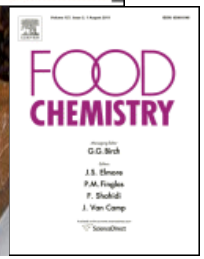
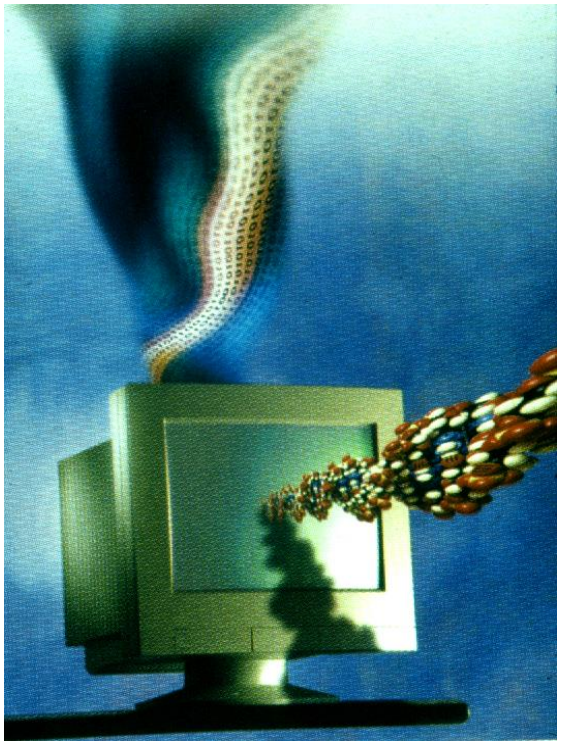
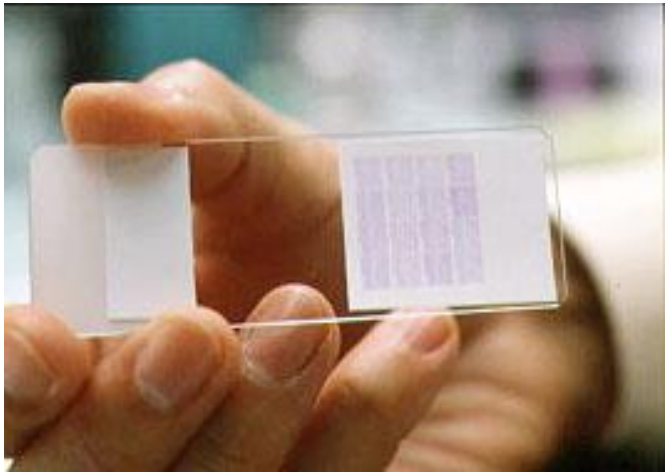
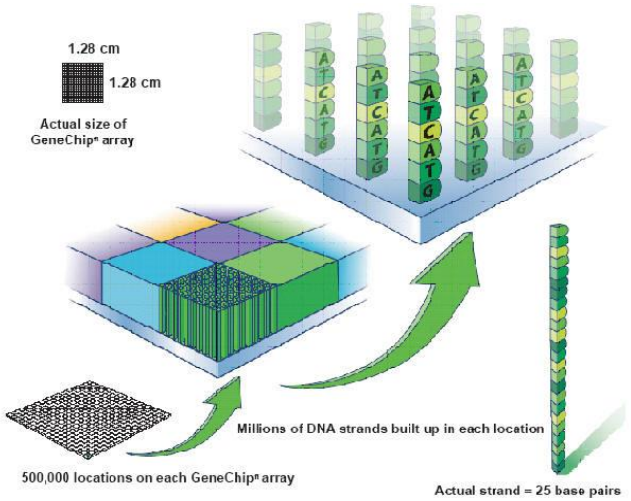

FOOD
CHEMISTRY


WORK IN PROGRESS

# ΒΙΟΠΛΗΡΟΦΟΡΙΚΗ







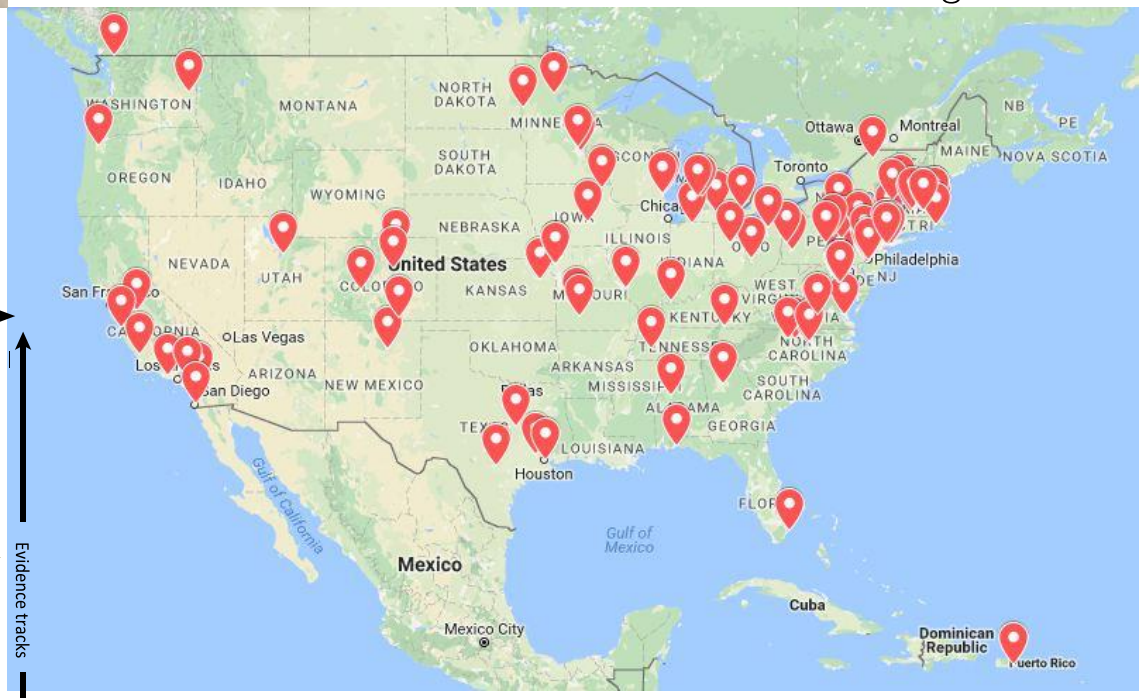


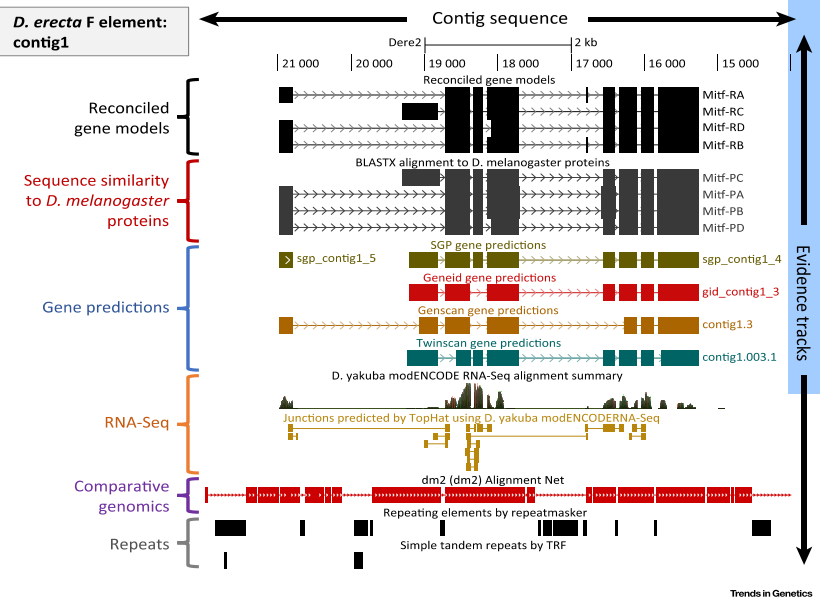
big
data

Trends in Genetics

## Scientific Life

# The GEP: Crowd-Sourcing Big Data Analysis with Undergraduates



# Γενετική

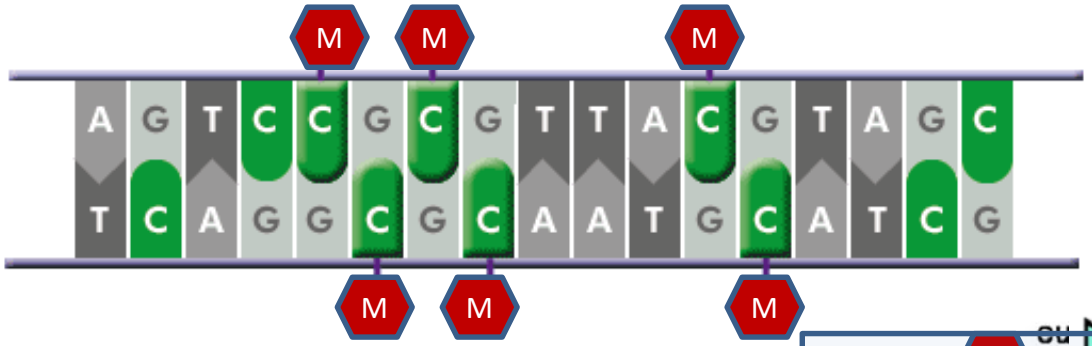
# Επιγενετική

*Κληρονομήσιμη αλλαγή χαρακτήρων που περιλαμβάνει αλλαγή στην αλληλουχία του DNA*

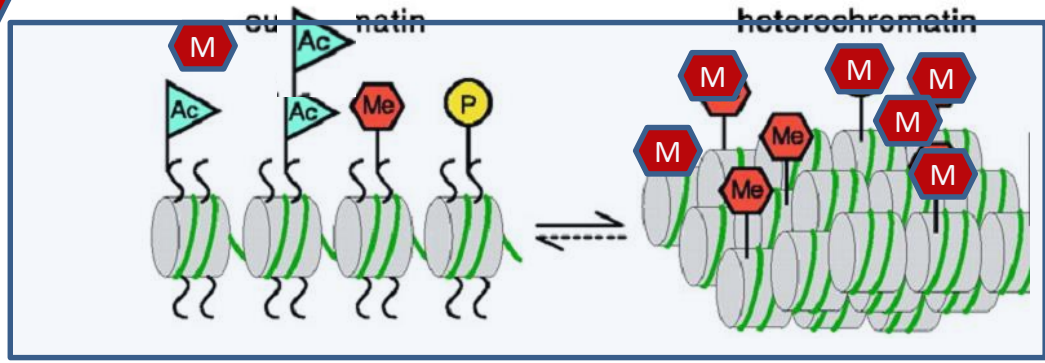
*Κληρονομήσιμη αλλαγή χαρακτήρων που δεν περιλαμβάνει αλλαγή στην αλληλουχία του DNA*


