




The InnoFOOD SEE Project

INSTITUTE OF APPLIED BIOSCIENCES
ΙΝΣΤΙΤΟΥΤΟ ΕΦΑΡΜΟΣΜΕΝΩΝ ΒΙΟΕΠΙΣΤΗΜΩΝ
CERTH

FOOD PRODUCTION IN THE GENOMICS ERA

Dr. Notis Argiriou

SOUTH EAST EUROPE
Jointly for our common future

INNO-FOOD SEE

THE CHALLENGES OF AGRICULTURE

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THE F OF AGRICULTURE

Food

Feed

Fiber

Flowers

Farmaceuticals and Parfums

Fuels

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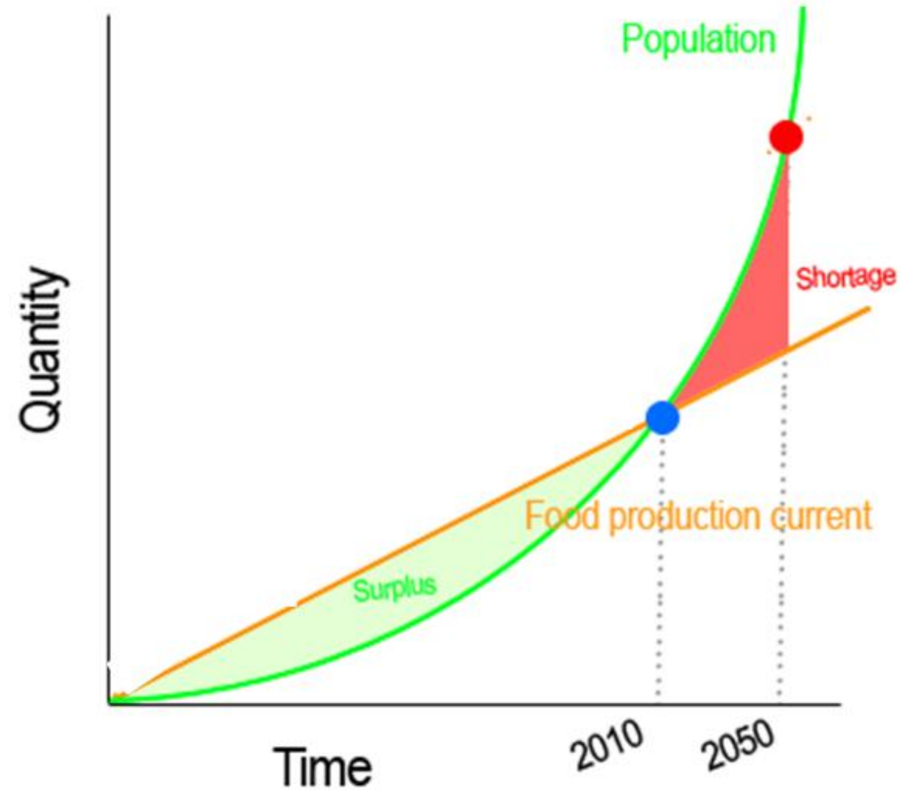
Food
Τρόφιμα

Current Food Production vs. Future Food Production In Relation to Growing World Populations Over Time



Less arable land

Less water and desertification

Less biodiversity and genetic material

Less pesticides and chemicals

High energy prices

INTRODUCTION AND TRAINING OBJECTIVES

TRAINING OBJECTIVES

- To demonstrate applications of the knowledge obtained from genomics
- To present some of the main genomic technologies
- To present the New Trends on Food Production
- To train on methods that can be easily introduced in other laboratories of the SEE area.
- To promote the exchange of experience between different laboratories and eventually set-up a network between them
- To demonstrate protocols for the traceability of PDO or high added value products
- To introduce innovations in the agri-food chain particularly those related to nucleic acid technologies.

THE AGRI-FOOD CHAIN

Seedling

Harvesting

Consumption

New Varieties and Breeds

- Selection of genotypes
- Production of germplasm and seeds

1º

Cultivation and Farming

- Cultivation and Farming Methods

2º

Transformation

- Harversting
- Mechanical, Chemical and Physical Transformation
- Packaging
- Promotion

3º

FROM GENETICS TO GENOMICS AND APPLICATIONS

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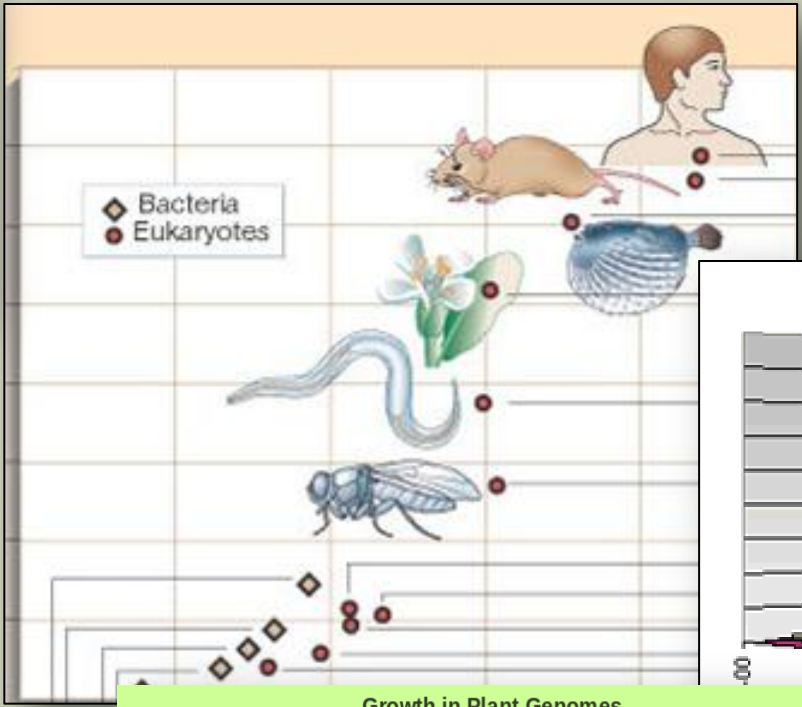
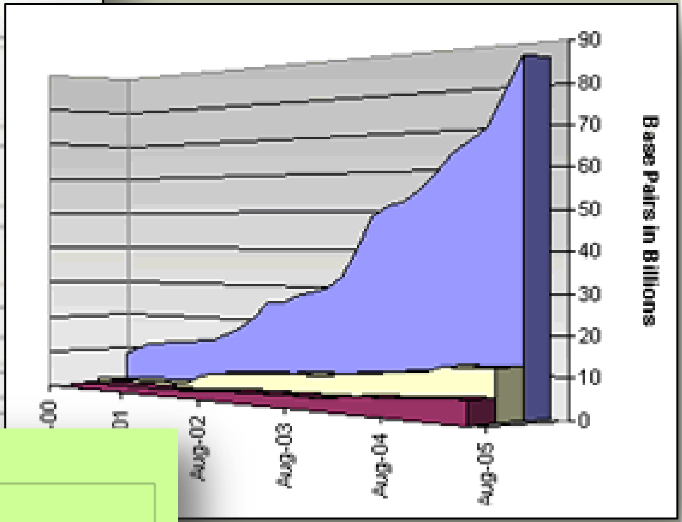
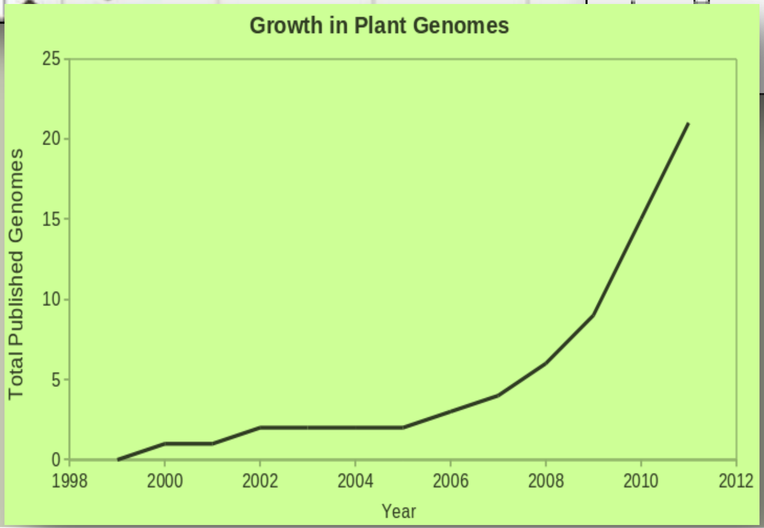
GENETICS → GENOMICS

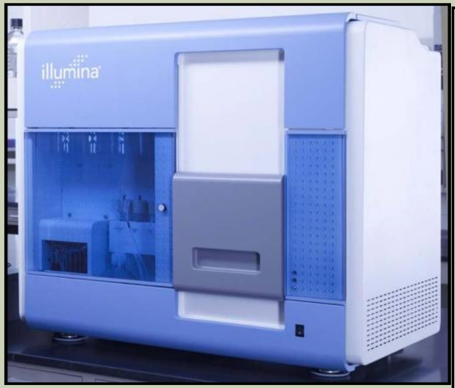




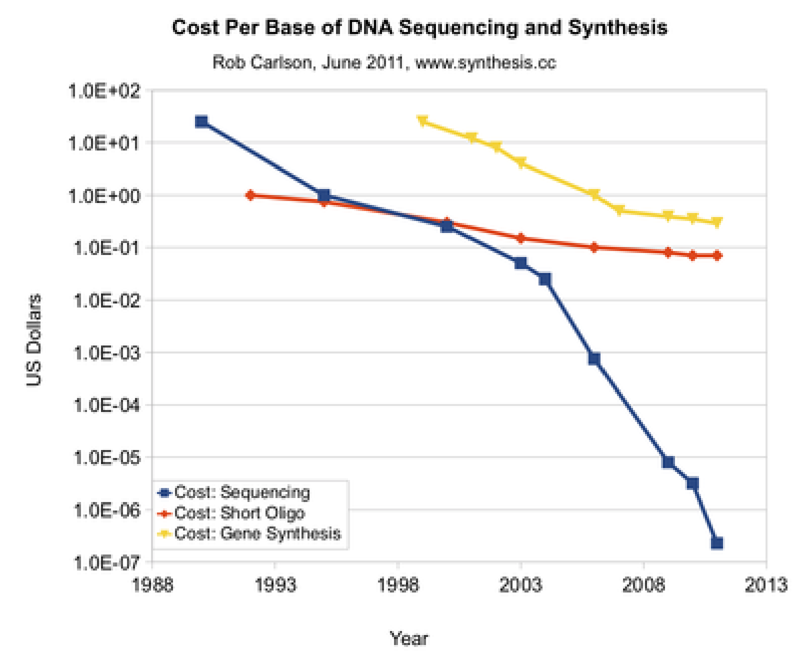


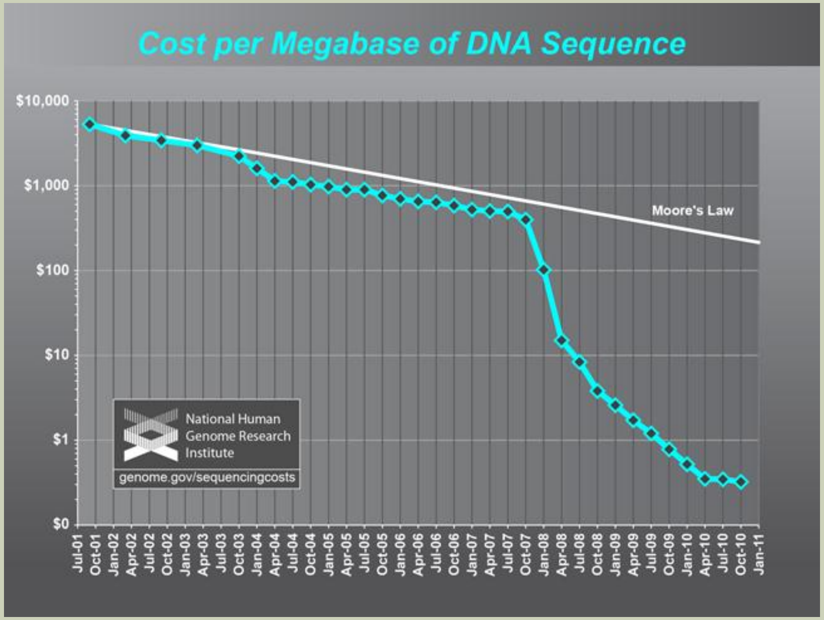
SEQUENCING PLATFORMS

- Roche/454 FLX: 2004
- Illumina Solexa Genome Analyzer: 2006
- Applied Biosystems SOLiD™ System: 2007
- Helicos Heliscope™ : 2009
- Pacific Biosciences SMRT: 2010
- Ion Torrent: 2011
- Ion Proton 2012