**ΚΑΛΟΣ** **ΠΑΝΩΡΑΙΑ**

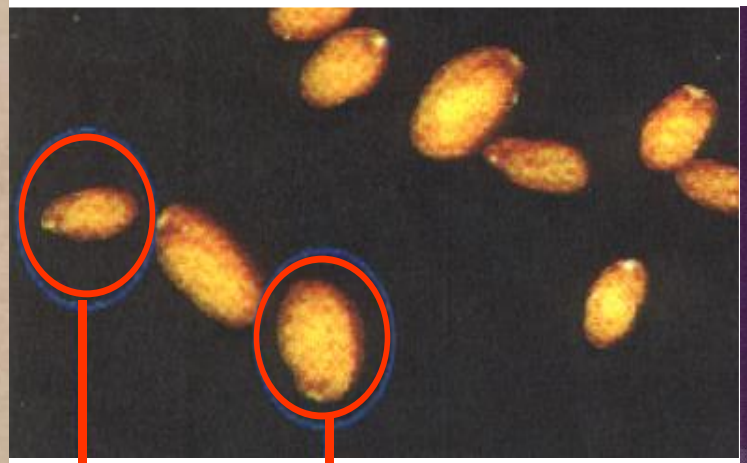
**ΚΑΚΟΣ** **ΩΡΑΙΑ**




**Καλός**
**Κάλος**

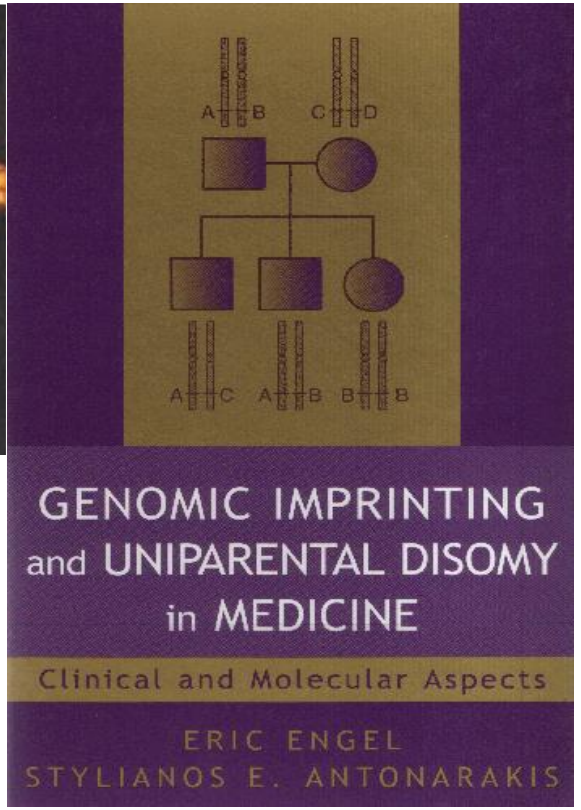


# Γονική αποτύπωση

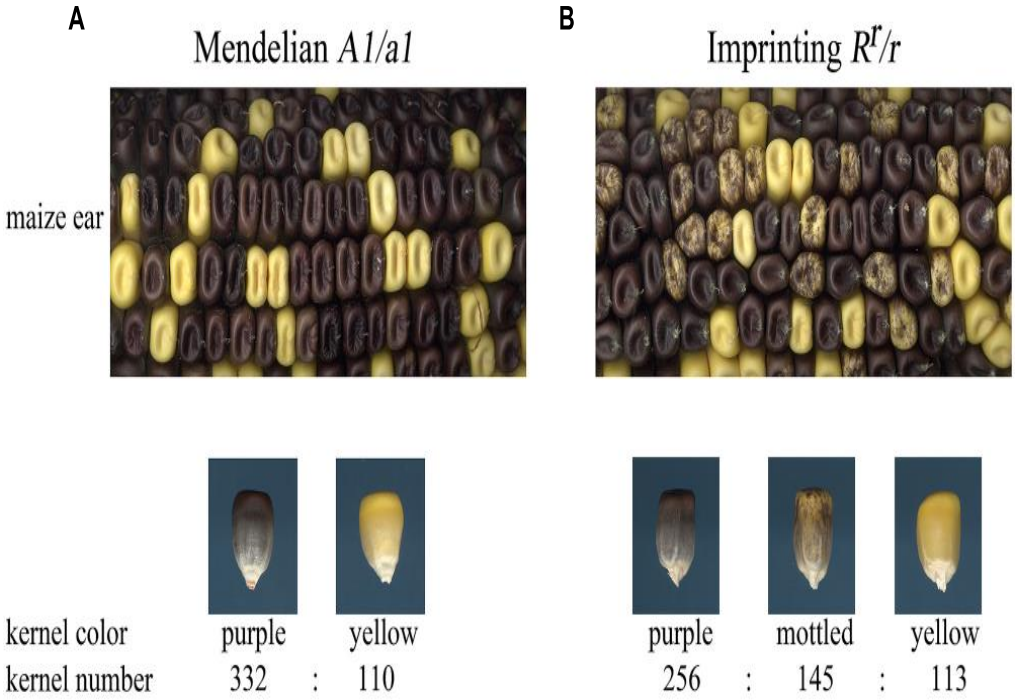


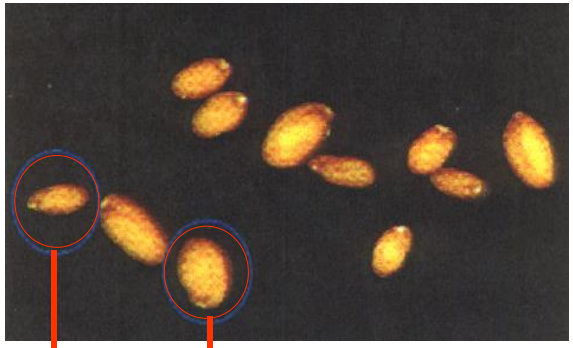
Μικρός καρπός

Μεγάλος καρπός



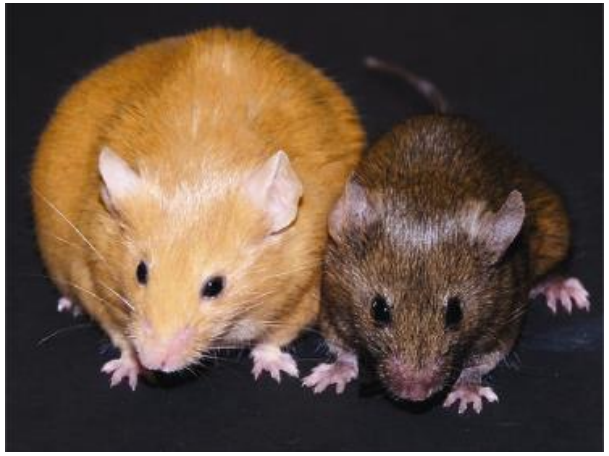
# Imprinting στο καλαμπόκι



**Small Seed**

**Large Seed**



# Βιβλιογραφία


**The Dutch famine and schizophrenia spectrum disorders**
Hoek HW, Brown AS, Susser E
Soc Psychiatry Psychiatr Epidemiol. 1998 Aug;33(8):373-9

**Prenatal exposure to the 1944-45 Dutch 'hunger winter' and addiction later in life.**
Franzek EJ, Sprangers N, Janssens AC, Van Duijn CM, Van De Wetering BJ
Addiction. 2008 Mar;103(3):433-8. Epub 2008 Jan 8

**Rates of adult schizophrenia following prenatal exposure to the Chinese famine of 1959-1961**
St Clair D, Xu M, Wang P, Yu Y, Fang Y, Zhang F, Zheng X, Gu N, Feng G, Sham P, He L
JAMA. 2005 Aug 3;294(5):557-62

**Epigenetic regulation in psychiatric disorders.**
Tsankova N, Renthal W, Kumar A, Nestler EJ.
*Nat Rev Neurosci. 2007 May;8(5):355-67*

LTR Hypomethylated

When to Intervene??

LTR Hypermethylated

Yellow Mouse

Agouti Mouse

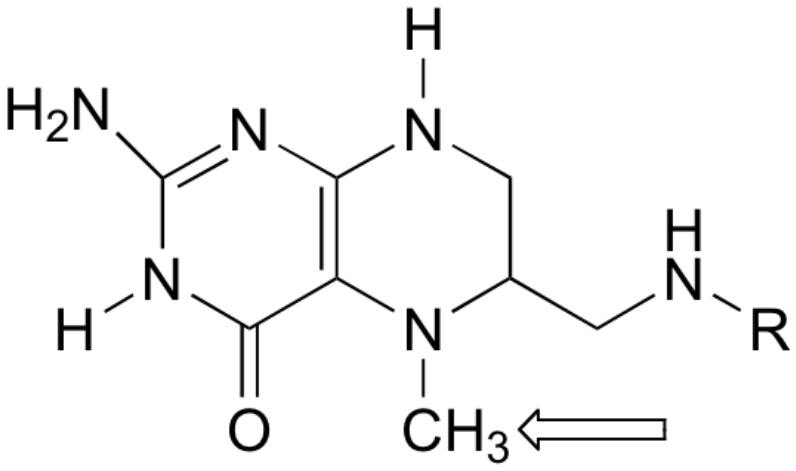
High risk cancer, diabetes, obesity & reduced lifespan

→

Lower risk of cancer, diabetes, obesity and prolonged life

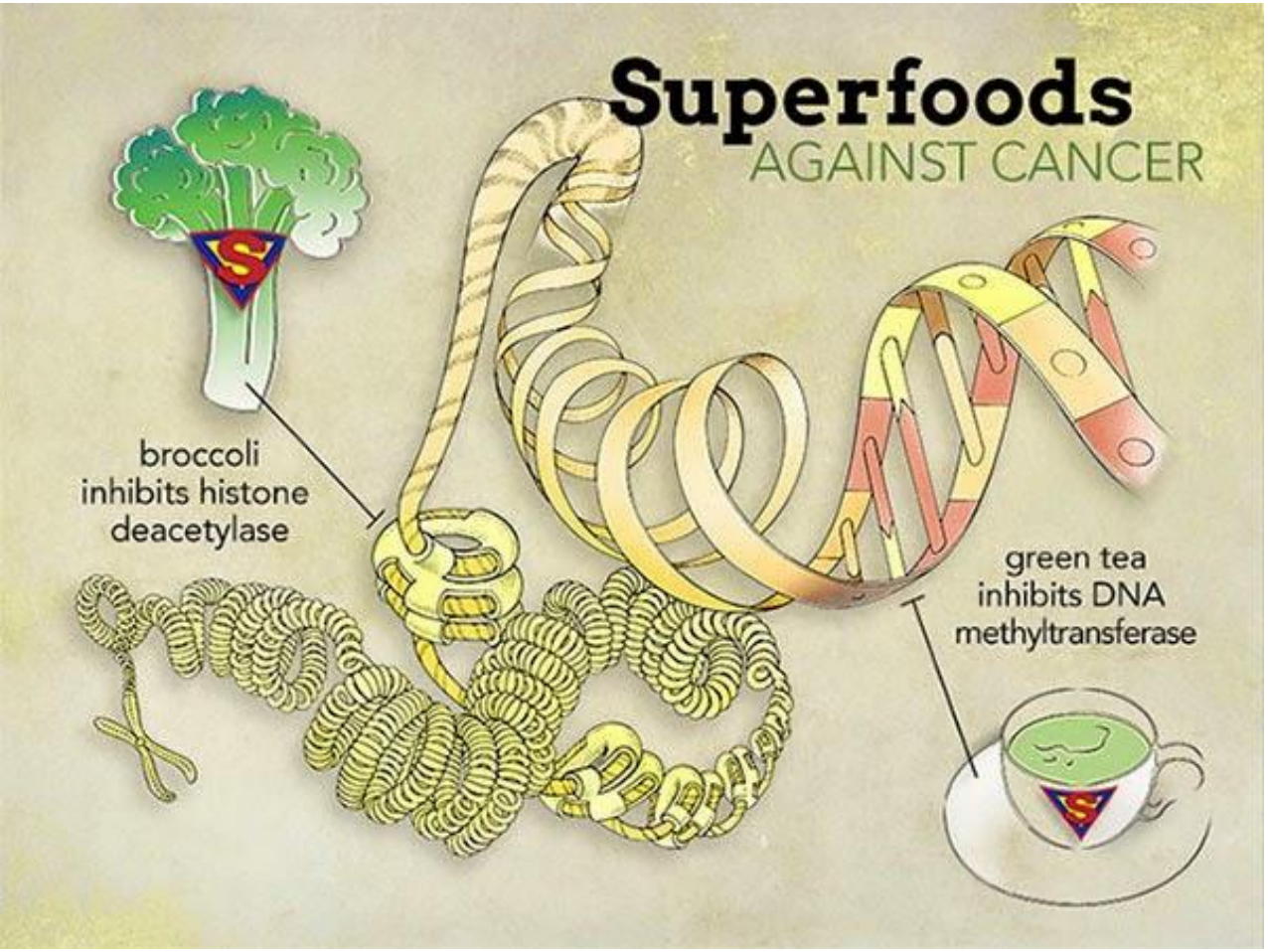
Maternal Supplements with zinc methionine betaine choline, folate $B_{12}$

Cooney et al. J Nutr 132:2393S (2002)




5-methyltetrahydrofolate



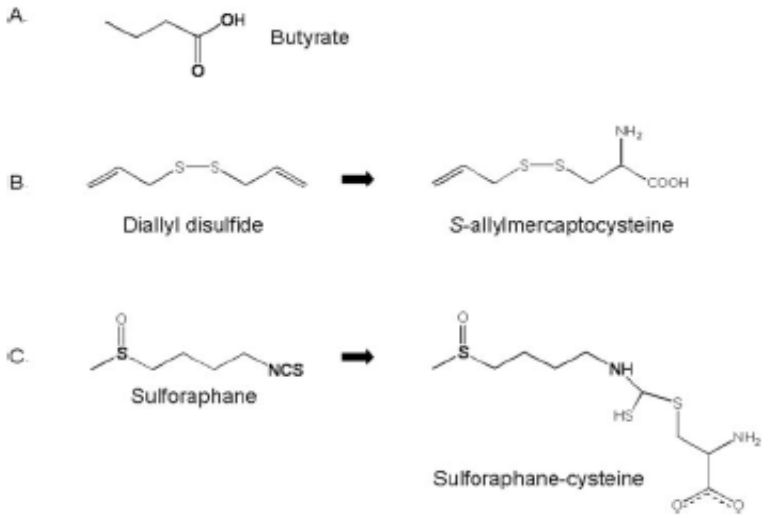



- ΒΡΟΥΒΕΣ
- ΜΟΥΣΤΑΡΔΑ
- ΡΑΔΙΚΙΑ
- ΡΕΠΑΝΑΚΙΑ
- ΖΩΧΟΙ
- ΡΟΚΑ
- ΣΤΑΜΝΑΓΚΑΘΙ

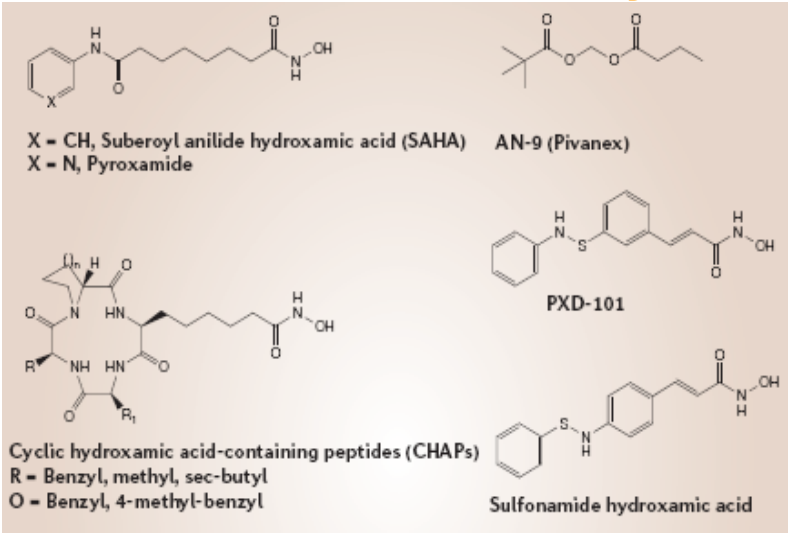
ΞΥΔΙ

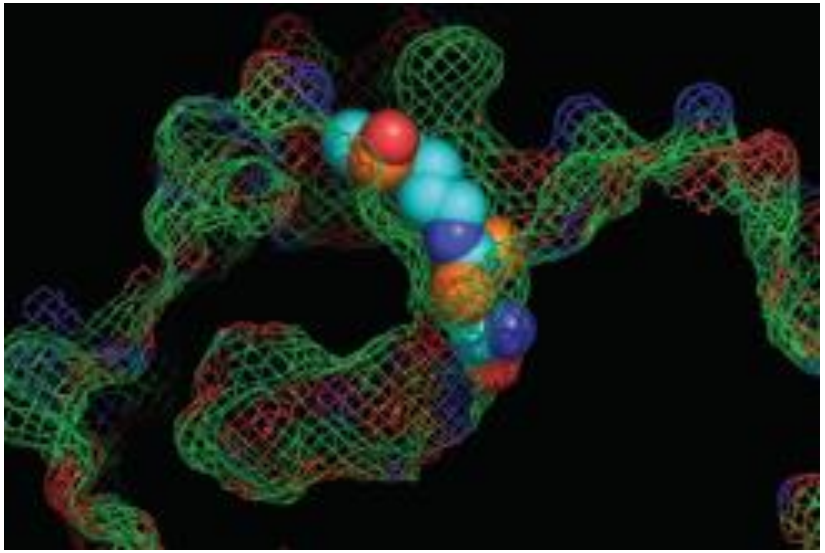
# ΑΝΑΣΤΟΛΕΙΣ ΤΗΣ ΑΠΟΑΣΕΤΥΛΑΣΗΣ

## Φυσικοί αναστολείς




## Συνθετικοί αναστολείς



# Epigenetic Bioactive compounds in plants

**Artichoke**
(Silymarin)

**Oleander**
(Oleanderin)

**Tomato**
(Lycopene)

**Garlic**
(Diallyl sulfide, ajoene, S-allyl cysteine, allicin)

**Carrots**
(β-carotenes)

**Tea**
(Catechins)

**Red grapes**
(Resveratrol)

**Red chilli**
(Capsaicin)

**Turmeric**
(Curcumin)

**Cloves**
(Eugenol & isoeugenol)

**Honey-bee propolis**
(Caffeic acid, CAPE)

**Cruciferous vegetables**
(Sulforaphane)

**Pomegranate**
(Ellagic acid)

**Ginger**
(6-Gingerol)

**Basil**
(Ursolic acid)

**Fennel,**
(Anethol)

**Soybean**
(Genistein)

**Aloe**
(Emodin)

ΓΟΝΙΔΙΩΜΑΤΙΚΗ → ΜΕΤΑΓΟΝΙΔΙΩΜΑΤΙΚΗ

# Evolution of Mammals and Their Gut Microbes

Ruth E. Ley,[1] Micah Hamady,[2] Catherine Lozupone,[1,3] Peter J. Turnbaugh,[1] Rob Roy Ramey,[4] J. Stephen Bircher,[5] Michael L. Schlegel,[6] Tammy A. Tucker,[6] Mark D. Schrenzel,[6] Rob Knight,[3] Jeffrey I. Gordon[1]*


Briefings in Functional Genomics Advance Access published December 18, 2014

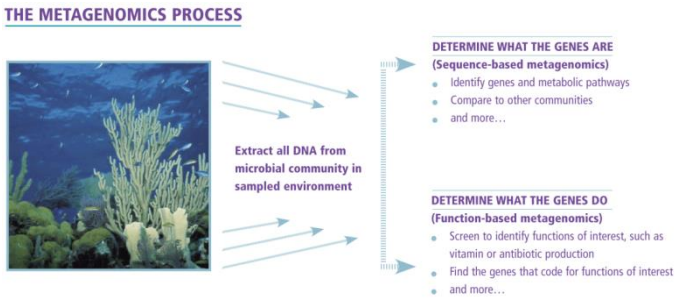
OXFORD

*Briefings in Functional Genomics*, 2014, 1–6

doi: 10.1093/bfgp/elu049
Letter to the Editor

## Functional marker development is challenged by the ubiquity of endophytes—a practical perspective

Birgit Arnholdt-Schmitt, Vera Valadas and Matthias Döring



# Ο άνθρωπος και τα βακτήρια

**10** τρισεκατομμύρια κύτταρα

**100** τρισεκατομμύρια Βακτήρια (χιλιάδες διαφορετικά είδη)

**23.000** γονίδια

## ΟΙ ΑΣΘΕΝΕΙΕΣ ΜΕ ΤΙΣ ΟΠΟΙΕΣ ΣΧΕΤΙΖΟΝΤΑΙ

### Παχυσαρκία
Στους παχύσαρκους παρατηρείται υπεραφθονία ενός τύπου Βακτηρίου (Firmicutes) σε σχέση με όλα τα υπόλοιπα

### Υποσιτισμός
Μερικές φορές τα βακτήρια δεν καταφέρνουν να διασπάσουν τους υδατάνθρακες και τις υπόλοιπες ουσίες με τις οποίες τροφόμαστε

### Υπέρταση
Τα Βακτήρια του πεπτικού συστήματος παράγουν φορμικό οξύ το οποίο «υποδεικνύει» στα νεφρά πόσο αλάτι πρέπει να απορροφήσουν από το αίμα

### Διαβήτης ενηλίκων
Εικάζεται πως τα βακτήρια επιδρούν στην αποτελεσματικότητα της ινσουλίνης αναφορικά με τη διάσπαση των σακχάρων του αίματος

### Προβλήματα ανάπτυξης του εγκεφάλου
Εικάζεται πως κάποιες τοξίνες που παράγονται από Βακτήρια του πεπτικού συστήματος μπορεί να επηρεάσουν την ανάπτυξη του εγκεφάλου στα μικρά παιδιά