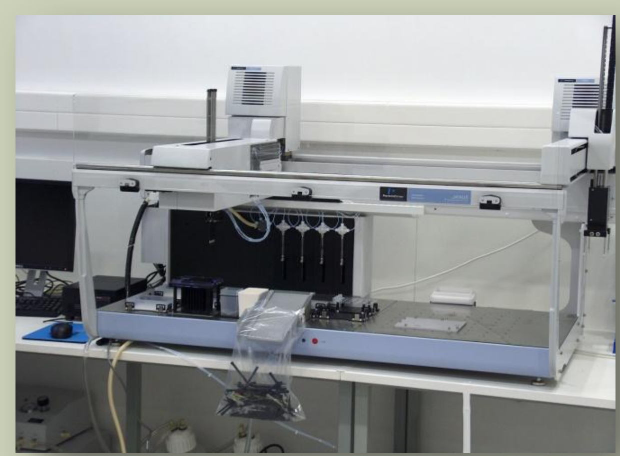
SEQUENCING COSTS



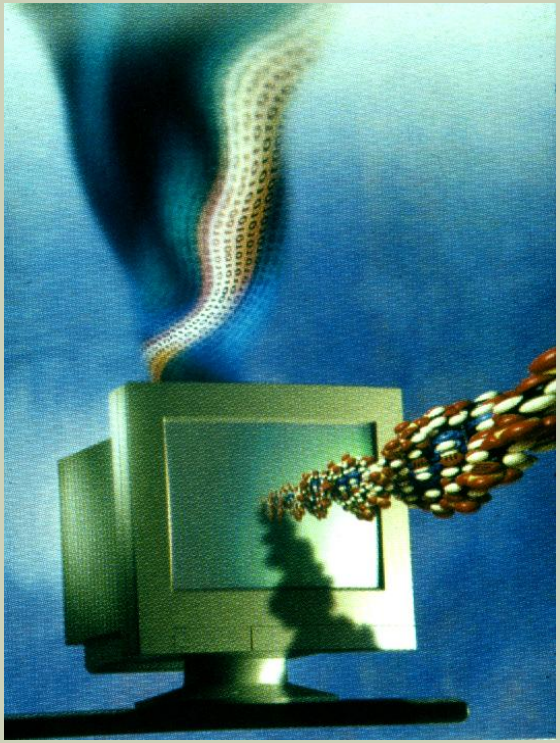


High cost, time consuming, high level of expertise

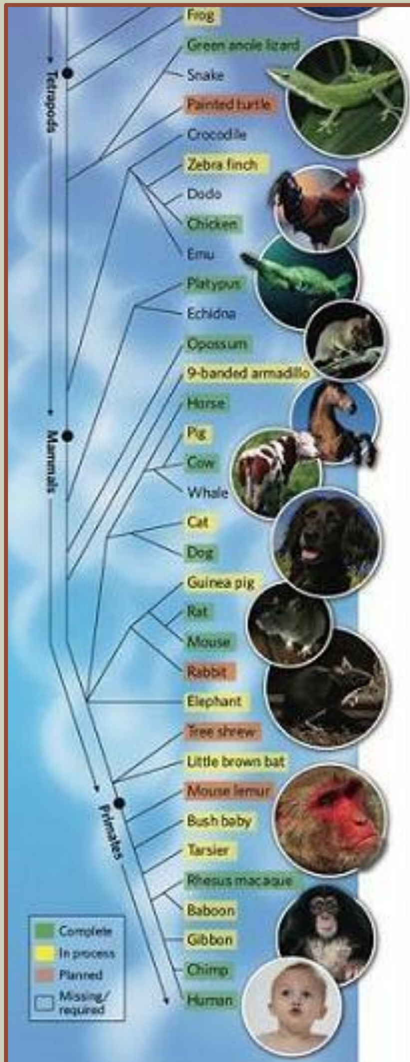
AUTOMATION

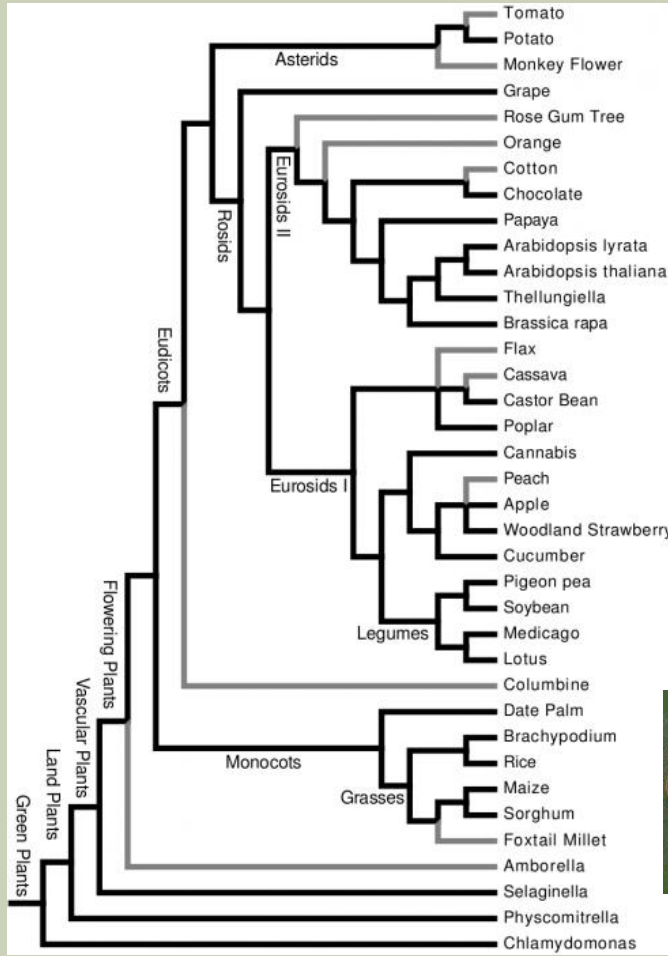


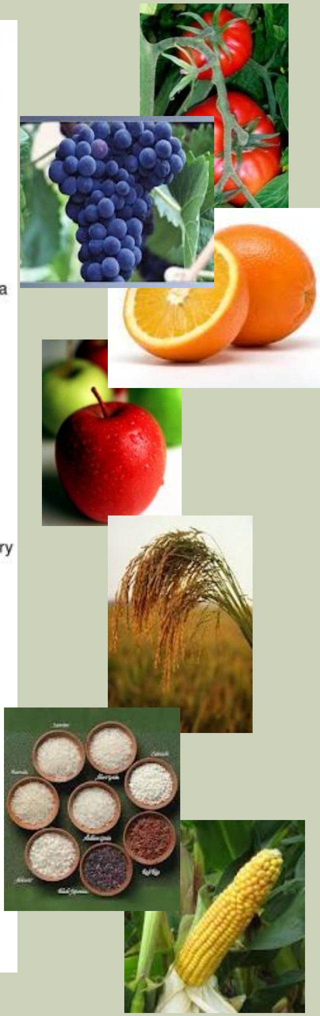
BIOINFORMATICS



SEQUENCED GENOMES







The First 50 Plant Genomes

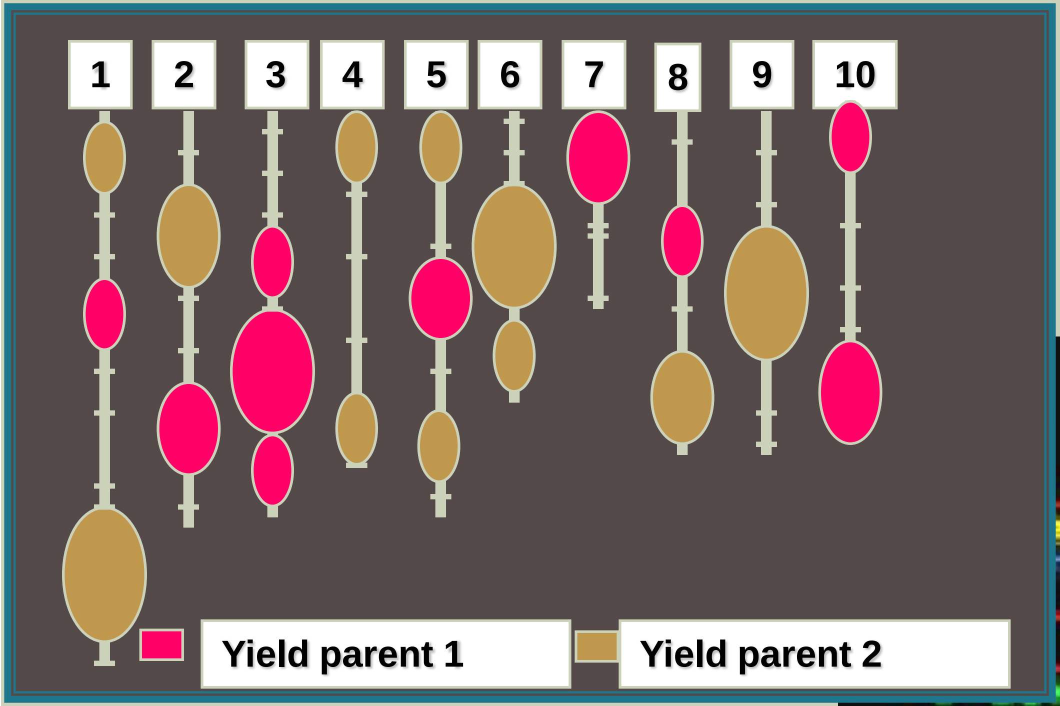
Todd P. Michael* and Scott Jackson

THE PLANT GENOME ▪ JULY 2013 ▪ VOL. 6, NO. 2

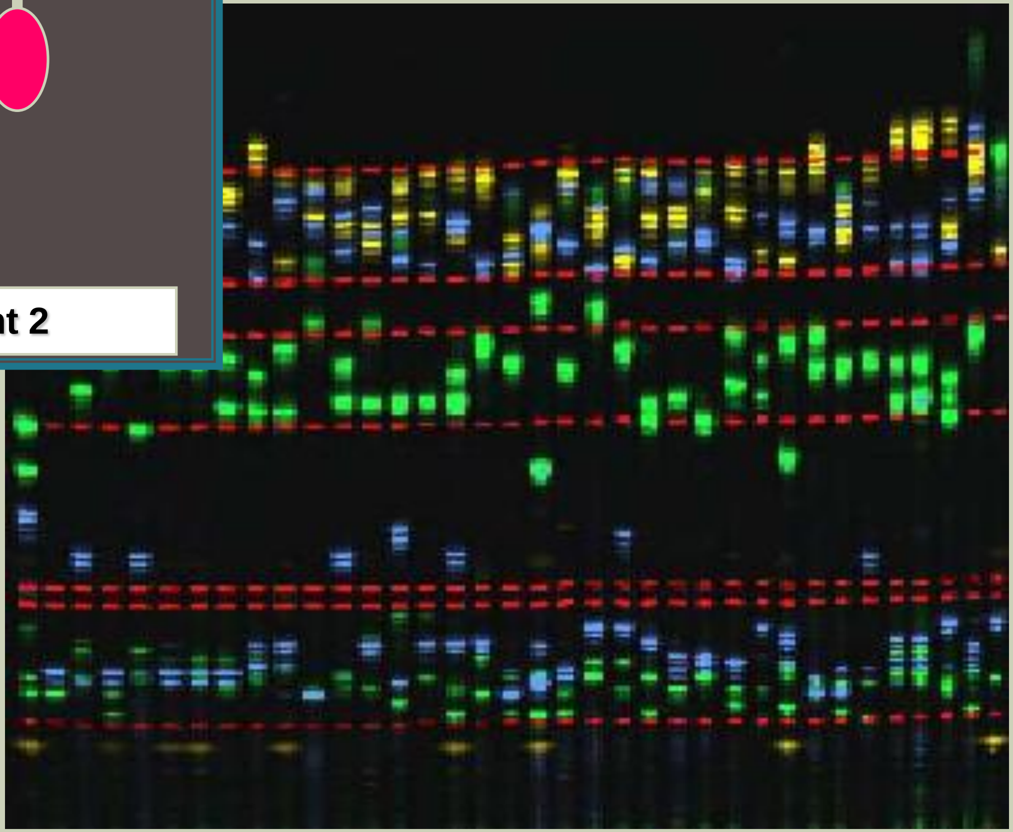
Table 1. Published plant genomes.†

	Scientific name	Common name	Year	Type	Division or monocot/dicot	Chr (#)	Size	Assembled	Assem	Gene (#)	Repeat	scaffold N50	contig N50	Sequencer types	Journal	PMID
							——Mb——		%		%	kb				
1	*Arabidopsis thaliana*	arabidopsis	2000	model	dicot	5	125	115	92	25,498	14	NA	NA	Sa	Nature	11130711
2	*Oryza sativa*	rice	2002	crop	monocot	12	430	362	84	59,855	26	12	7	Sa	Science	11935017
3	*Oryza sativa*	rice	2002	crop	monocot	12	420	389	93	61,668	NA	NA	NA	Sa	Science	11935018
4	*Oryza sativa*	rice	2005	crop	monocot	12	389	371	95	37,544	26	NA	NA	Sa	Nature	16100779
5	*Populus trichocarpa*	black cottonwood	2006	crop	dicot	19	485	410	84	45,555	NA	3100	126	Sa	Science	16973872
6	*Vitis vinifera*	grape	2007	crop	dicot	19	475	487	103	30,434	41	2065	66	Sa	Nature	17721507
7	*Physcomitrella patens*	moss	2008	model	bryophyta	27	510	480	94	35,938	16	1320	292	Sa	Science	18079367
8	*Vitis vinifera*	grape	2007	crop	dicot	19	505	477	95	29,585	27	1330	18	Sa,4	PlosOne	18094749
9	*Carica papaya*	papaya	2008	crop	dicot	9	372	370	99	28,629	43	1000	11	Sa	Nature	18432245
10	*Lotus japonicus*	lotus	2008	model	dicot	6	472	315	67	30,799	56	NA	NA	Sa	DNA Research	18511435
11	*Sorghum bicolor*	sorghum	2009	crop	monocot	10	818	739	90	34,496	62	62,400	195	Sa	Nature	19189423
12	*Cucumis sativus*	cucumber	2009	crop	dicot	7	367	244	66	26,682	24	1140	20	Sa,I	Nature Genetics	19881527
13	*Zea mayes*	maize	2009	crop	monocot	10	2300	2048	89	32,540	85	76	40	Sa	Science	19965430
14	*Glycine max*	soybean	2010	crop	dicot	20	1115	973	87	46,430	57	47,800	189	Sa	Nature	20075913
15	*Brachypodium distachyon*	brachypodium	2010	model	monocot	5	272	272	100	25,532	21	59,300	348	Sa	Nature	20148030
16	*Ricinus communis*	castor bean	2010	crop	dicot	10	320	326	102	31,237	50	561	21	Sa	Nature Biotechnology	20729833
17	*Malus x domestica*	apple	2010	crop	dicot	17	742	604	81	57,386	67	1542	13	Sa,4	Nature Genetics	20802477
18	*Jatropha curcas*	jatropha	2010	crop	dicot	NA	380	286	75	40,929	37	NA	4	Sa,	DNA Research	21149391
19	*Theobroma cacao*	cocoa	2011	crop	dicot	10	430	327	76	28,798	24	473	20	Sa,4,I	Nature Genetics	21186351
20	*Fragaria vesca*	strawberry	2011	crop	dicot	7	240	210	87	34,809	23	1361	NA	4,S,I	Nature Genetics	21186353
21	*Arabidopsis lyrata*	lyrata	2011	model	dicot	8	207	207	100	32,670	30	24,500	227	Sa	Nature Genetics	21478890
22	*Selaginella moellendorffii*	spikemoss	2011	non-model	lycopod	NA	110	213	193	22,285	38	1700	120	Sa	Science	21551031
23	*Phoenix dactylifera*	date palm	2011	crop	monocot	18	658	381	58	28,890	40	30	6	I	Nature Biotechnology	21623354
24	*Solanum tuberosum*	potato	2011	crop	dicot	12	844	727	86	39,031	62	1318	31	Sa,4,I	Nature	21743474
25	*Thellungiella parvula*	thellungiella	2011	model	dicot	7	140	137	98	30,419	8	5290	NA	4,I	Nature Genetics	21822265
26	*Cucumis sativus*	cucumber	2011	crop	dicot	7	367	323	88	26,587	NA	319	323	Sa,4	PlosOne	21829493
27	*Brassica rapa*	chinese cabbage	2011	crop	dicot	10	485	284	59	41,174	40	1971	27	I	Nature Genetics	21873998
28	*Cannabis sativa*	hemp	2011	crop	dicot	?	820	787	96	30,074	NA	16	2	4,I	Genome Biology	22014239
29	*Cajanus cajan*	pigeon pea	2011	crop	dicot	11	833	605	72	48,680	52	516	22	Sa,I	Nature Biotechnology	22057054
30	*Medicago truncatula*	medicago	2011	model	dicot	8	454	262	58	62,388	31	1270	NA	Sa,4,I	Nature	22089132
31	*Setaria italica*	setaria	2012	model	monocot	9	490	423	86	38,801	46	1007	25	I	Nature Biotechnology	22580950
32	*Setaria italica*	setaria	2012	model	monocot	9	510	397	80	35,471	40	47,300	126	Sa	Nature Biotechnology	22580951
33	*Solanum lycopersicum*	tomato	2012	crop	dicot	12	900	760	84	34,727	63	16,467	87	Sa,4,S,I	Nature	22660326
34	*Cucumis melo*	melon	2012	crop	dicot	12	450	375	83	27,427	NA	4680	18	Sa,4,I	PNAS	22753475
35	*Linum usitatissimum*	flax	2012	crop	dicot	15	373	318	85	43,484	24	132	20	I	Plant Journal	22757964
36	*Musa acuminata malaccensis*	banana	2012	crop	monocot	11	523	472	90	36,542	44	1311	43	Sa,4,I	Nature	22801500
37	*Gossypium raimondii*	cotton D	2012	crop	dicot	13	880	775	88	40,976	60	2284	45	I	Nature Genetics	22922876
38	*Azadirachta indica*	neem	2012	crop	dicot	NA	364	NA	NA	20,169	13	452	1	4,I	BMC Genomics	22958331
39	*Hordeum vulgare*	barely	2012	crop	monocot	7	5100	4980	98	30,400	84	NA	NA	NA	Nature	23075845

	Scientific name	Common name	Year	Type	Division or monocot/dicot	Chr (#)	Size	Assembled	Assem	Gene (#)	Repeat	scaffold N50	contig N50	Sequencer types	Journal	PMID
							——Mb——		%		%	kb				
40	*Pyrus bretschneideri*	pear	2013	crop	dicot	17	527	512	97	42,812	53	541	36	I	Genome Research	23149293
41	*Citrullus lanatus*	watermelon	2012	crop	dicot	11	425	354	83	23,440	45	2380	26	I	Nature Genetics	23179023
42	*Triticum aestivum*	wheat	2012	crop	monocot	21	17,000	3800	22	94,000	80	NA	1	4	Nature	23192148
43	*Gossypium raimondii*	cotton D	2012	crop	dicot	13	880	738	84	37,505	61	18,800	136	Sa,4,I	Nature	23257886
44	*Prunus mume*	chinese plum	2012	crop	dicot	8	280	237	85	31,390	45	578	32	I	Nature Communications	23271652
45	*Cicer arietinum*	chickpea	2013	crop	dicot	8	738	532	72	28,269	49	39,990	24	Sa,I	Nature Biotechnology	23354103
46	*Hevea brasiliensis*	rubber tree	2013	crop	dicot	18	2150	1119	52	68,955	72	3	NA	4,S,I	BMC Genomics	23375136
47	*Phyllostachys heterocycla*	moso bamboo	2013	non-model	monocot	24	2075	2051	99	31,987	59	329	12	I	Nature Genetics	23435089
48	*Oryza brachyantha*	rice relative	2013	non-model	monocot	12	300	263	88	32,038	29	1013	20	I	Nature Communications	23481403
49	*Prunus persica*	peach	2013	crop	dicot	8	265	227	86	27,852	37	27,400	214	Sa	Nature Genetics	23525075
50	*Aegilops tauschii*	wheat DD	2013	crop	monocot	7	4360	4244	97	43,150	66	58	5	4,I	Nature	23535592
51	*Triticum urartu*	wheat AA	2013	crop	monocot	7	4940	4660	94	34,879	67	64	3	I	Nature	23535596
52	*Nelumbo nucifera*	ancient lotus	2013	non-model	dicot	8	929	804	87	26,685	57	3400	39	I	Genome Biology	23663246
53	*Utricularia gibba*	bladderwort	2013	non-model	dicot	16	77	82	106	28,500	3	95	26	4,I	Nature	23665961
54	*Picea abies*	norway spruce	2013	crop	gymnosperm	12	19,600	12,000	61	28,354	NA	NA	NA		Nature	23698360
55	*Capsella rubella*	capsella	2013	non-model	dicot	8	219	135	62	26,521	NA	15,100	134	Sa	Nature Genetics	23749190