## ΟΙ ΠΙΟ ΚΟΙΝΕΣ ΜΟΡΦΕΣ ΒΑΚΤΗΡΙΑΚΩΝ ΚΥΤΤΑΡΩΝ

1 μικρόμετρο

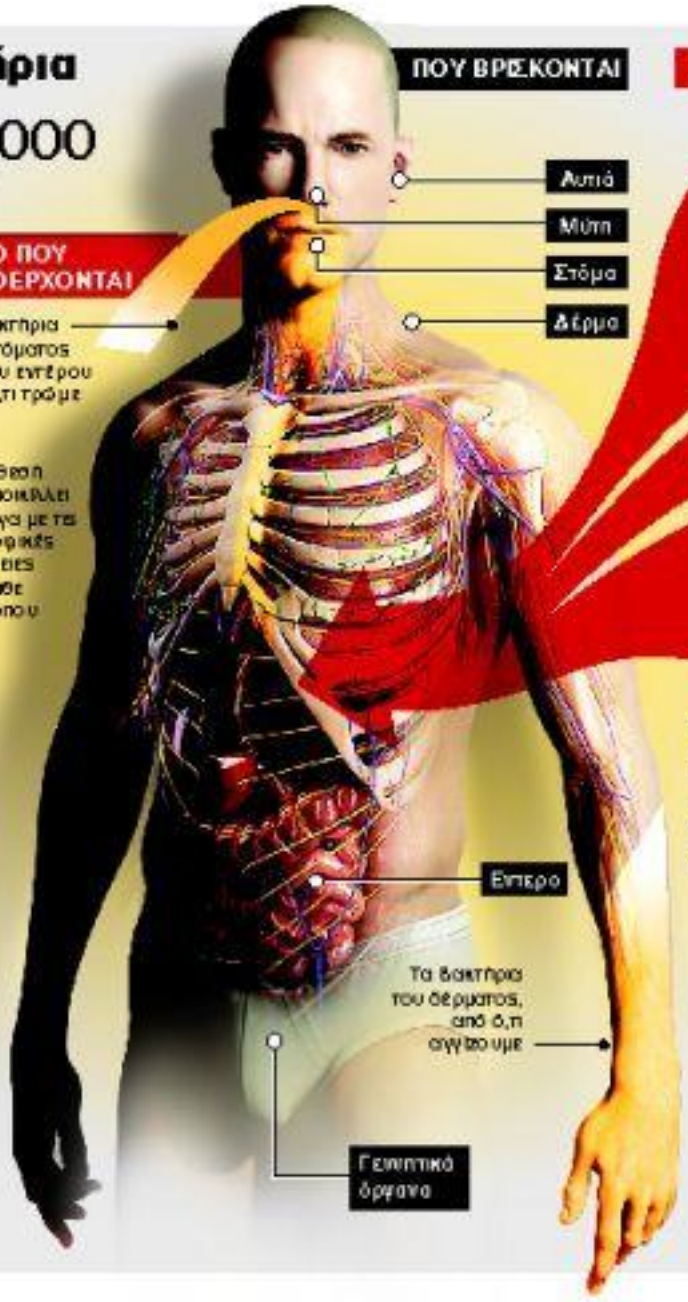
Κόκκος · Βάκιλος · Σπειρίλιο · Σπειροχαίτη

## ΑΠΟ ΠΟΥ ΠΡΟΕΡΧΟΝΤΑΙ

Τα βακτήρια του στόματος και του εντέρου από ό,τι τρώμε

Η ανάπτυξη τους ποικίλλει ανάλογα με τις διατροφικές συνήθειες του κάθε ανθρώπου

## ΠΟΥ ΒΡΙΣΚΟΝΤΑΙ




## ΟΙ ΛΕΙΤΟΥΡΓΙΕΣ ΤΟΥΣ

### ΕΠΙΤΡΕΠΟΥΝ
την πέψη τροφών ενώσεων που ο ανθρώπινος οργανισμός δεν θα μπορούσε να διασπάσει και των οποίων η διατροφική αξία κοστίζει με το 10% των θερμίδων που ένας άνθρωπος καταναλώνει σε ημερήσια βάση

### ΚΑΤΑΠΟΛΕΜΟΥΝ
τα επιβλαβή για την υγεία μας βακτήρια

### ΠΑΡΑΓΟΥΝ
- Βιταμίνες από έντερό μας
- Φολικό οξύ
- Βιταμίνη B2
- Βιταμίνη B12

## The Economist

το τελευταίο τεύχος του βρετανικού περιοδικού είναι αφιερωμένο στις πιο πρόσφατες ανακαλύψεις σχετικά με τις λειτουργίες των μικροβίων που συμβιώνουν μαζί μας: «Το 99% των κυττάρων του ανθρώπινου σώματος είναι Βακτήρια».

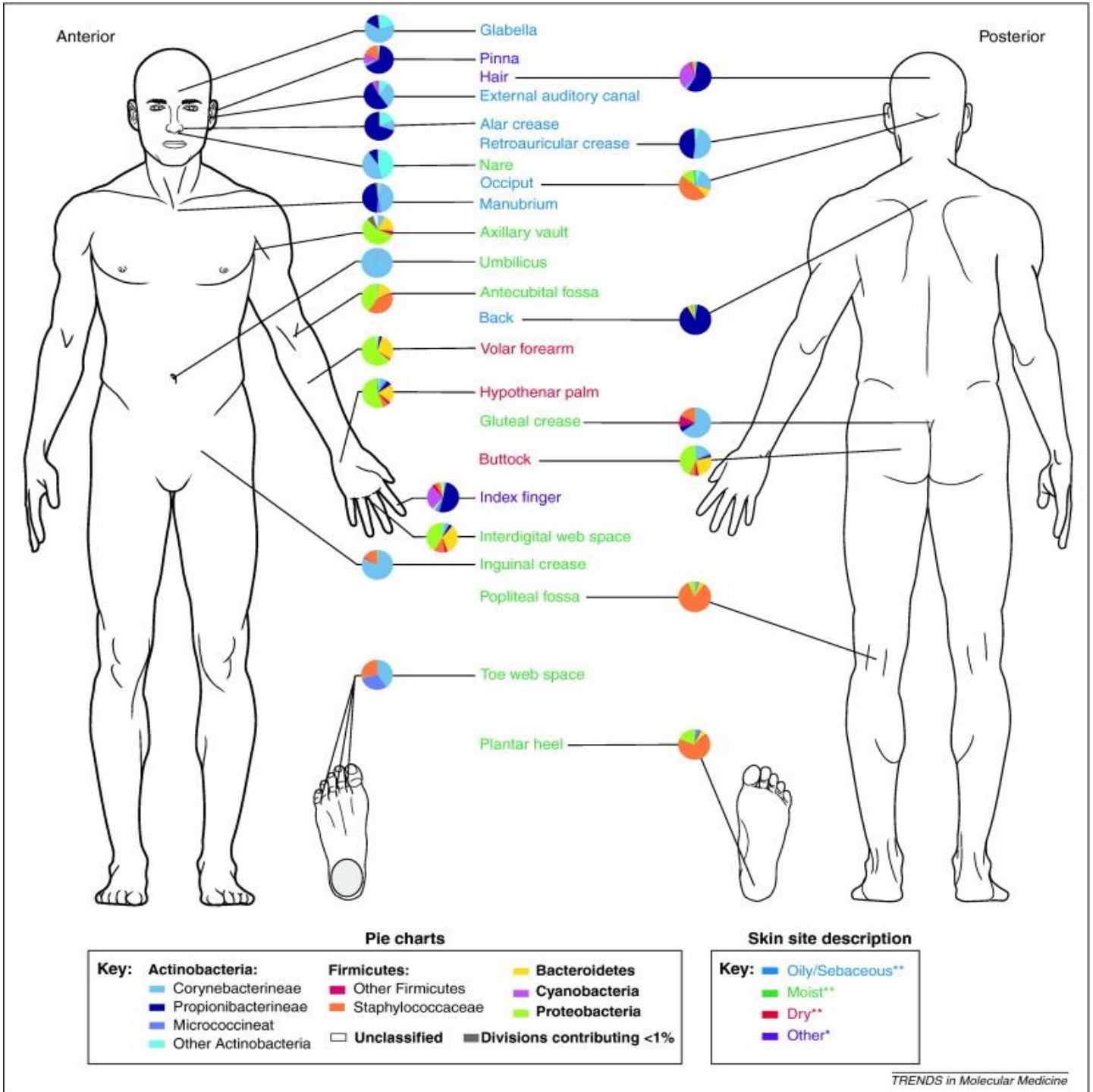
# Oral Microbiome

The community of microbes living in the oral cavity performs multiple functions. While the microbial composition for individuals is relatively stable, it can vary substantially among individuals.[54] Altered oral microbiomes are informative of health status, such as nutritional deficiencies[55] and cardiovascular disease.[56]

The microbial communities in the oral cavity are organized in compartments and biofilms. Excessive buildup can form plaque and cause oral diseases. Metagenomic studies have identified specific metabolic pathways of oral disease.[57] During oral diseases—such as chronic periodontitis, dental caries, and gingivitis—the subgingival microbiome undergoes dynamic changes that are associated with infection of dental implants by oral pathogens[58] and smoking.[59] These changes can be monitored to assess disease progression and therapy effectiveness.[60]

During oral diseases—such as chronic periodontitis, dental caries, and gingivitis—the subgingival microbiome undergoes dynamic changes that can be monitored to assess disease progression an therapy effectiveness.

Periodontitis.

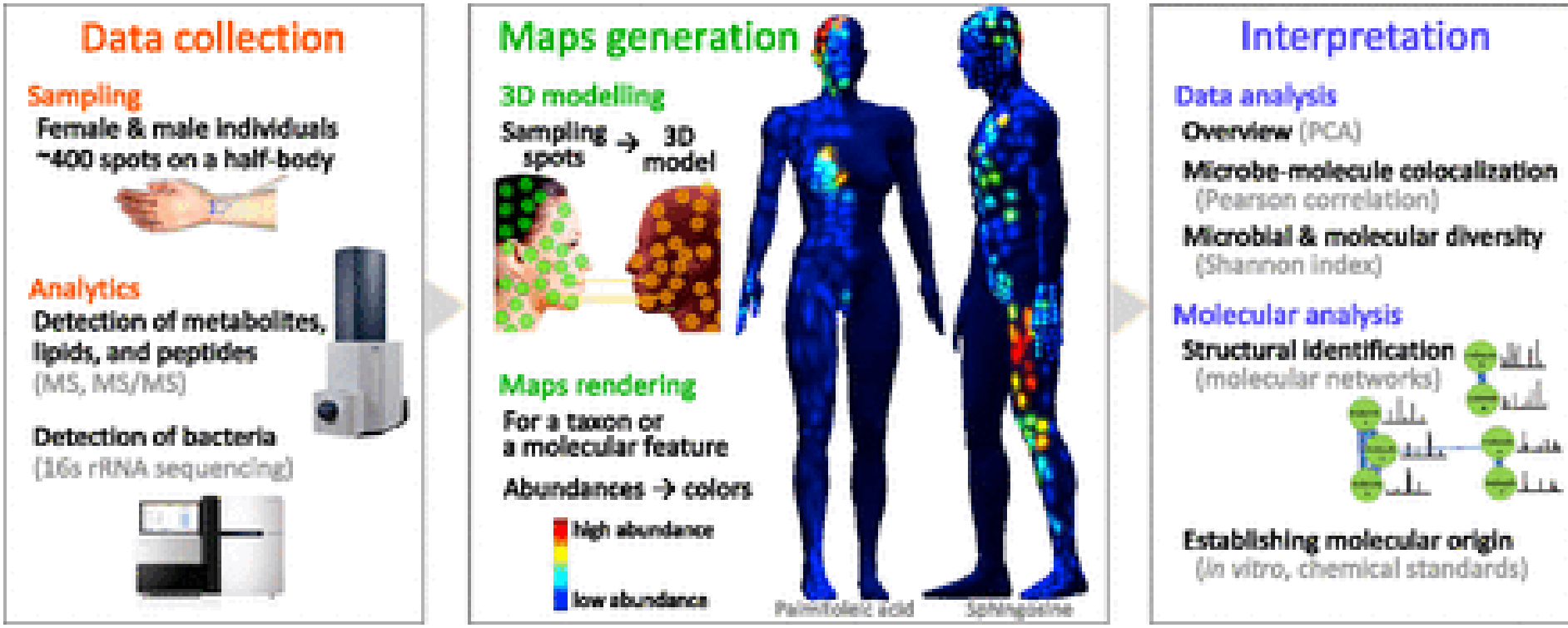

Anterior
Posterior
Glabella
Pinna
Hair
External auditory canal
Alar crease
Retroauricular crease
Nare
Occiput
Manubrium
Axillary vault
Umbilicus
Antecubital fossa
Back
Volar forearm
Hypothenar palm
Gluteal crease
Buttock
Index finger
Interdigital web space
Inguinal crease
Popliteal fossa
Toe web space
Plantar heel
Pie charts
Key:
Actinobacteria:
Corynebacterineae
Propionibacterineae
Micrococcineat
Other Actinobacteria
Firmicutes:
Other Firmicutes
Staphylococcaceae
Unclassified
Bacteroidetes
Cyanobacteria
Proteobacteria
Divisions contributing <1%
Skin site description
Key:
Oily/Sebaceous**
Moist**
Dry**
Other*

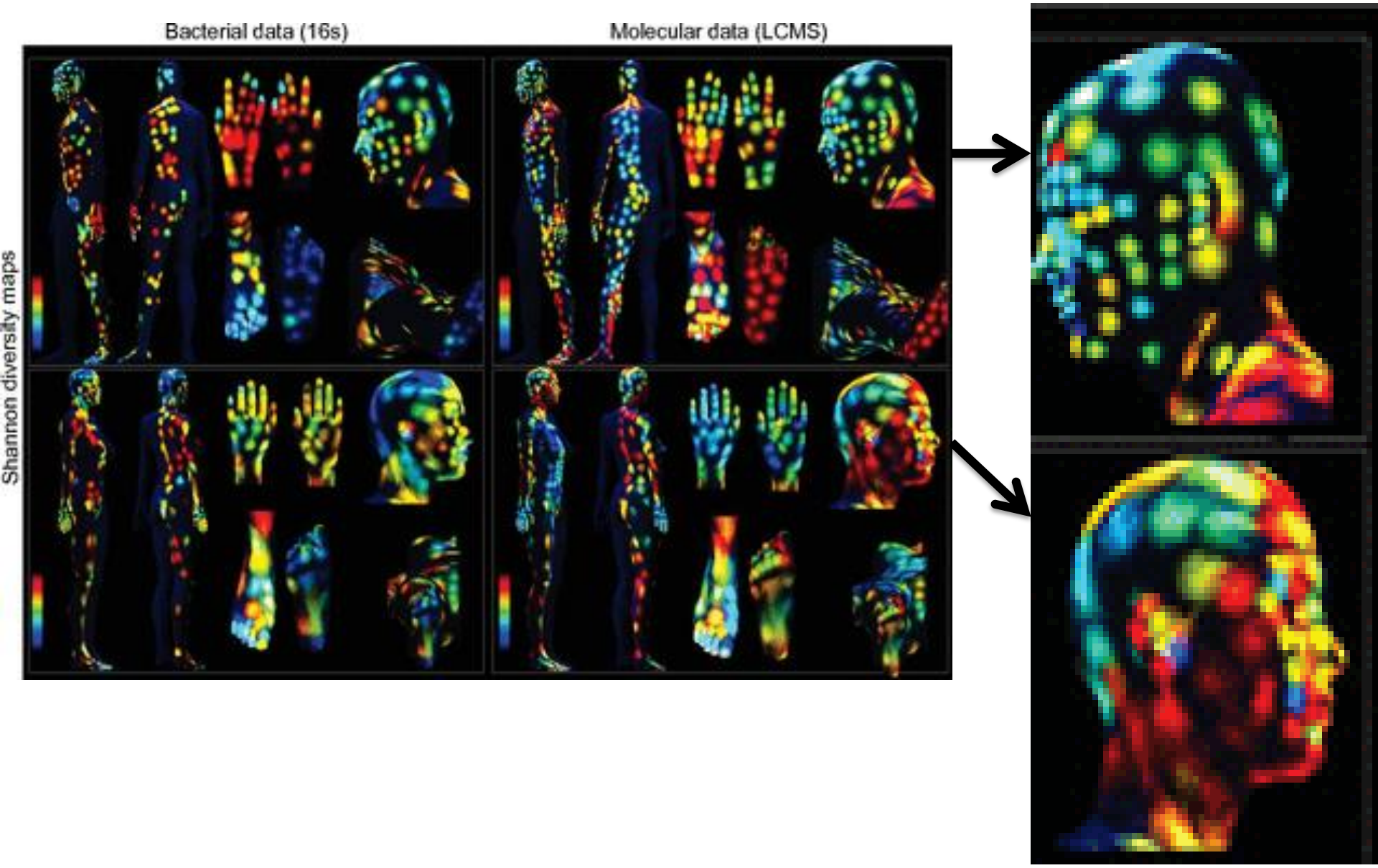
# Molecular cartography of the human skin surface in 3D

Amina Bouslimani[a,1], Carla Porto[a,1], Christopher M. Rath[a,1], Mingxun Wang[b], Yurong Guo[c], Antonio Gonzalez[d,e], Donna Berg-Lyon[d,e], Gail Ackermann[d,e], Gitte Julie Moeller Christensen[a,f], Teruaki Nakatsuji[g], Lingjuan Zhang[g], Andrew W. Borkowski[g], Michael J. Meehan[a], Kathleen Dorrestein[a], Richard L. Gallo[g], Nuno Bandeira[a,b,h,2], Rob Knight[b,c,d,e,i,2], Theodore Alexandrov[a,j,k,l,2], and Pieter C. Dorrestein[a,m,n,o,2]

[a]Skaggs School of Pharmacy and Pharmaceutical Sciences, [c]School of Medicine, [g]Division of Dermatology, and Departments of [m]Biochemistry, [n]Pharmacology, and [o]Chemistry, University of California, San Diego, La Jolla, CA 92037; [b]Department of Computer Science and Engineering and [h]Center for Computational Mass Spectrometry, University of California, San Diego, La Jolla, CA 92093; [d]Department of Chemistry and Biochemistry, [e]BioFrontiers Institute, and [i]Howard Hughes Medical Institute, University of Colorado at Boulder, Boulder, CO 80309; [f]Department of Biomedicine, Aarhus University, DK-8000 Aarhus C, Denmark; [j]Center for Industrial Mathematics, University of Bremen, 28359 Bremen, Germany; [k]SCiLS GmbH, 28359 Bremen, Germany; and [l]European Molecular Biology Laboratory, Meyerhofstrasse 1, 69117 Heidelberg, Germany

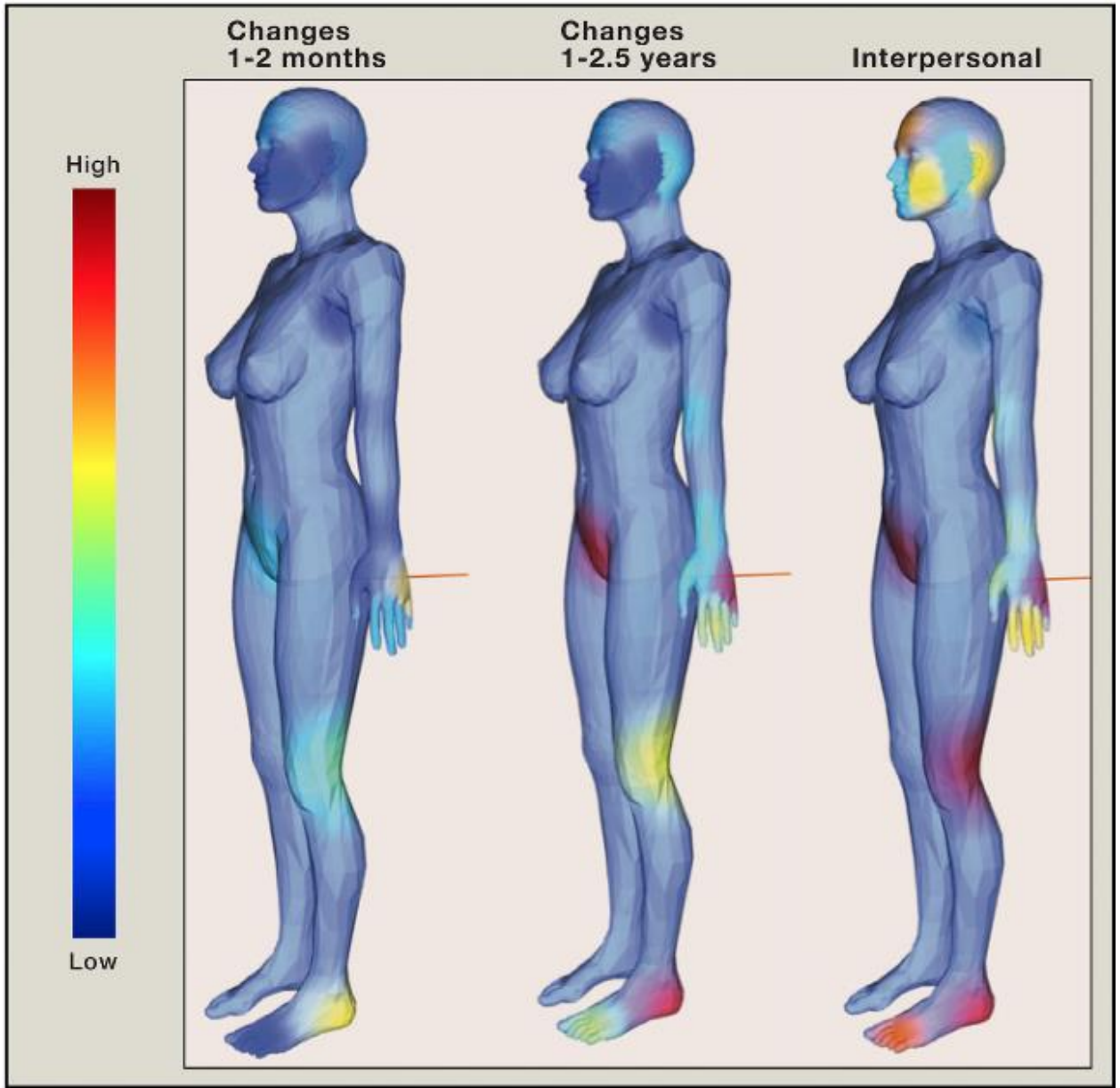
Edited by Jerrold Meinwald, Cornell University, Ithaca, NY, and approved March 6, 2015 (received for review December 30, 2014)