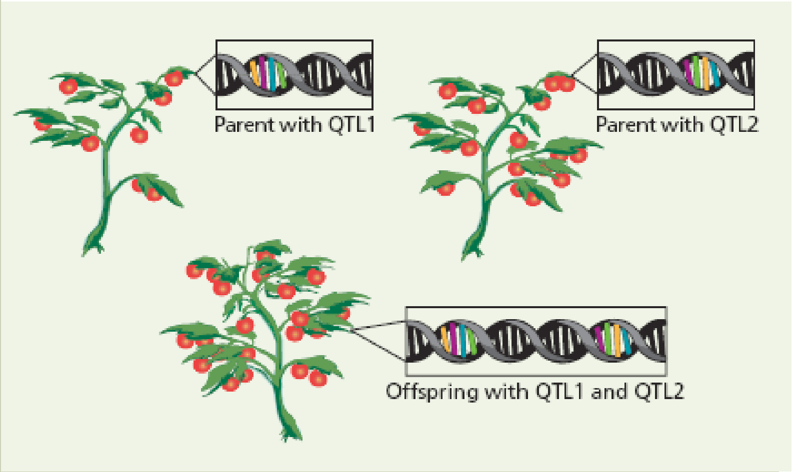


•*Molecular Breeding*

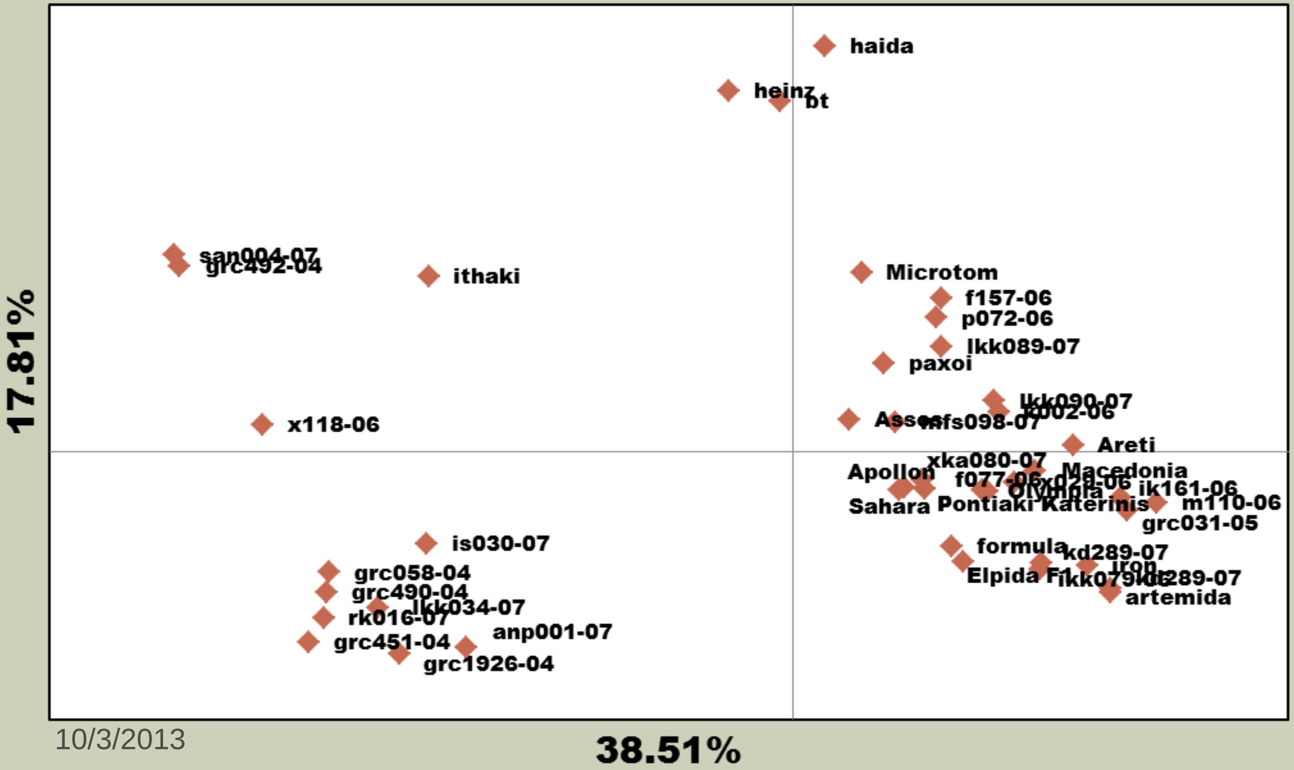


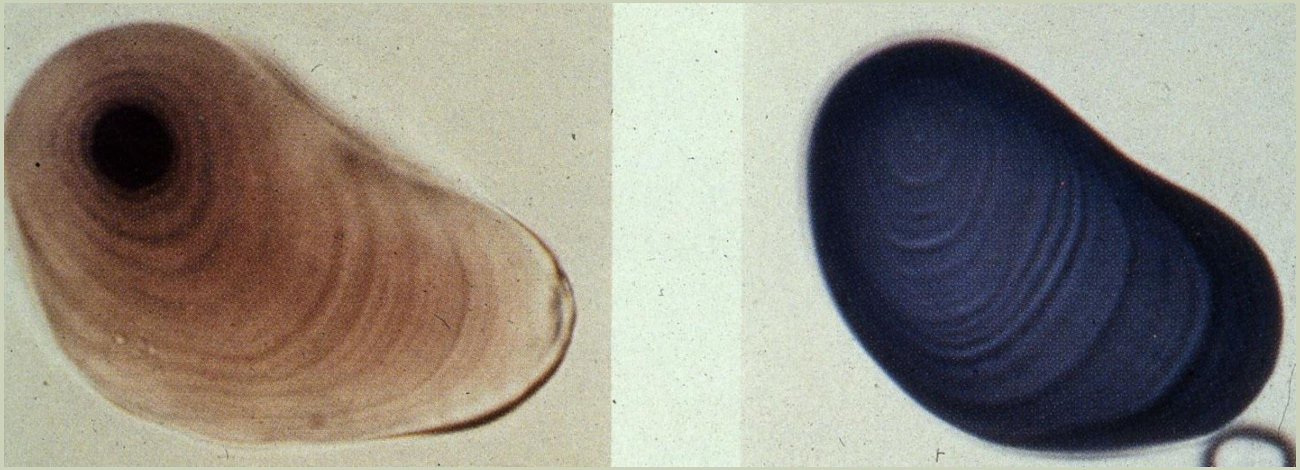
•*Molecular markers (genotyping)*

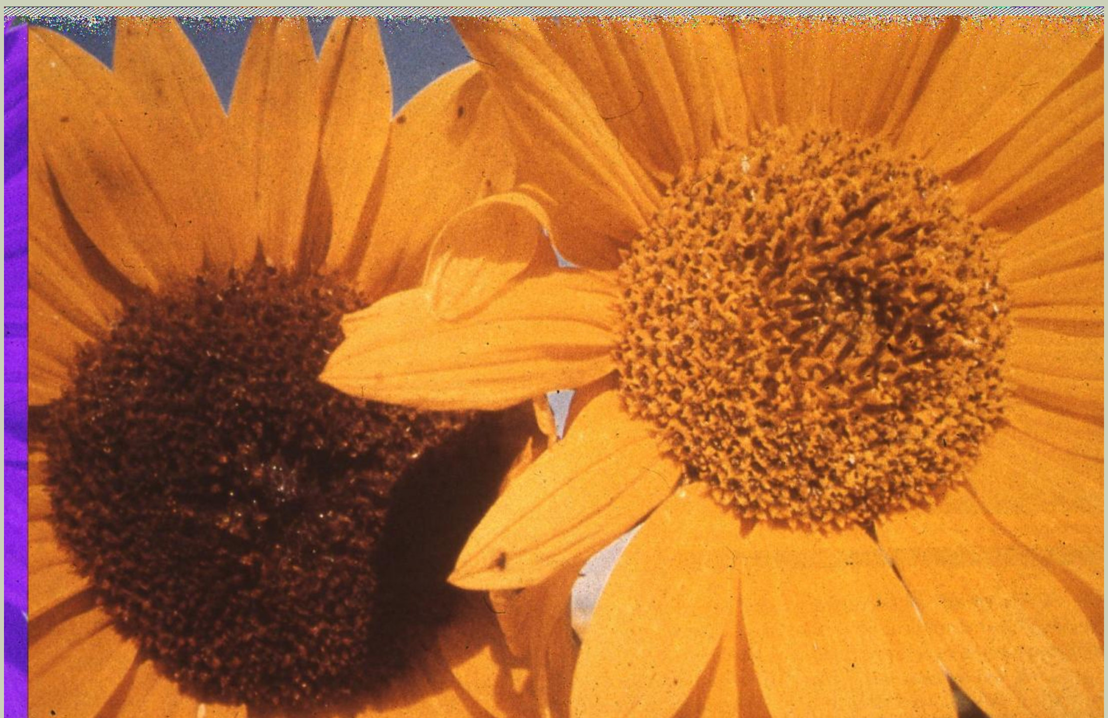
NUTRITOM

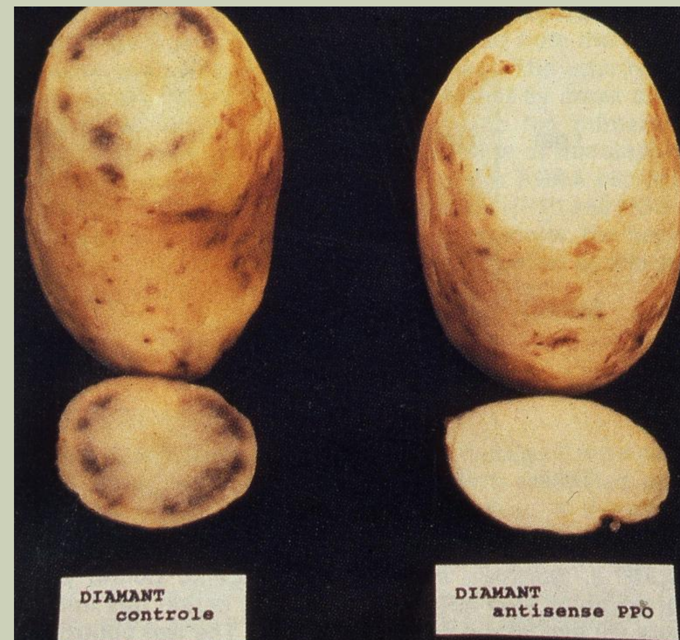


Principal Coordinates





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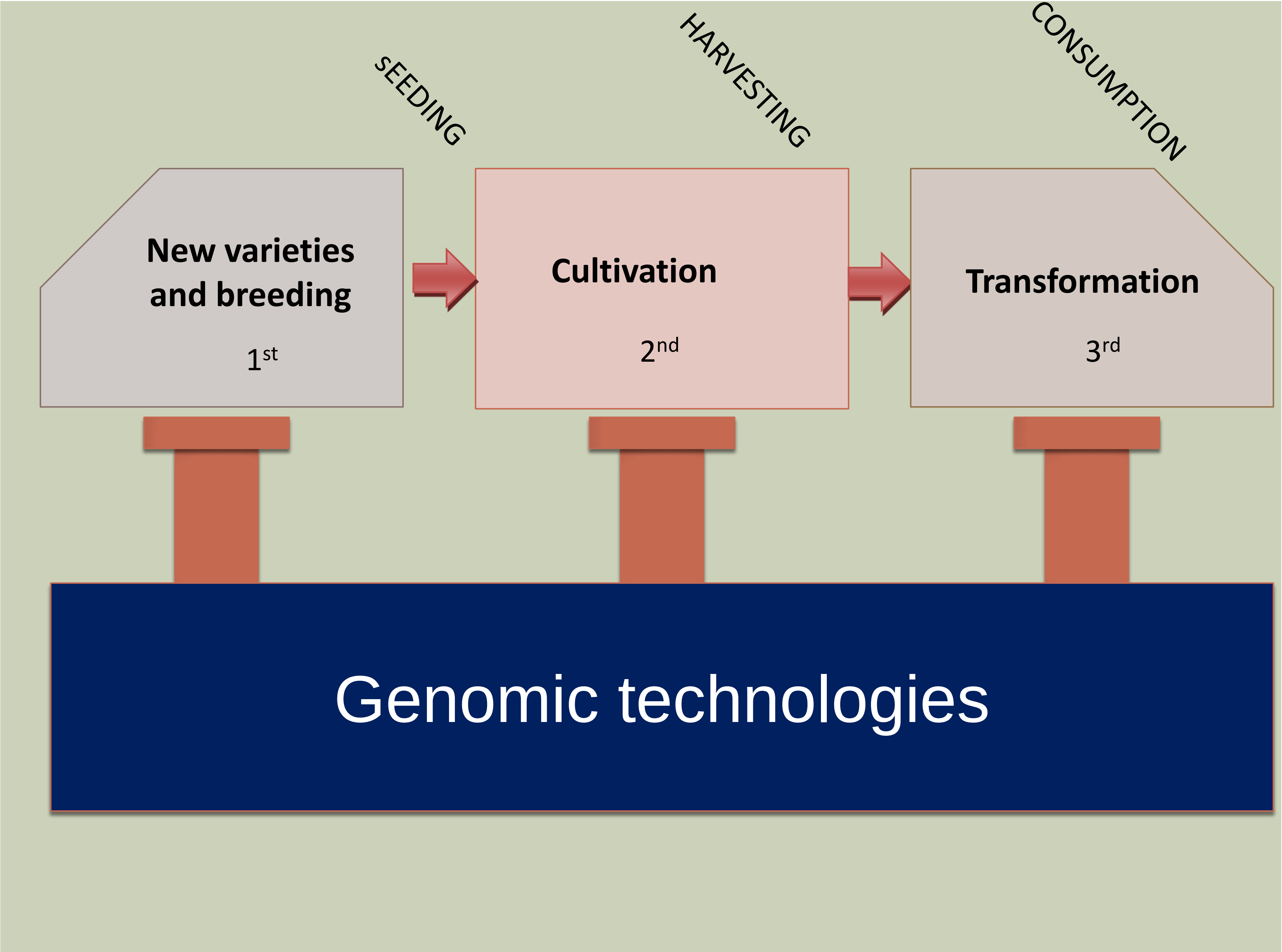
SEEDING
HARVESTING
CONSUMPTION
New varieties and breeding
1st
Cultivation
2nd
Transformation
3rd
Genomic technologies