Bacterial data (16s)
Molecular data (LCMS)
Shannon diversity maps

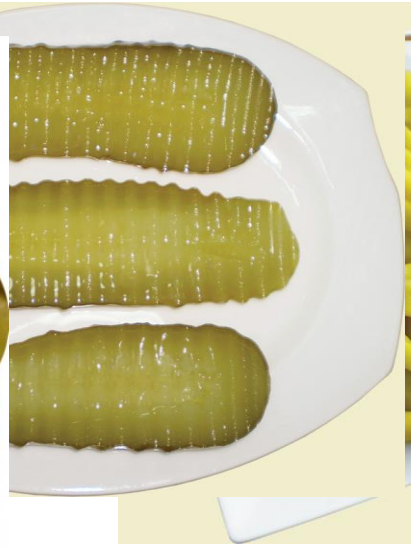
Cell

# Microbial Skin Inhabitants: Friends Forever



ΓΟΝΙΔΙΩΜΑΤΙΚΗ → ΜΕΤΑΓΟΝΙΔΙΩΜΑΤΙΚΗ





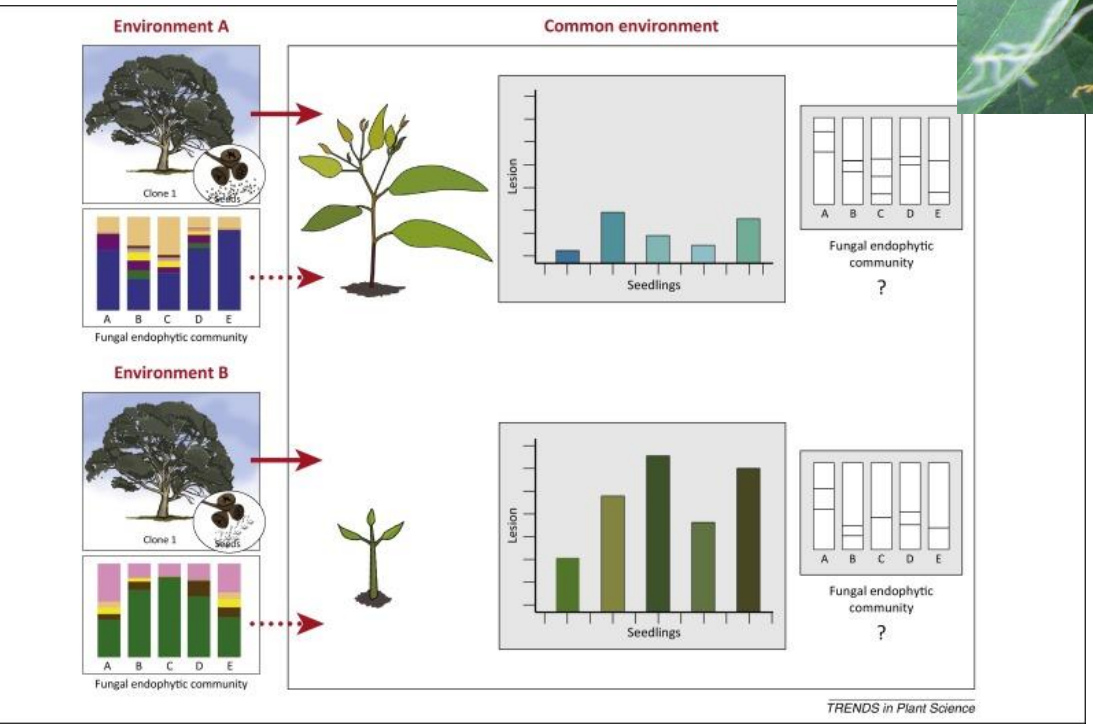


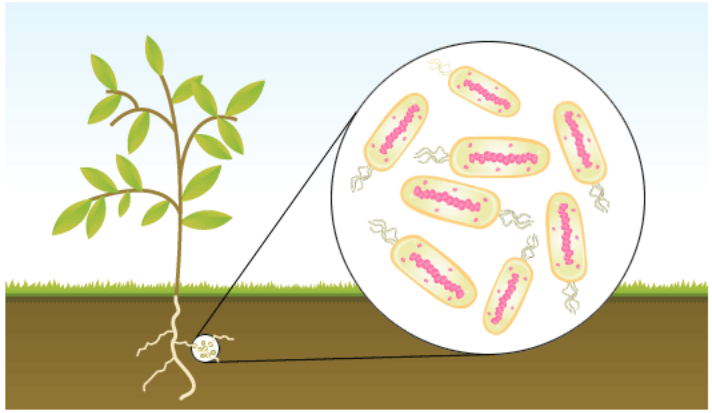
ΓΟΝΙΔΙΩΜΑΤΙΚΗ → ΜΕΤΑΓΟΝΙΔΙΩΜΑΤΙΚΗ

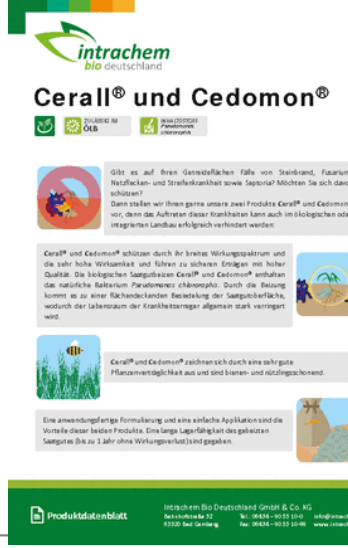
frontiers in Microbiology

OPINION
published: 10 February 2016
doi: 10.3389/fmicb.2016.00073

# Back to the Future of Soil Metagenomics


Environment A
Common environment
Clone 1
Seeds
A B C D E
Fungal endophytic community
Lesion
Seedlings
Fungal endophytic community
?
Environment B
Clone 1
Seeds
A B C D E
Fungal endophytic community
Lesion
Seedlings
Fungal endophytic community
?
TRENDS in Plant Science




| Bioagent | Trade Name/Formulation |
|---|---|
| *Agrobacterium radiobacter* strain K1026 | Nogall, |
| *A. radiobacter* strain K84 | Galltrol, Diegall |
| *Azospirillum brasilense/Azotobacter chroococcum* | Gmax Nitromax |
| *A. brasilense* | Azo-Green |
| *B. subtilis* MB1600 | BaciGold, HiStick N/T, Subtilex |
| *B. subtilis* strain FZB24 | Rhizo-Plus, Serenade, Rhapsody, Taegro, Tae-Technical |
| *Bacillus chlororaphis* 63-28 | AtEze |
| *Bacillus cereus* BPO1 | Pix plus |
| *Bacillus pumilus* GB 34 | Concentrate; YieldShield |
| *B. pumilus* QST2808 | Sonata ASO, Ballard |
| *B. subtilis* GB03 | Companion, System 3, Kodiak, Kodiak HB, Epic |
| *Bacillus amyloliquefaciens* GB99 | Quantum 4000 |
| *Bacillus licheniformis* SB3086 | EcoGuard, Green Releaf |
| *Burkholderia cepacia* | Blue Circle, Deny, Intercept |
| *P. fluorescens* A506 | BlightBan A506, Conquer, Victus |
| *Pseudomonas syringae* ESC-100 | Bio-Save 10, 11, 100, 110,1000, and 10 LP |
| *Pseudomonas chlororaphis* | Cedomon |
| *Pseudomonas cepacia* | Intercept |
| *Streptomyces griseovirdis* K61 | Mycostop |
| *B. subtilis* + *B. amyloliquefaciens* | Bio Yield |
| *Pseudomonas* spp. + *Azospirillum* spp. | BioJet |

ΓΟΝΙΔΙΩΜΑΤΙΚΗ → ΜΕΤΑΓΟΝΙΔΙΩΜΑΤΙΚΗ

Cell Systems
Article

# Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics

Ebrahim Afshinnekoo,[1,2,3,21] Cem Meydan,[1,2,21] Shanin Chowdhury,[1,2,4] Dyala Jaroudi,[1,2] Collin Boyer,[1,2] Nick Bernstein,[1,2] Julia M. Maritz,[5] Darryl Reeves,[1,2,6] Jorge Gandara,[1,2] Sagar Chhangawala,[1,2] Sofia Ahsanuddin,[1,2,7] Amber Simmons,[1,2] Timothy Nessel,[8] Bharathi Sundaresh,[8] Elizabeth Pereira,[8] Ellen Jorgensen,[9] Sergios-Orestis Kolokotronis,[10] Nell Kirchberger,[1,2] Isaac Garcia,[1,2] David Gandara,[1,2] Sean Dhanraj,[7] Tanzina Nawrin,[7] Yogesh Saletore,[1,2,6] Noah Alexander,[1,2] Priyanka Vijay,[1,2,6] Elizabeth M. Hénaff,[1,2] Paul Zumbo,[1,2] Michael Walsh,[11] Gregory D. O'Mullan,[3] Scott Tighe,[12] Joel T. Dudley,[13] Anya Dunaif,[14] Sean Ennis,[15,16] Eoghan O'Halloran,[15] Tiago R. Magalhaes,[15,16] Braden Boone,[17] Angela L. Jones,[17] Theodore R. Muth,[7] Katie Schneider Paolantonio,[5] Elizabeth Alter,[18] Eric E. Schadt,[13] Jeanne Garbarino,[14] Robert J. Prill,[19] Jane M. Carlton,[5] Shawn Levy,[17] and Christopher E. Mason[1,2,20,*]

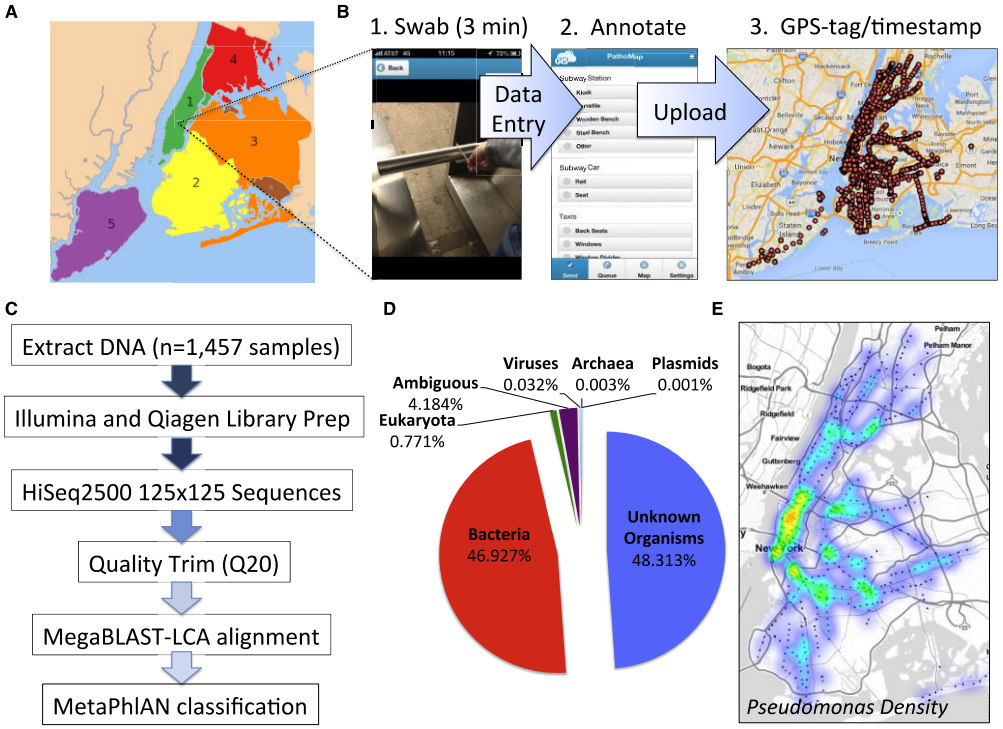



Figure 1. The Metagenome of New York City

# Are we all identical?

Elderly


Pregnant

Celiac

Overweight

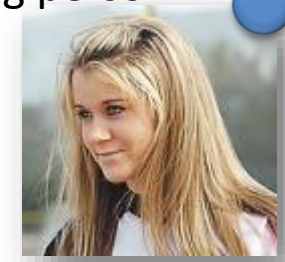
Cancer patient

Babies

Athlete


Kidney patient

Young person



Diabetic

# Οργάνωση της Γεωργικής Παραγωγής

ΣΠΟΡΑ

ΣΥΓΚΟΜΙΔΗ

ΚΑΤΑΝΑΛΩΣΗ

**ΔΗΜΙΟΥΡΓΙΑ ΝΕΩΝ ΠΟΙΚΙΛΙΩΝ**

- Δημιουργία παραλ/κότητας
- Επιλογή επιθυμητών γενοτύπων
- Αναπολλαπλασιασμός

**ΚΑΛΛΙΕΡΓΕΙΑ**

- Όλες οι καλλιεργητικές φροντίδες για την προστασία και την θρέψη του φυτού

**ΜΕΤΑΠΟΙΗΣΗ**

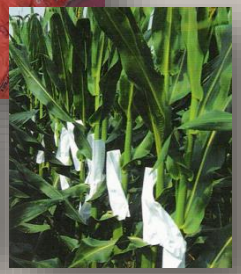
- Διαλογή
- Μηχανική, Φυσική, Χημική Επεξεργασία
- Συσκευασία-Τυποποίηση
- Διαφήμηση-Διάθεση

**1ο** **2ο** **3ο**

# ΤΥΧΑΙΟ

| WHEAT VARIETIES |
|---|
| ACHELOOS(ΑΧΕΛΩΟΣ) |
| ACHERON (ΑΧΕΡΩΝ) |
| AIGES (ΑΙΓΕΣ) |
| ALFIOS (ΑΛΦΕΙΟΣ) |
| APOLLONIA |
| APOTEOSI |
| ARACHTHOS (ΑΡΑΧΘΟΣ) |
| AXIOS (ΑΞΙΟΣ) |
| CENTAURO |
| DIO (ΔΙΟ) |
| ……. |
| VERDI |
| VERTICO |



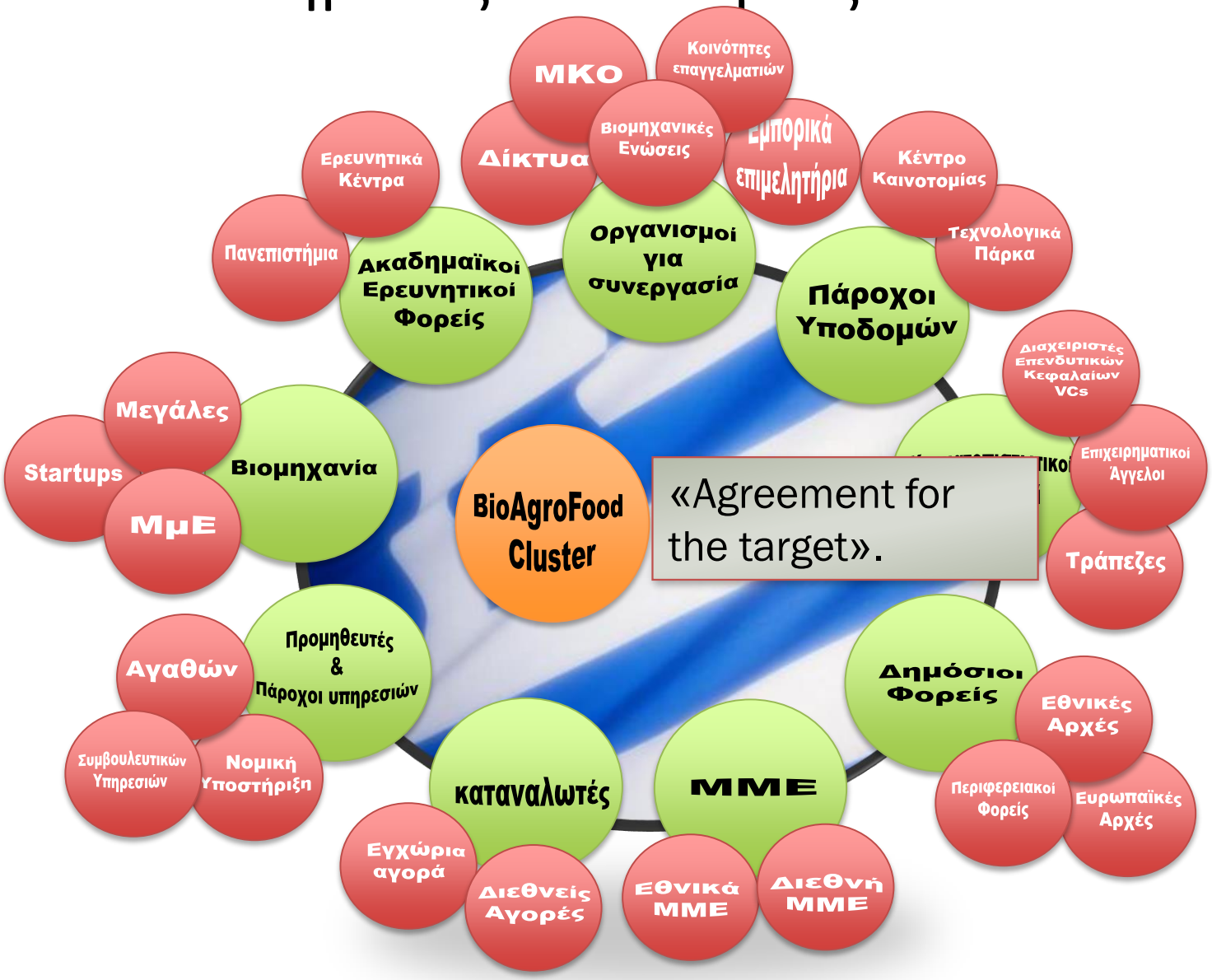



# ΤΥΧΑΙΟ

## Fine mapping and marker-assisted selection (MAS) of a low glutelin content gene in rice

| WHEAT VARIETIES |
|---|
| ACHELOOS(ΑΧΕΛΩΟΣ) |
| ACHERON (ΑΧΕΡΩΝ) |
| AIGES (ΑΙΓΕΣ) |
| ALFIOS (ΑΛΦΕΙΟΣ) |
| APOLLONIA |
| APOTEOSI |
| ARACHTHOS (ΑΡΑΧΘΟΣ) |
| AXIOS (ΑΞΙΟΣ) |
| CENTAURO |
| DIO (ΔΙΟ) |
| …… |
| VERDI |
| VERTICO |

# Τα συστατικά για τη δημιουργία ενός Οικοσυστήματος Καινοτομίας - > Cluster



# ΕΥΧΑΡΙΣΤΩ ΓΙΑ ΤΗΝ ΠΡΟΣΟΧΗ ΣΑΣ

# DNA barcoding-Biodiversity identification and discovery


PNAS

## Use of DNA barcodes to identify flowering plants

W. John Kress*†, Kenneth J. Wurdack*‡, Elizabeth A. Zimmer*, Lee A. Weigt‡, and Daniel H. Janzen§

*Department of Botany and ‡Laboratories of Analytical Biology, National Museum of Natural History, Smithsonian Institution, P.O. Box 37012, Washington, DC 20013-7012; and §Department of Biology, University of Pennsylvania, Philadelphia, PA 19104

Contributed by Daniel H. Janzen, April 15, 2005

Methods for identifying species by using short orthologous DNA sequences, known as "DNA barcodes," have been proposed and initiated to facilitate biodiversity studies, identify juveniles, associate sexes, and enhance forensic analyses. The cytochrome c

paper is not to debate the validity of using barcodes for plant identification, but rather to determine appropriate DNA regions for use in flowering plants.

A portion of the mitochondrial CO1 gene was deliberately

BIOTROPICA 40(4): 405–406

## DNA Barcoding—a Windfall for Tropical Biology?

W. John Kress[1] and David L. Erickson

PLoS one

OPEN ACCESS Freely available online

## A Two-Locus Global DNA Barcode for Land Plants: The Non-Coding *trnH-*

## *rbcL* Gene Complements

## Region

NEWSFOCUS

TAXONOMY

## Wanted: A Barcode for Plants

PNAS

COMMENTARY

## DNA barcodes: Genes, genomics, and bioinformatics

W. John Kress* and David L. Erickson

*Department of Botany, MRC-166, National Museum of Natural History, Smithsonian Institution, P.O. Box 37012, Washington, DC 20013-7012*