FROM GENOMICS TO META-GENOMICS AND APPLICATIONS

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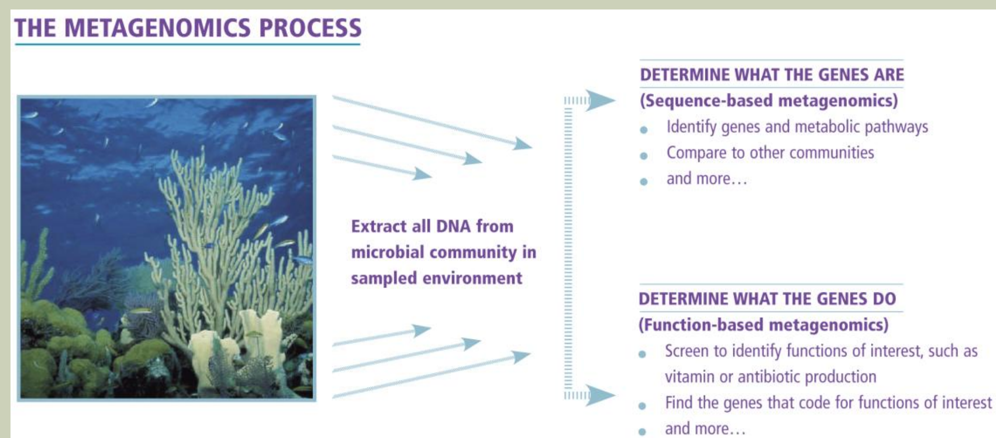
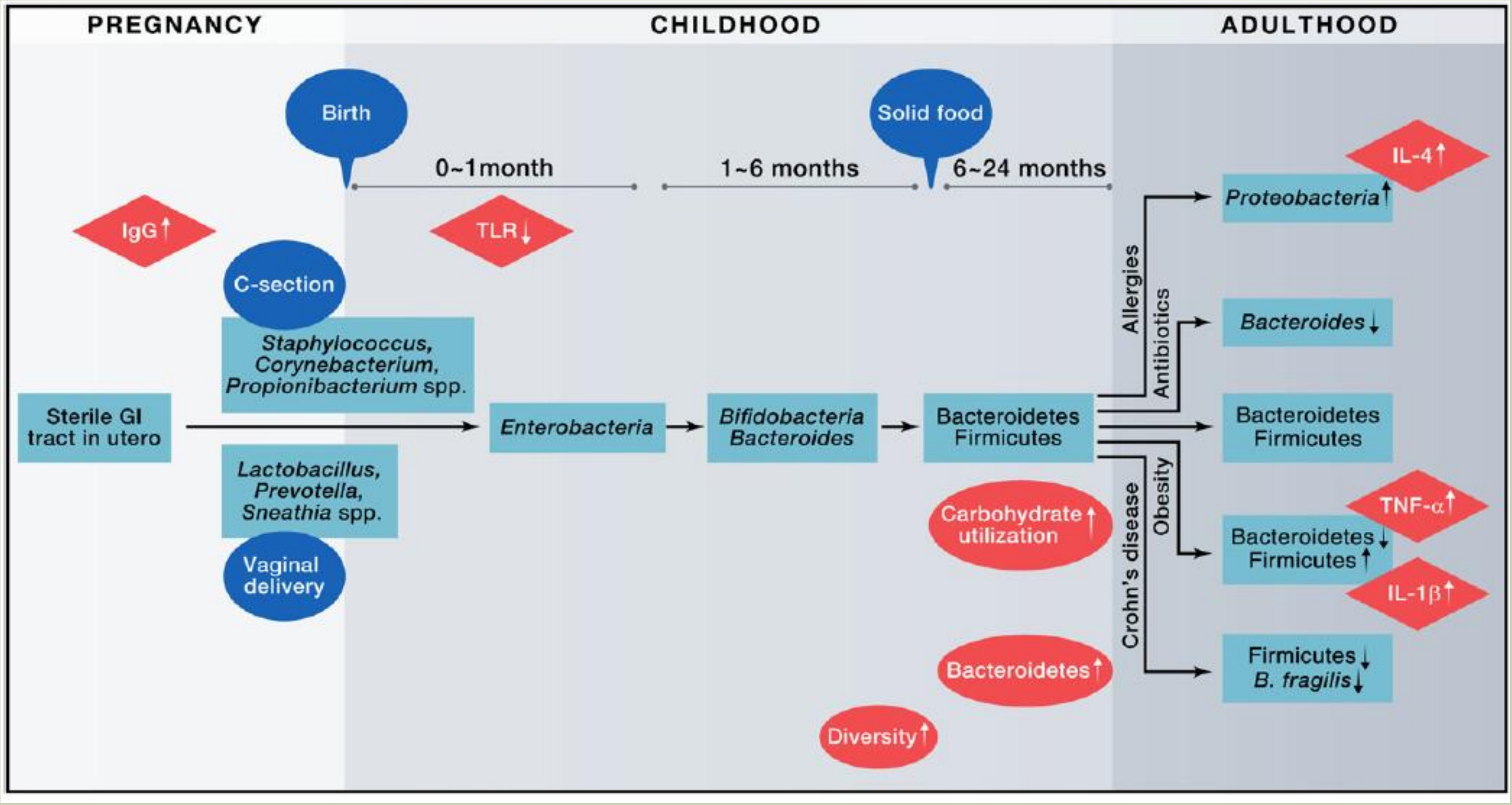
GENOMICS → METAGENOMICS

Evolution of Mammals and Their Gut Microbes

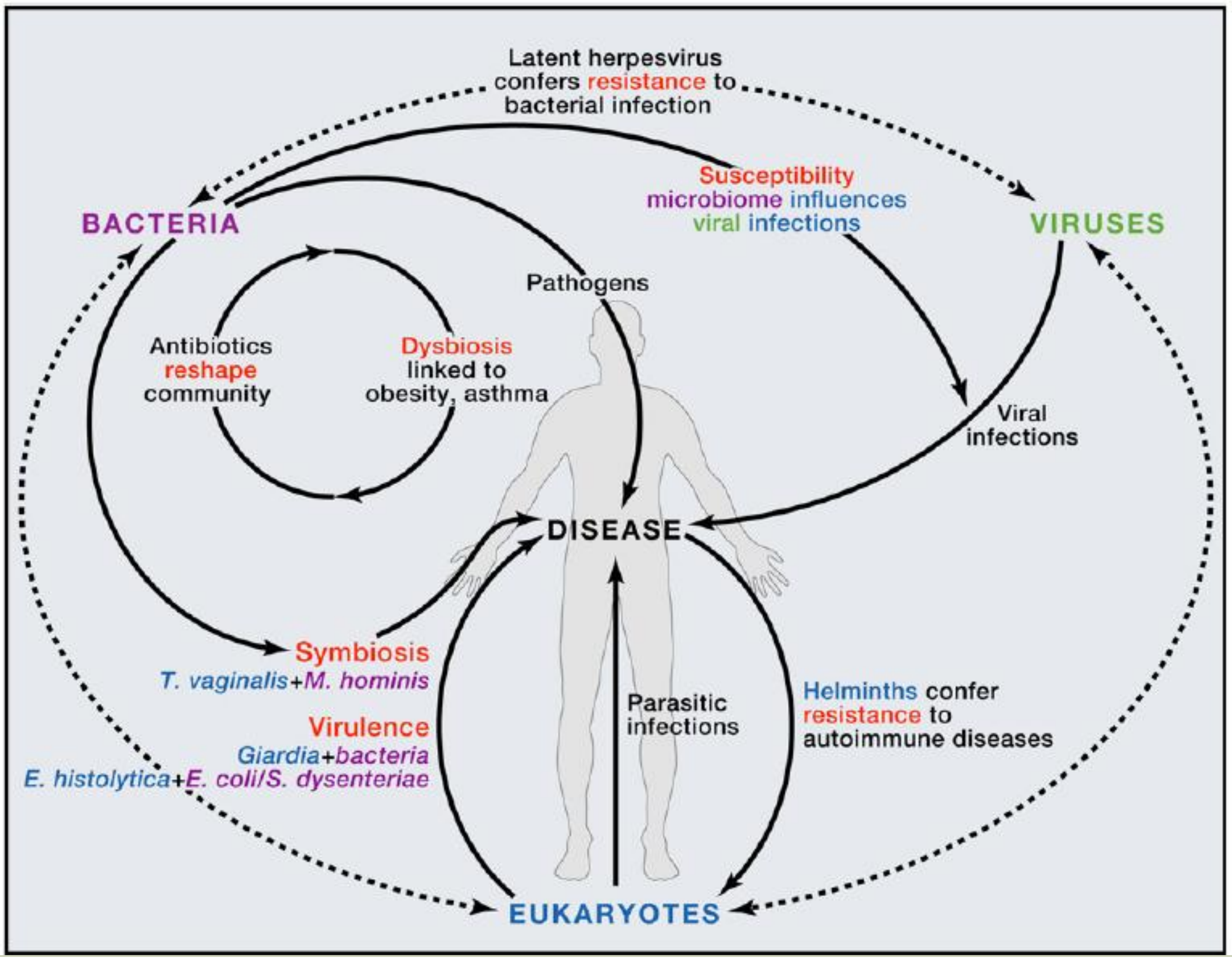
Ruth E. Ley,[1] Micah Hamady,[2] Catherine Lozupone,[1,3] Peter J. Turnbaugh,[1] Rob Roy Ramey,[4] J. Stephen Bircher,[5] Michael L. Schlegel,[6] Tammy A. Tucker,[6] Mark D. Schrenzel,[6] Rob Knight,[3] Jeffrey I. Gordon[1]*



DEVELOPMENT OF MICROORGANISMS IN HUMANS



INTERACTIONS OF BACTERIA, VIRUS AND EUKARYOTIC ORGANISMS IN HUMANS



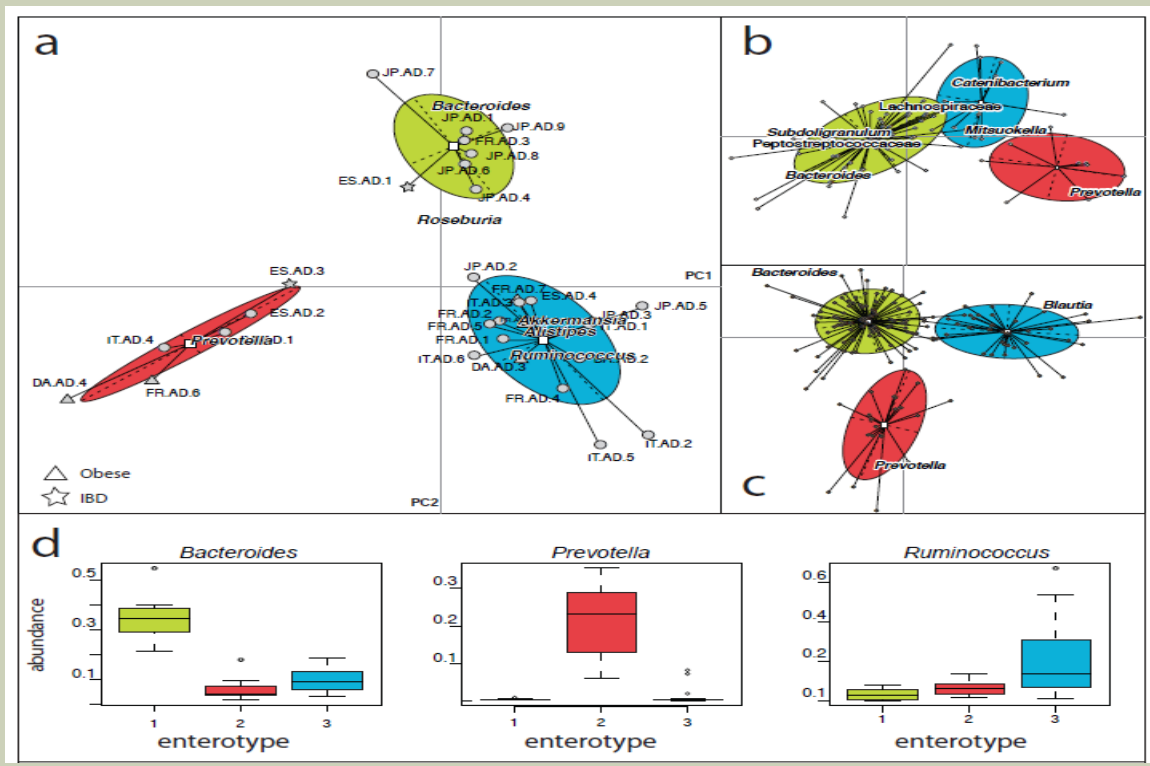
ARTICLE

doi:10.1038/nature09944

Enterotypes of the human gut microbiome

Manimozhiyan Arumugam[1]*, Jeroen Raes[1,2]*, Eric Pelletier[3,4,5], Denis Le Paslier[3,4,5], Takuji Yamada[1], Daniel R. Mende[1], Gabriel R. Fernandes[1,6], Julien Tap[1,7], Thomas Bruls[3,4,5], Jean-Michel Batto[7], Marcelo Bertalan[8], Natalia Borruel[9], Francesc Casellas[9], Leyden Fernandez[10], Laurent Gautier[8], Torben Hansen[11,12], Masahira Hattori[13], Tetsuya Hayashi[14], Michiel Kleerebezem[15], Ken Kurokawa[16], Marion Leclerc[7], Florence Levenez[7], Chaysavanh Manichanh[9], H. Bjørn Nielsen[8], Trine Nielsen[11], Nicolas Pons[7], Julie Poulain[3], Junjie Qin[17], Thomas Sicheritz-Ponten[8,18], Sebastian Tims[15], David Torrents[10,19], Edgardo Ugarte[3], Erwin G. Zoetendal[15], Jun Wang[17,20], Francisco Guarner[9], Oluf Pedersen[11,21,22,23], Willem M. de Vos[15,24], Søren Brunak[8], Joel Doré[7], MetaHIT Consortium†, Jean Weissenbach[3,4,5], S. Dusko Ehrlich[7] & Peer Bork[1,25]

Europeans, Americans, Asians. n=33; Sanger



Danes n=85;

US n=154; 454

Human individuals studied so far belong to 3 enterotypes

SEVENTH FRAMEWORK PROGRAMME

FROM GENOMICS TO EPI-GENOMICS AND APPLICATIONS

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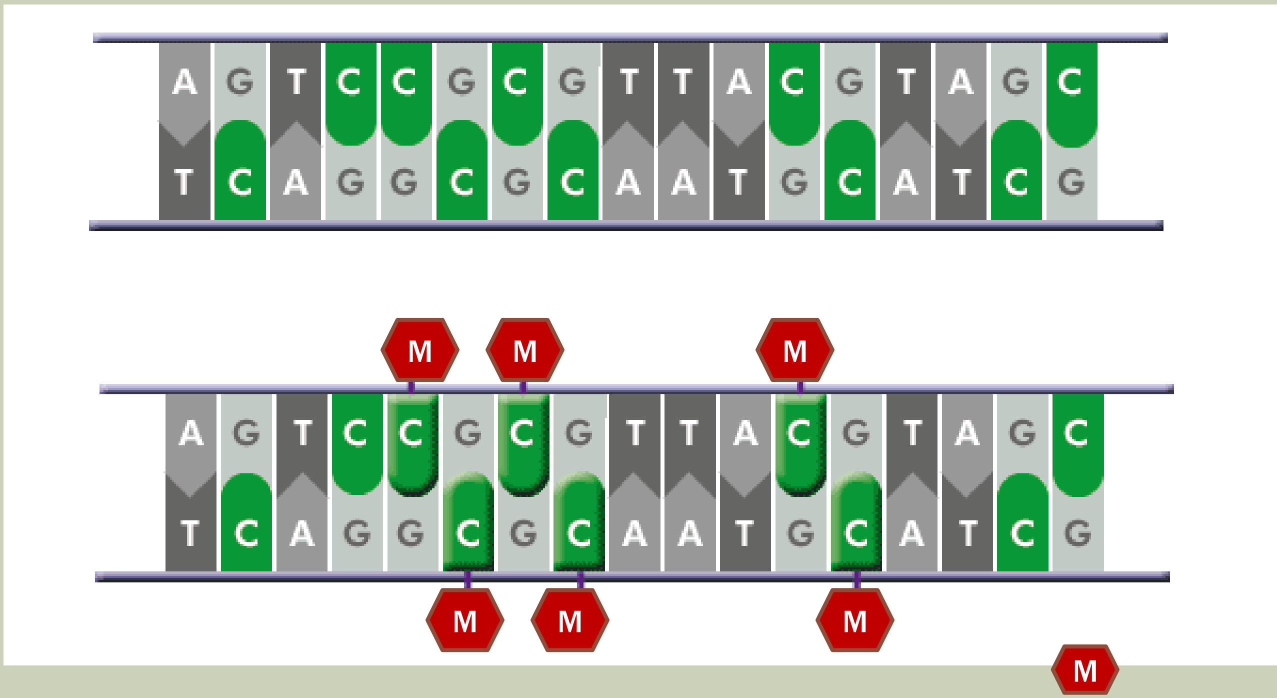
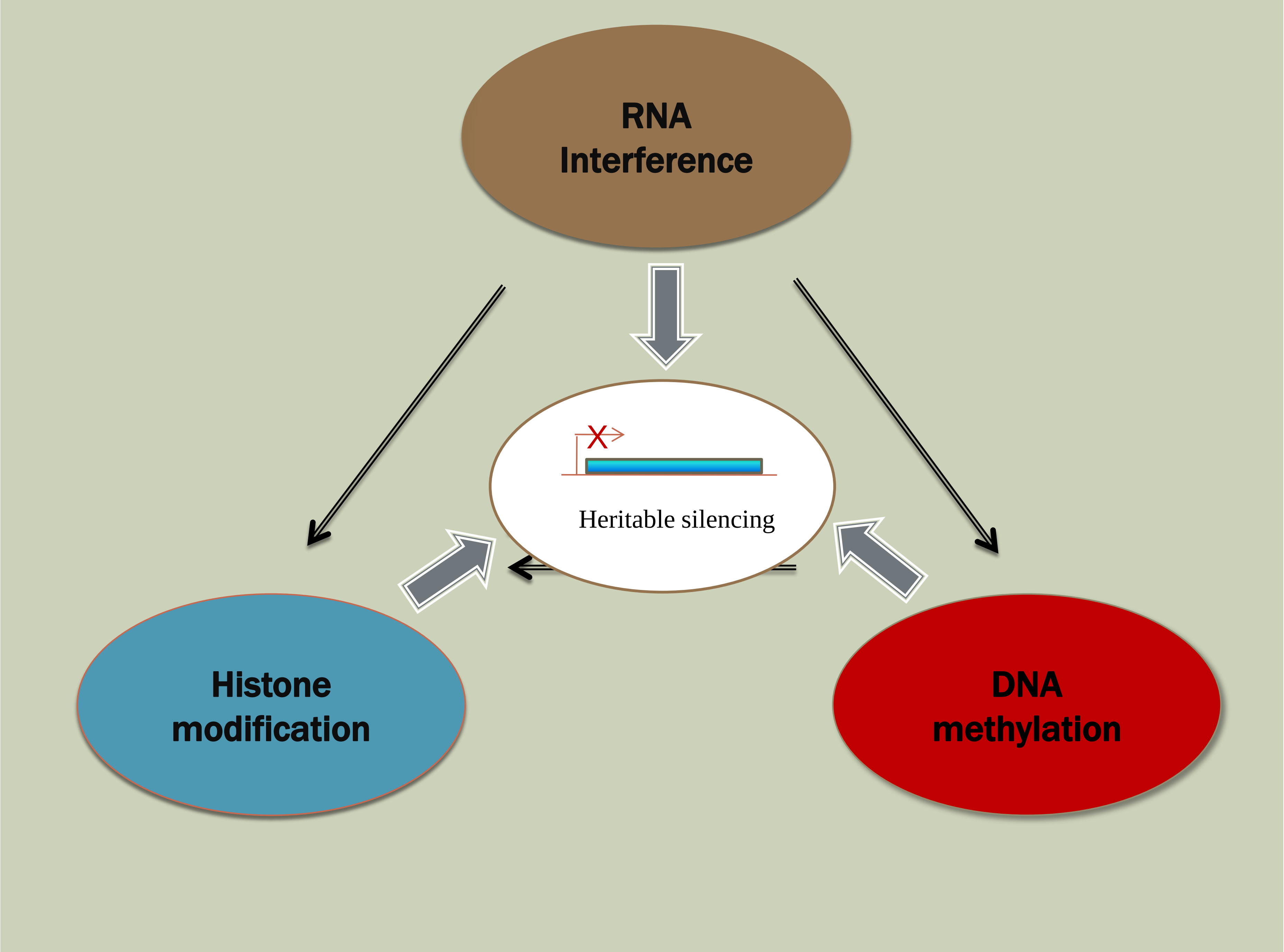
GENOMICS → EPI-GENOMICS