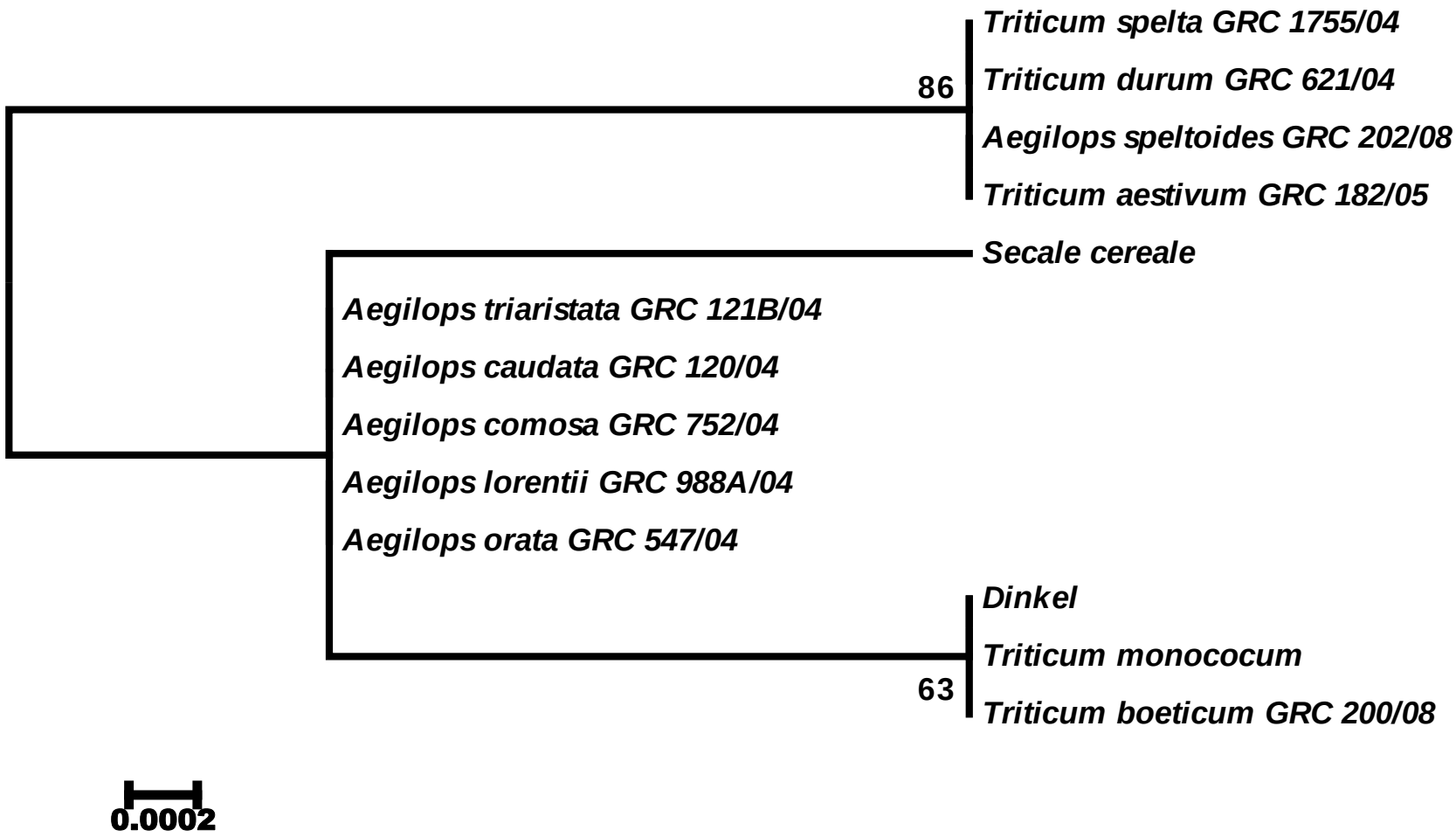
It is not a coincidence that DNA barcoding has developed in concert with genomics-based investigations. DNA barcoding (a tool for rapid species identification based on DNA

DNA Barcoding

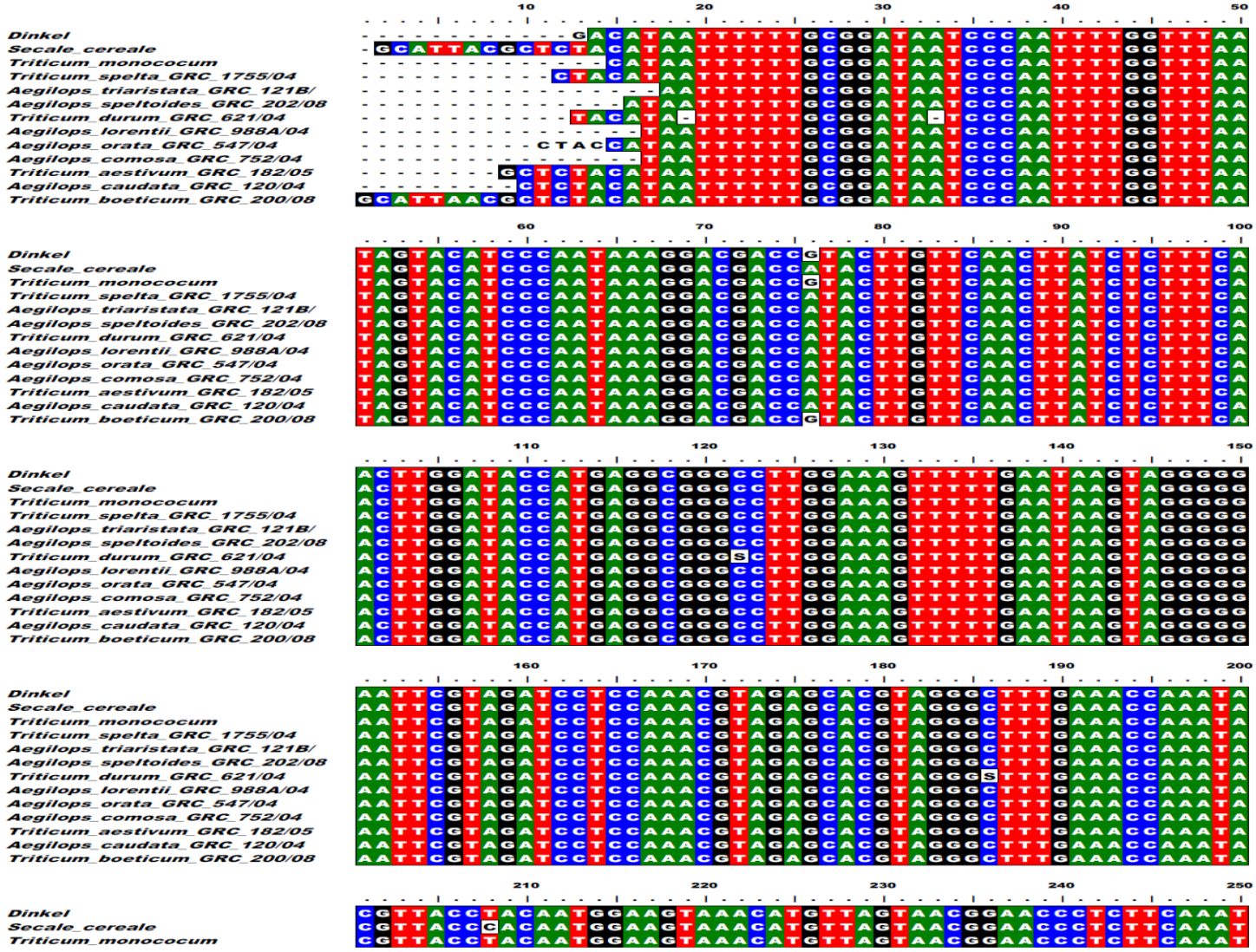
Genomics

# Triticaceae

# Triticaceae



# Triticaceae



RESEARCH ARTICLE

# A chromosome-based draft sequence of the hexaploid bread wheat (*Triticum aestivum*) genome

The International Wheat Genome Sequencing Consortium (IWGSC)[*,†]

+ [illegible]

*Science* [illegible]

## Ερευνητές αποκωδικοποιούν το γονιδίωμα του σιταριού

**Σκοπός η καλύτερη διατροφή του παγκόσμιου πληθυσμού**

ΥΓΕΙΑ

15:22 • 18/07/2014

ARTICLE

OPEN

doi:10.1038/nature22043

# A chromosome conformation capture ordered sequence of the barlev genome

## Διαβάστηκε το DNA του κριθαριού

**ΔΗΜΟΣΙΕΥΣΗ**: 27/04/2017 10:08 |

the plant journal

SEB Society for Experimental Biology

*The Plant Journal* (2017)

doi: 10.1111/tpj.13515

RESOURCE

# The pangenome of hexaploid bread wheat

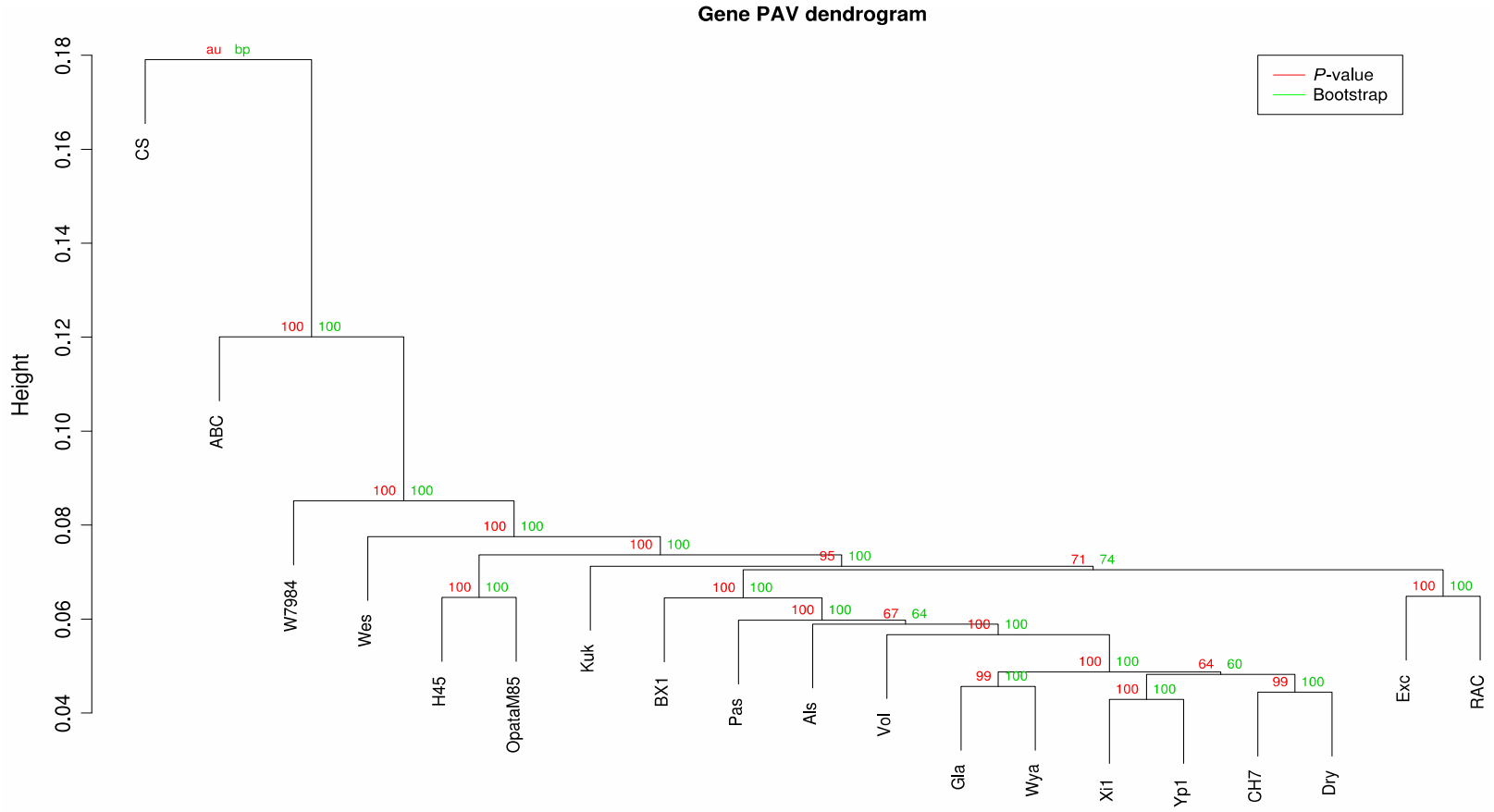



**Figure 2.** Dendrogram of the 19 cultivars based on the presence–absence variation of genes in each cultivar.