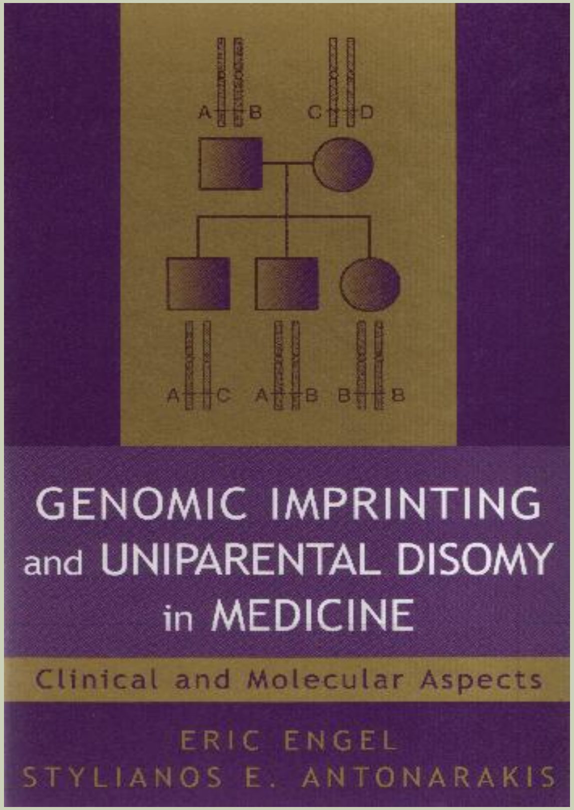
Epi-therapy

Epi-nutrition



RNA
Interference
Heritable silencing
Histone
modification
DNA
methylation

IMRINTING


A B
C D
A C
A B
B B
GENOMIC IMPRINTING
and UNIPARENTAL DISOMY
in MEDICINE
Clinical and Molecular Aspects
ERIC ENGEL
STYLIANOS E. ANTONARAKIS

LTR Hypomethylated

When to Intervene??

LTR Hypermethylated

Yellow Mouse

Agouti Mouse

High risk cancer, diabetes, obesity & reduced lifespan

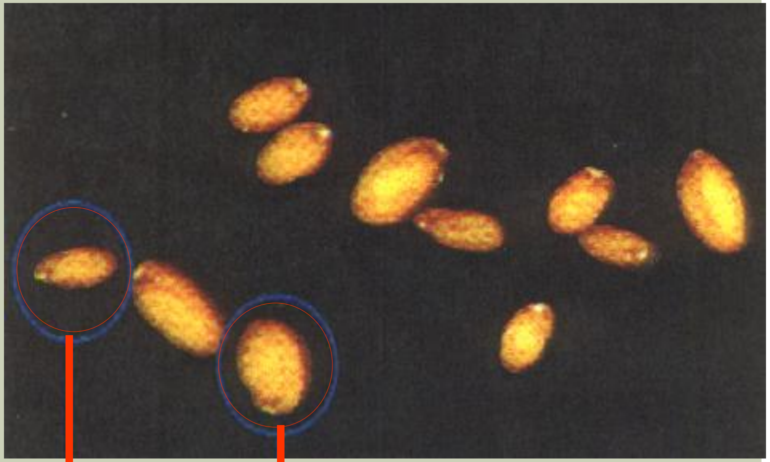
→

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)

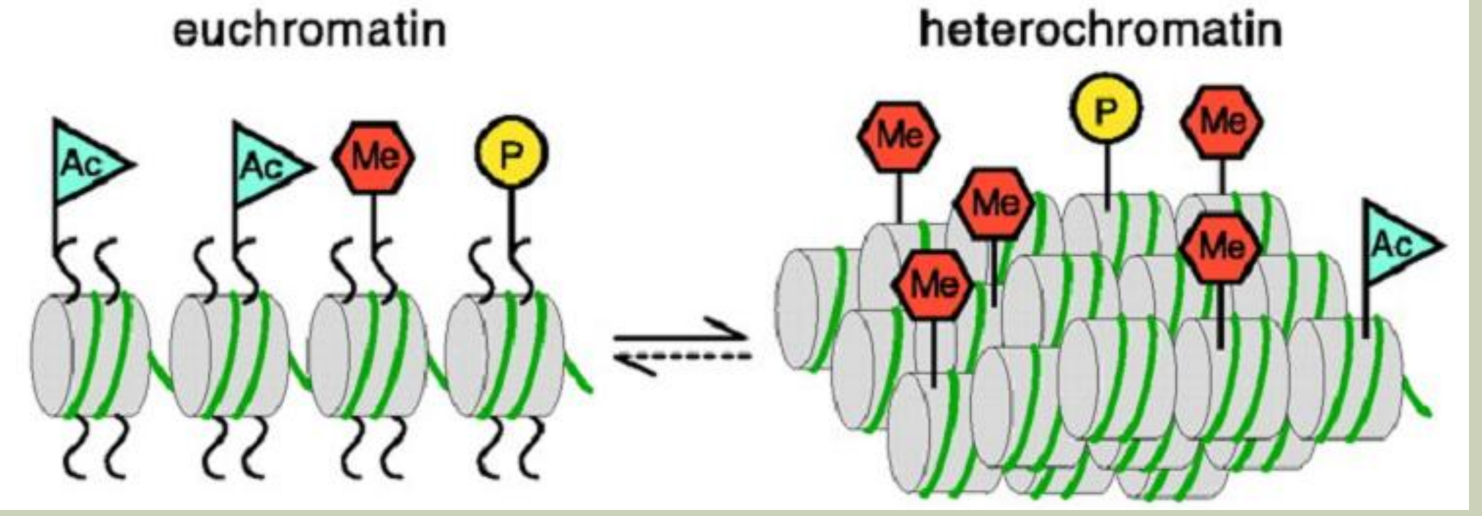
IMPRINTNG



Small Seed

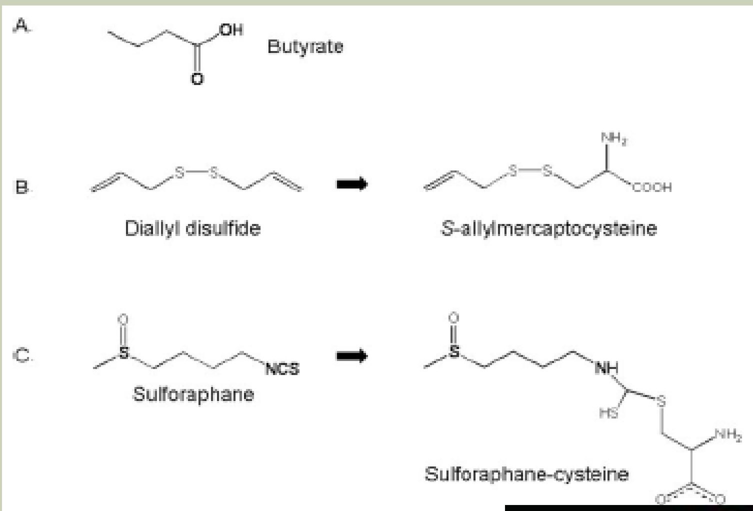
Large Seed

EPIGENETIC HISTONE MODIFICATION

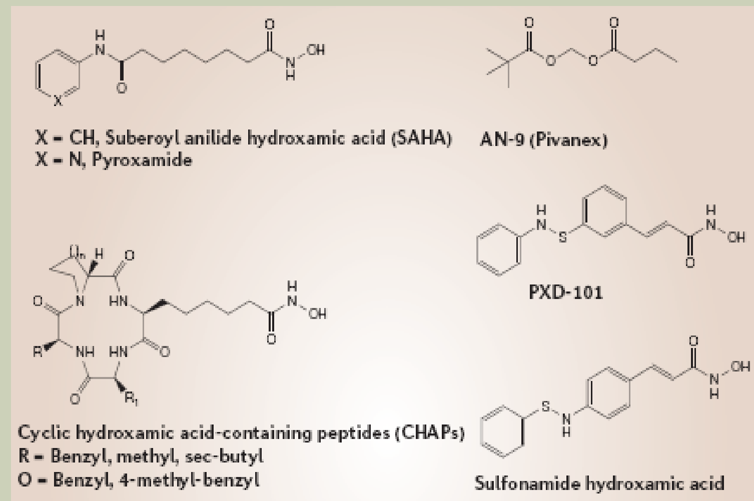


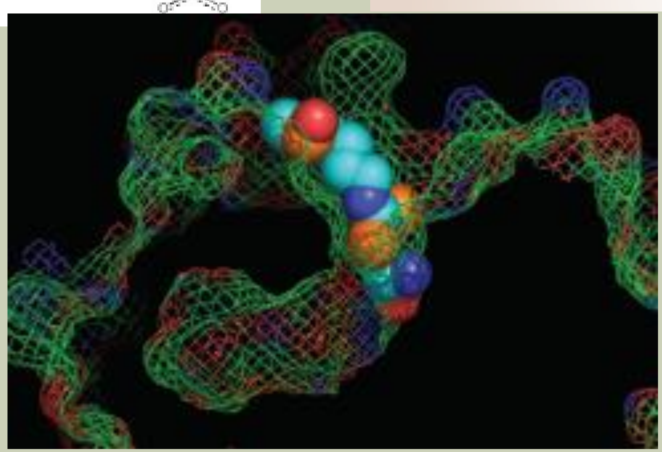
INHIBITORS OF HISTONE DEACETYLASES

Natural Inhibitors

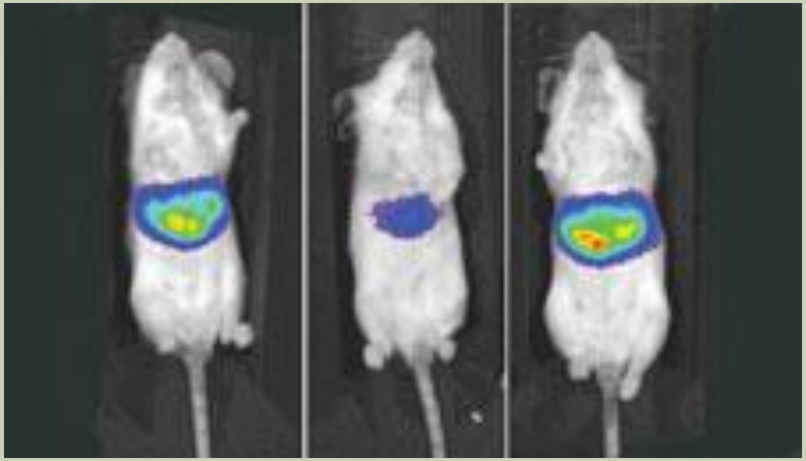


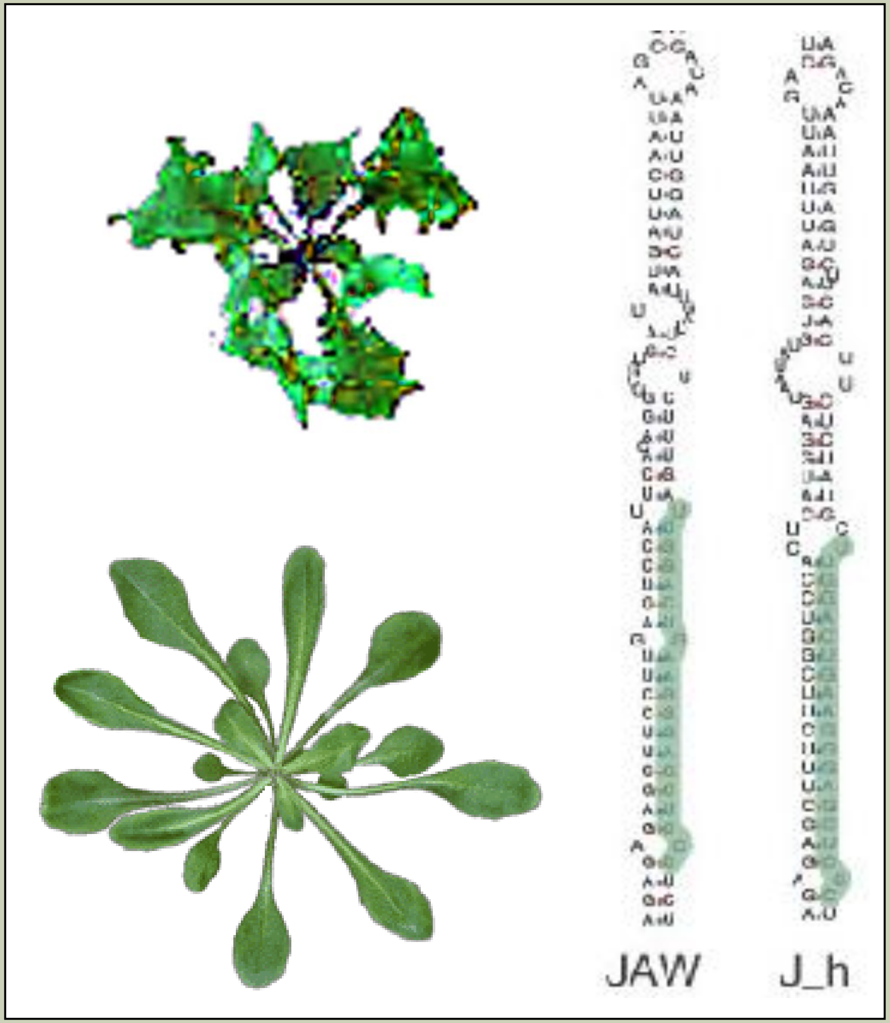
Synthetic Inhibitors



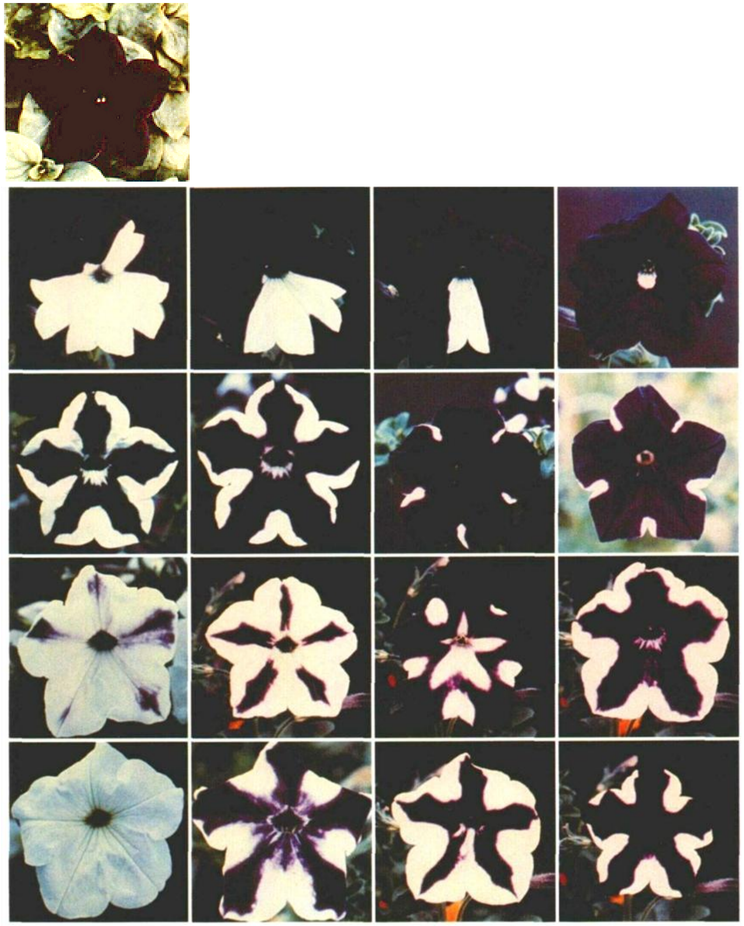


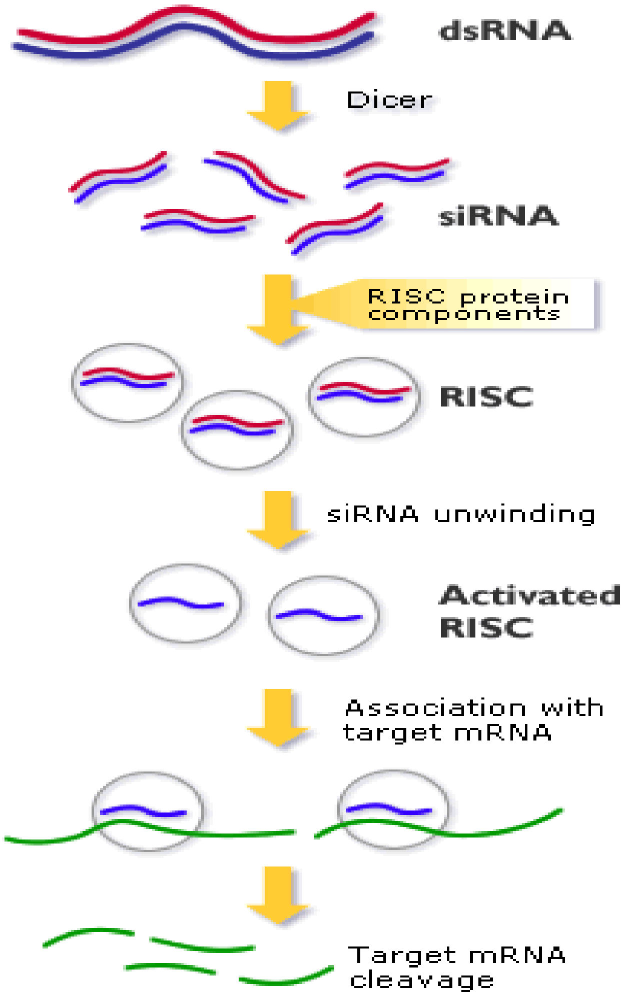
GENE SILENCING





RNA INTERFERENCE

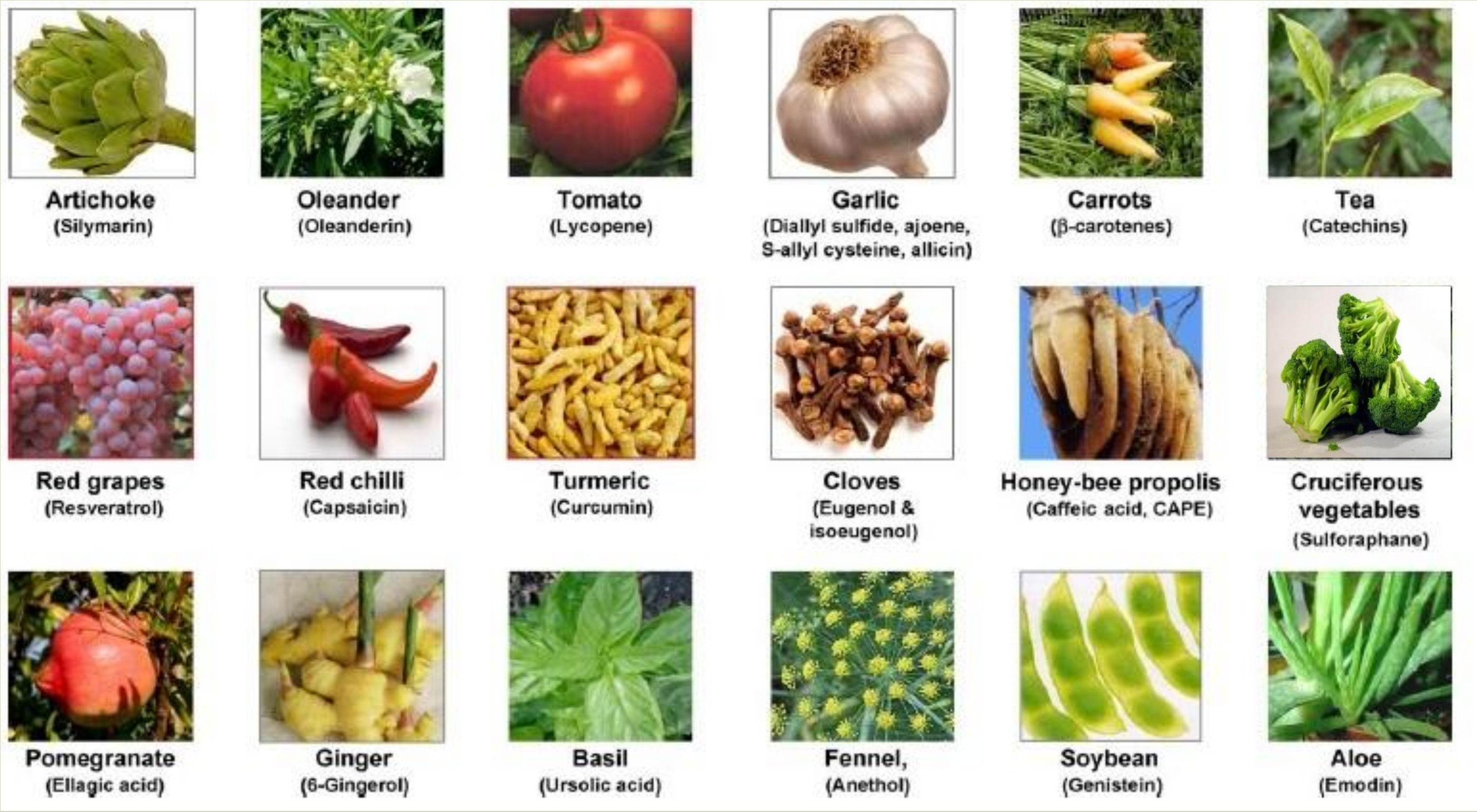




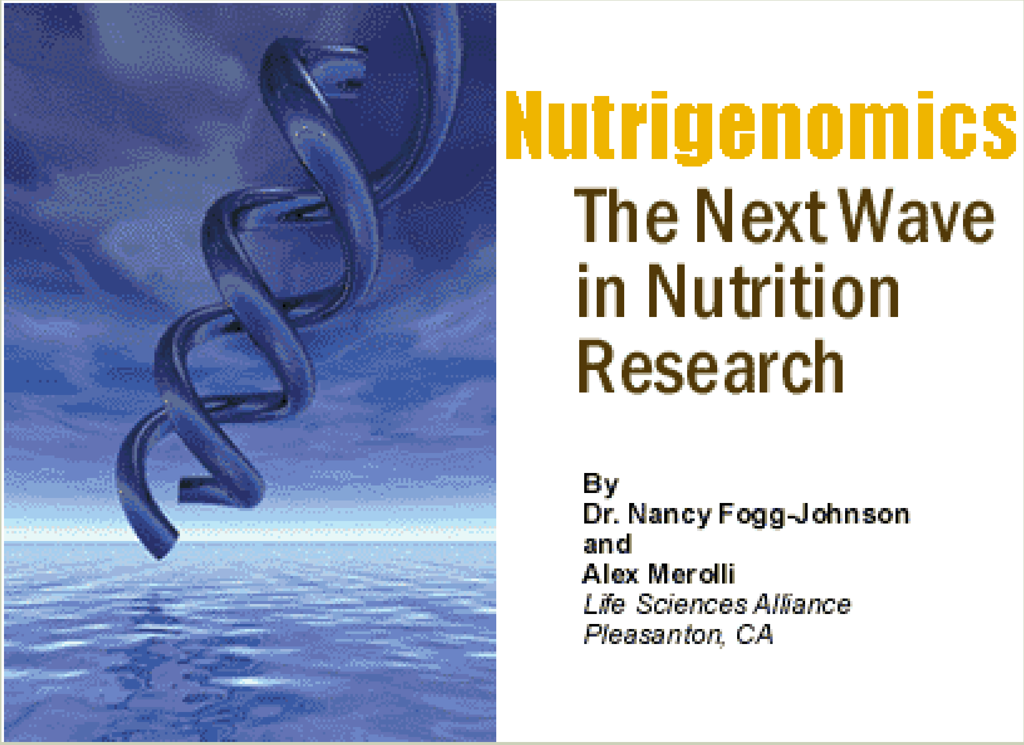
EPIGENETICS AND EPITHERAPY

Target	Drug
DNA Methylation	5-Azacytidine 5-Aza-2'-deoxycytidine FCDR Zebularine Procainamide EGOG Peammaplin A
Histone acetylation	Phenylbutiric acid SAHA Valproic acid Sulforaphanes
RNA interference	Antagomirs

EPIGENETICS AND EPINUTRITION: «EPIGENETIC» FOODS



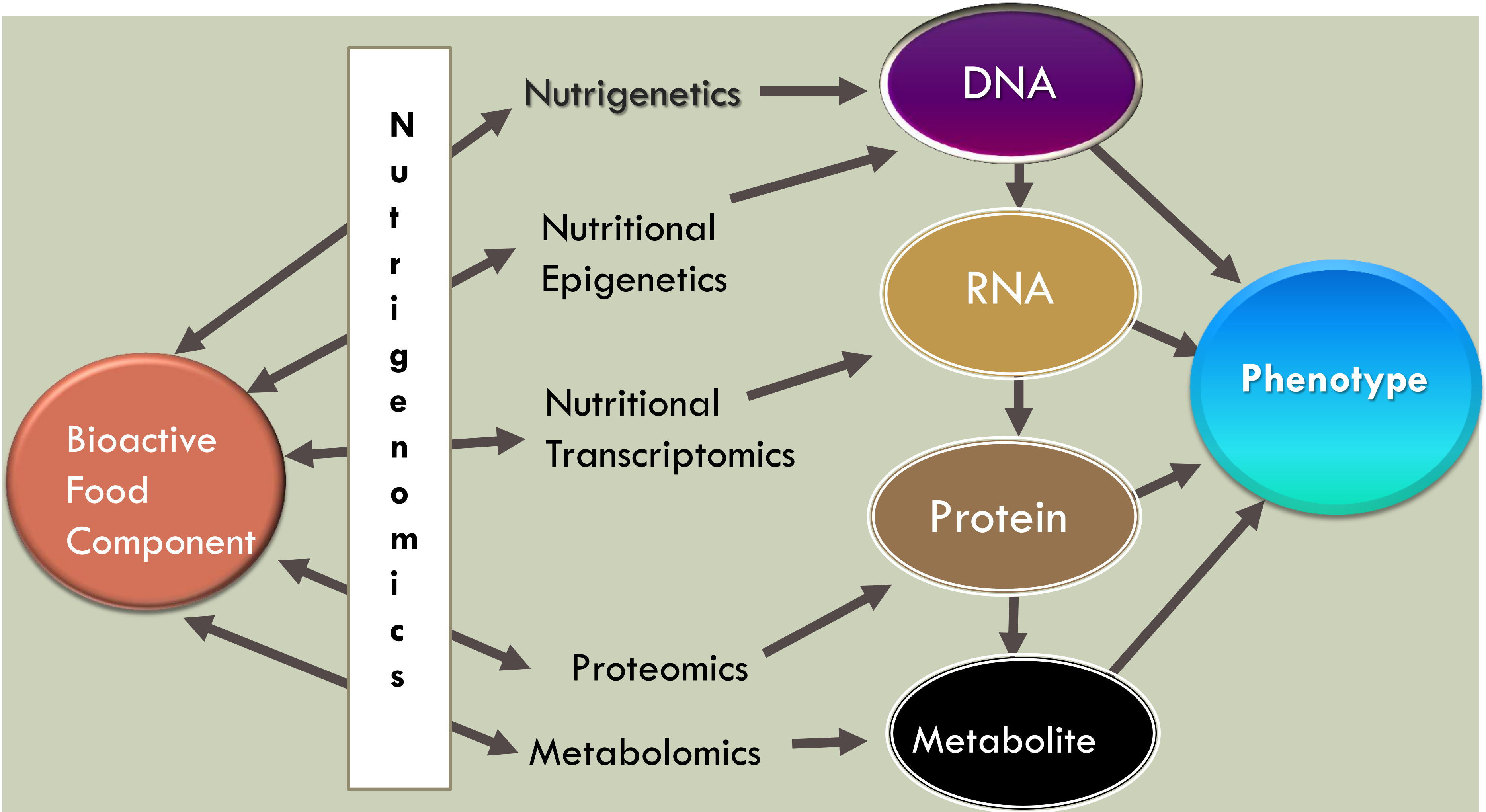
THE NEW ERA IN NUTRITION SCIENCE IS CALLED "NUTRIGENOMICS". IT IS BELIEVED THAT NUTRIGENOMICS WILL REVOLUTIONIZE WELLNESS AND DISEASE MANAGEMENT.



« …Untill the synergistic activities between humans, their diet and their commensals have been elucidated, the understanding of human biology will remain incomplete »

Julian Davies. Science, March 2001

THE "OMICS" OF NUTRITION



GENOMICS AND FOOD PRODUCTION

ARE WE ALL IDENTICAL?

Elderly

Pregnant

Cancer patient

Athlete

Kidney patient

Celiac

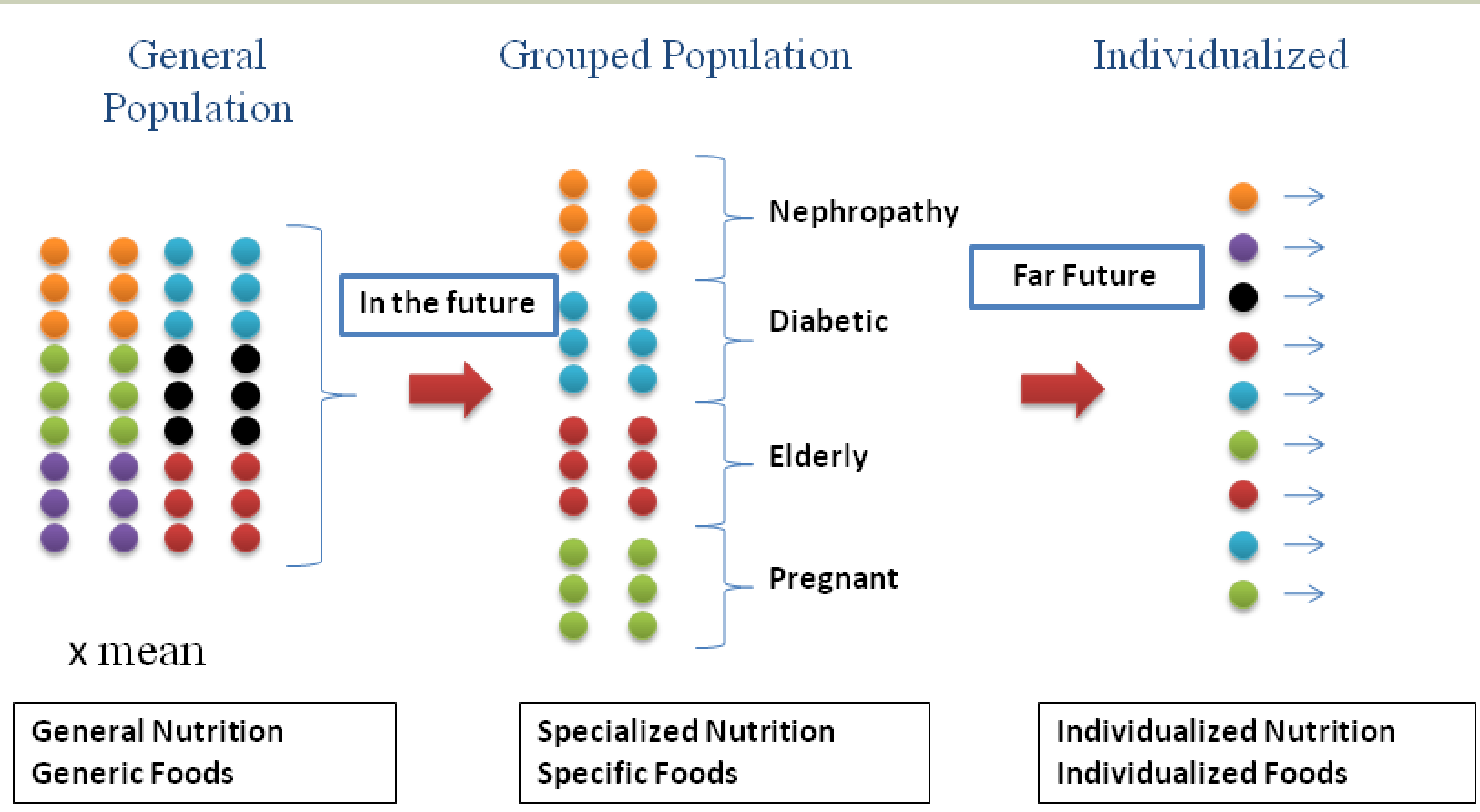
Overweight

Babies

Young person

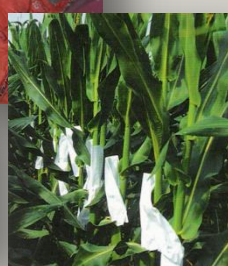
Diabetic

IMPROVING THE QUALITY OF LIFE



RANDOM

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


















RANDOM

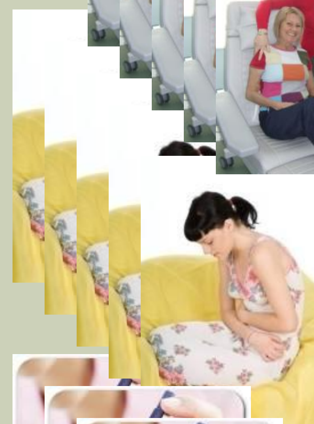
Fine mapping and marker-assisted selection (MAS) of a low glutelin content gene in rice

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

FOOD FOR DIFFERENT GROUPS

Food for Kidney patients

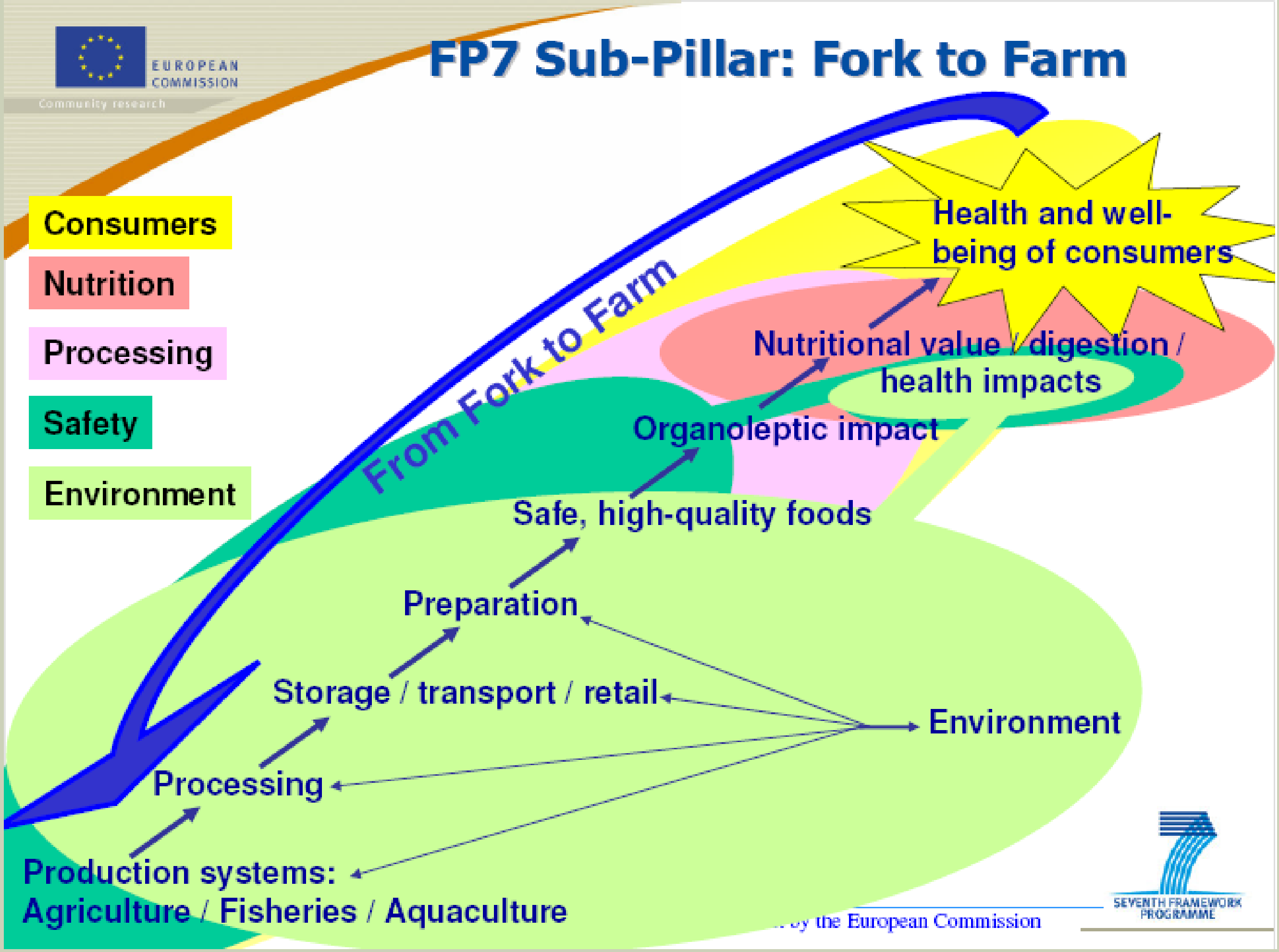
Food for Celiacs



Food for Diabetics

Food for Elderly

FROM FORK TO FARM: A BOTTOM UP APPROACH

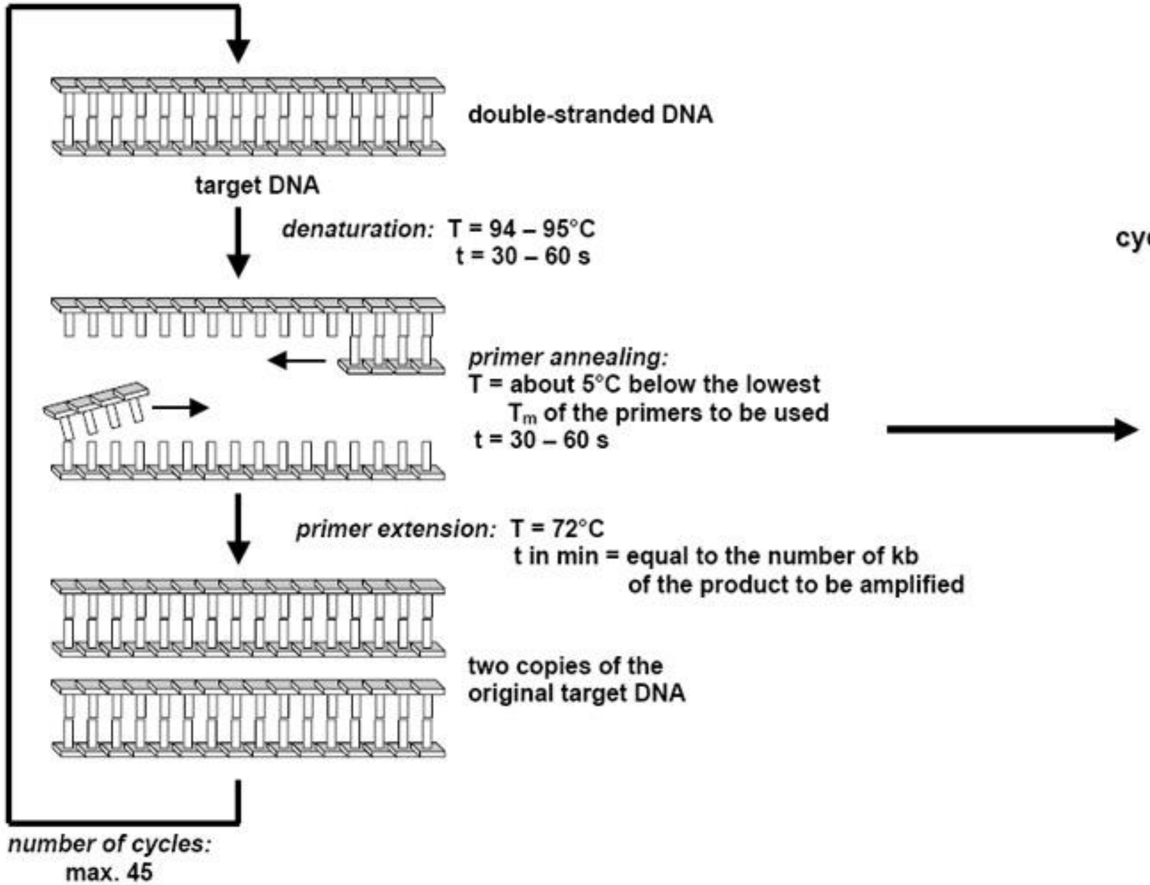


DNA METHODS TO IDENTIFY ORGANISMS

SOME NUCLEIC ACID BASED METHODS

- Polymerase Chain Reaction (PCR)
- Restriction Fragment Length Polymorphisms (RLFPs)
- Random Amplification of Polymorphic DNA (RAPDs)
- Amplified fragment length polymorphisms (AFLPs)
- Simple Sequence Repeats (SSRs)
- DNA microarrays
- Nucleic acid sequence based amplification (NASBA)
- Pulsed-Field Gel Electrophoresis (PFGE)

POLYMERASE CHAIN REACTION (PCR)



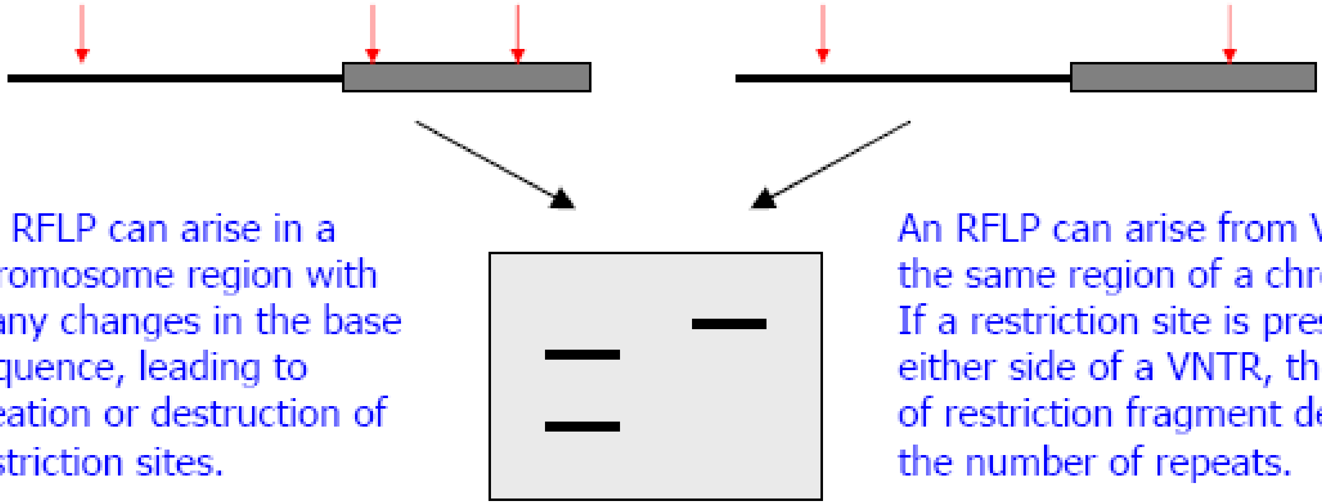
cycle number	target copies
1	2
2	4
3	8
4	16
5	32
6	64
20	1,048,576
30	1,073,741,824

Methods for DNA Fingerprinting

1. ______________________________ (RFLPs)

- Variations in the DNA revealed by differences in the banding pattern of DNA fragments from different individuals of a species, when subjected to restriction enzyme analysis.
  - Uses restriction enzymes and Southern hybridization
  - Lengthy procedures, but reproducible
  - Co-dominant markers, sequence knowledge/probes required

An RFLP can arise in a chromosome region with many changes in the base sequence, leading to creation or destruction of restriction sites.



An RFLP can arise from VNTRs in the same region of a chromosome. If a restriction site is present on either side of a VNTR, the length of restriction fragment depends on the number of repeats.

RFLP Loci: Family and Segregation Studies

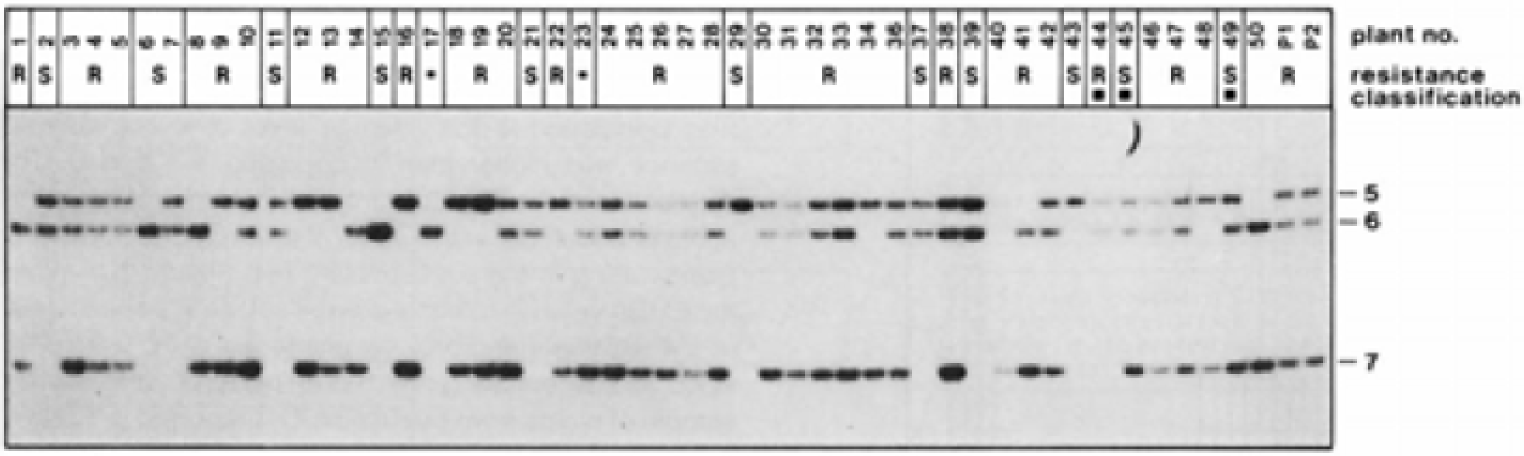


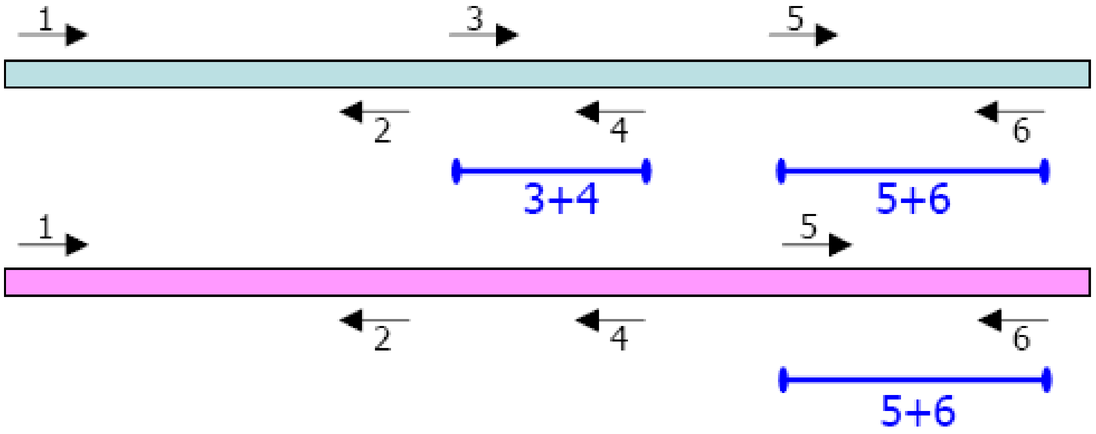
Figure **3.** Segregation of marker GS3.
Resistance (R) or susceptibility (S) to rhizomania is indicated above the corresponding lane below the plant number. Genomic DNA from 49 plants of population A (numbered 1-34 and 36-50) was digested with *TaqI,* separated and hybridized as described in Experimental procedures. The hybridizing fragments are numbered from 1 to 7. Only the lower part of the autoradiogram is shown. Fragment 7 reveals the RFLP marker GSSd, fragments 5 and 6 segregate independently from the rhizomania resistance gene. Plants 44, 45 and 49 are presumably recombinants between the DNA sequence hybridizing to the probe and the putative resistance locus. Plants 17 and 23, indicated by an asterisk, were not evaluated in the resistance test. P1 = single plant from population B (R01 x N01); P2 = single plant from population C (R02 x N02).

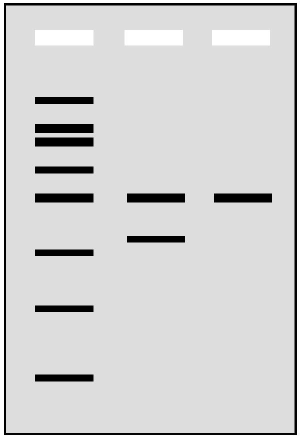
Barzen E, Mechelke W, Ritter E, Seitzer JF, Salamini F (1992) RFLP markers for sugar beet breeding: chromosomal linkage maps and location of major genes for rhizomania resistance, monogermy and hypocotyl colour. Plant J 2: 601-611.

PCR-based DNA Typing

2. ______________________ (RAPDs)

- Involve the use of a single "arbitrary" primer to amplify chromosomal DNA under non-stringent conditions. The number and sizes of PCR products vary among different individuals due to variations in DNA.
  - Use PCR and agarose gel electrophoresis
  - Several primers can be used to generate a unique profile for the individual.
  - No prior sequence knowledge required
  - Difficult to reproduce
  - Dominant markers

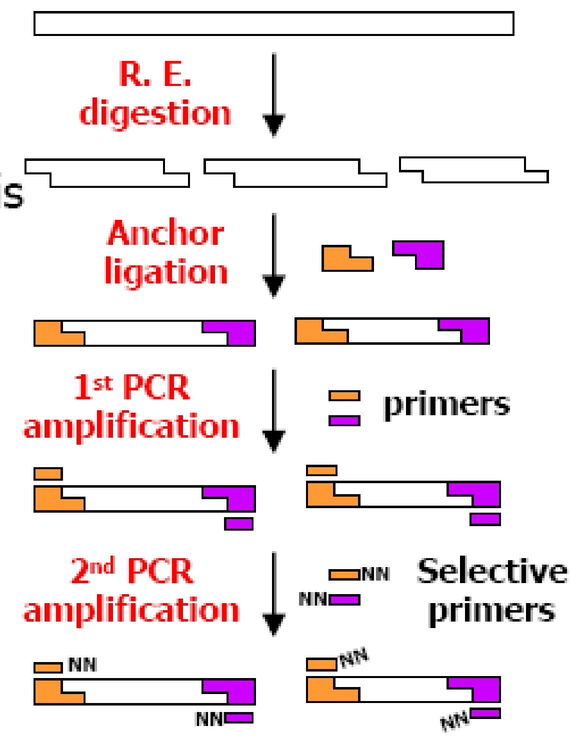




PCR-based DNA Typing

3. ______________________________ (AFLPs)

- Detects DNA restriction fragments by means of PCR amplification.
  - Use restriction enzymes, DNA ligase, PCR, and polyacrylamide gel electrophoresis
  - Reproducibility ~ RFLP >> RAPD
  - No prior sequence knowledge required
  - Dominant markers



PCR-based DNA Typing

4. ___________ or ______________________ (SSR)

- Highly polymorphic DNA marker comprised of mono-, di-, tri- or tetra- nucleotides that are repeated in tandem and distributed throughout the genome
- Microsatellites are abundant and frequently used for gene mapping
- Marker identification:
  - Sequencing ⇨ SSRs id ⇨ design primers corresponding to the flanking sequences ⇨ Use PCR/electrophoresis in actual analyses
  - Initial marker development: expensive and time-consuming
  - Highly sensitive and reproducible
  - Co-dominant markers

Length Polymorphism

Forward primer

5' ►►►►►►►►►►►

tagtttccacttttcattgaaaagaaggatctctttctttccctctctctctctctctctccctctctctctcacacacacacacacaca

cacacacaggaccttgttgggttatgctgttctctgttgtgaaccttgcctgttcagttatctagcacaaagcacatca

◄◄◄◄◄◄◄◄◄◄◄ 3"

Reverse primer

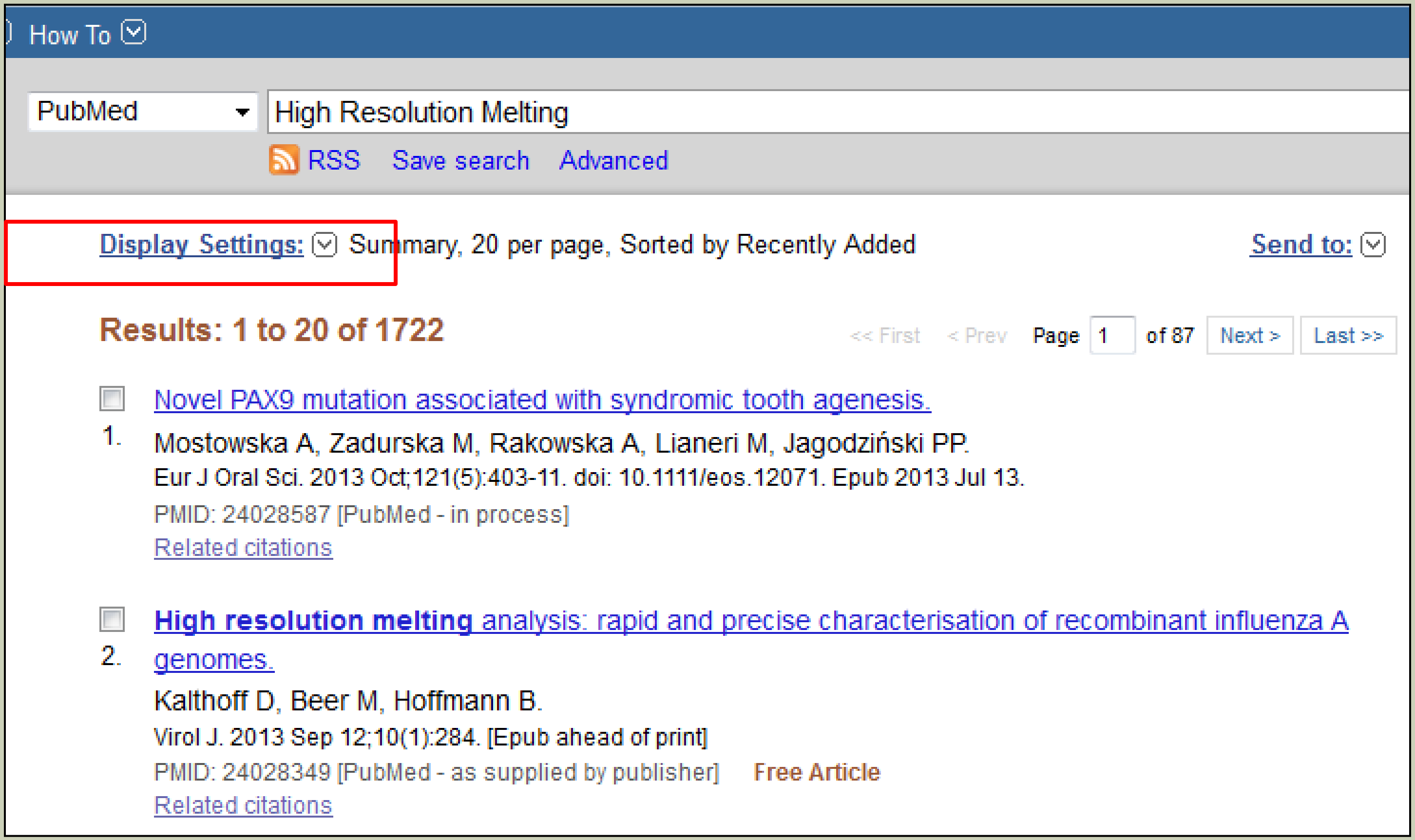
description

- ➡ tandem repeats
- ➡ a low degree of repetition
- ➡ length polymorphism detected by PCR.
- ➡ short motifs (1 to 6 bp)
- ➡ a random distribution

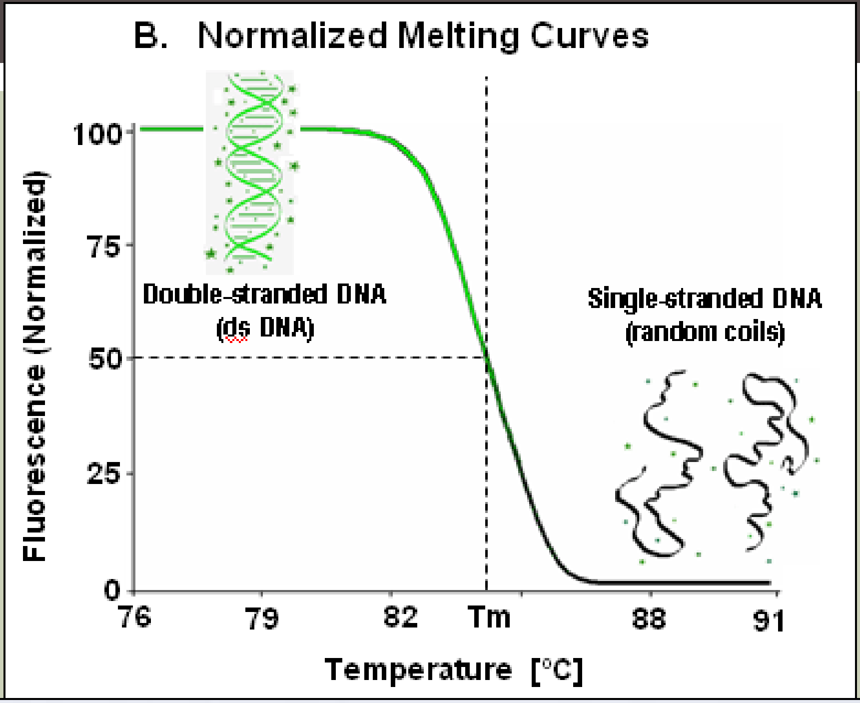
advantages

- ➡ specific
- ➡ highly polymorphic
- ➡ even distribution throughout the nuclear genome
- ➡ frequent occurrence
- ➡ a co-dominant inheritance
- ➡ reproducible

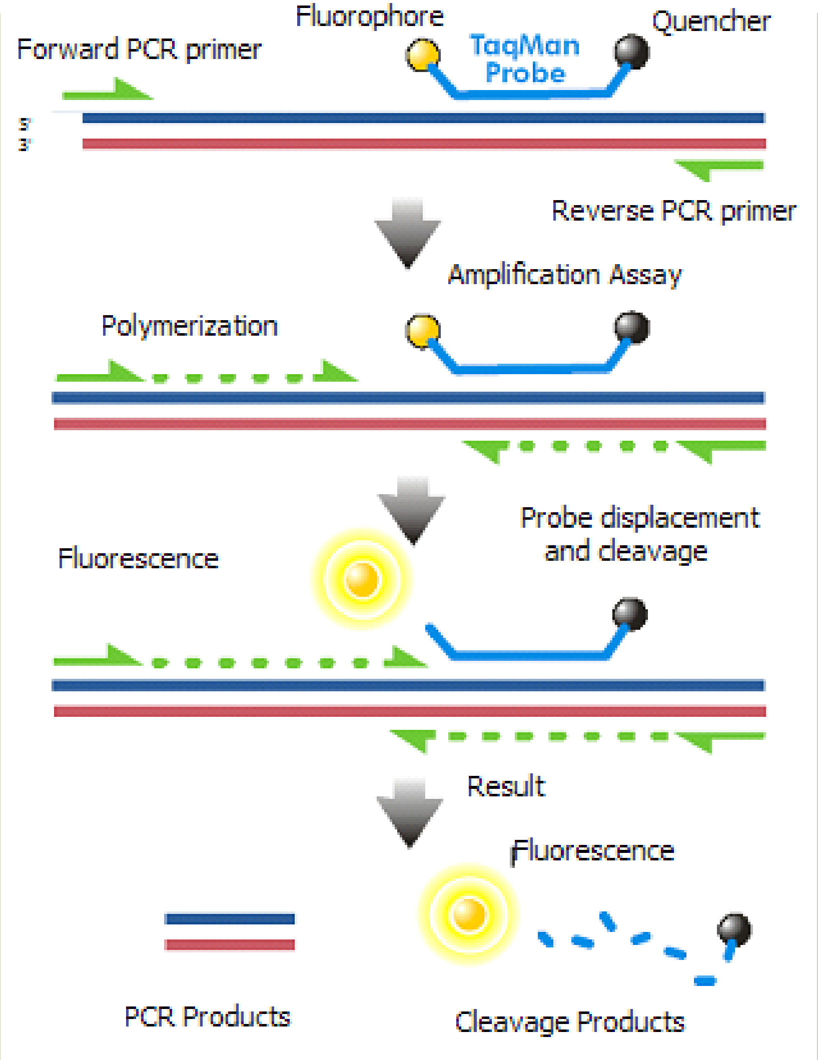
HIGH RESOLUTION MELTING (HRM)



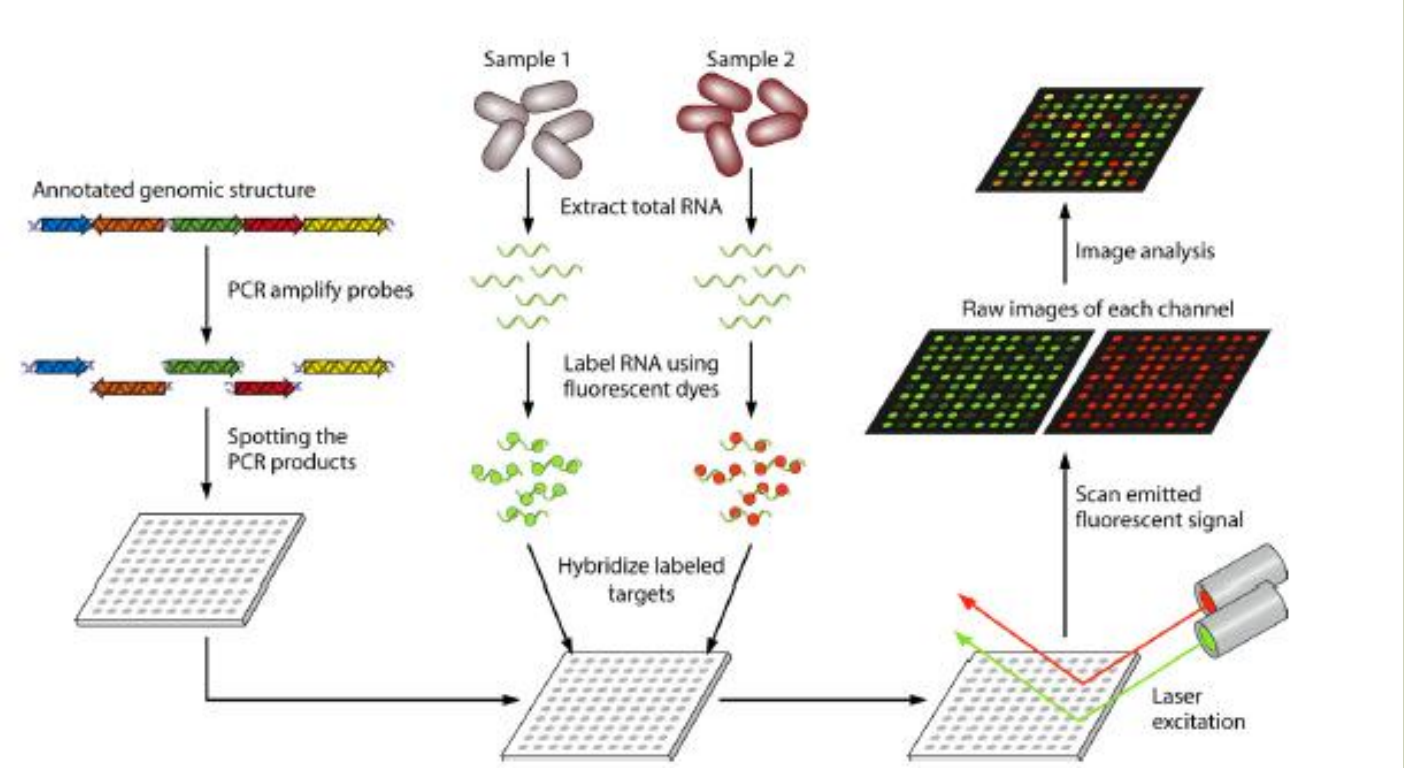
HIGH RESOLUTION MELTING (HRM) PRINCIPLE



TAQMAN ASSAY

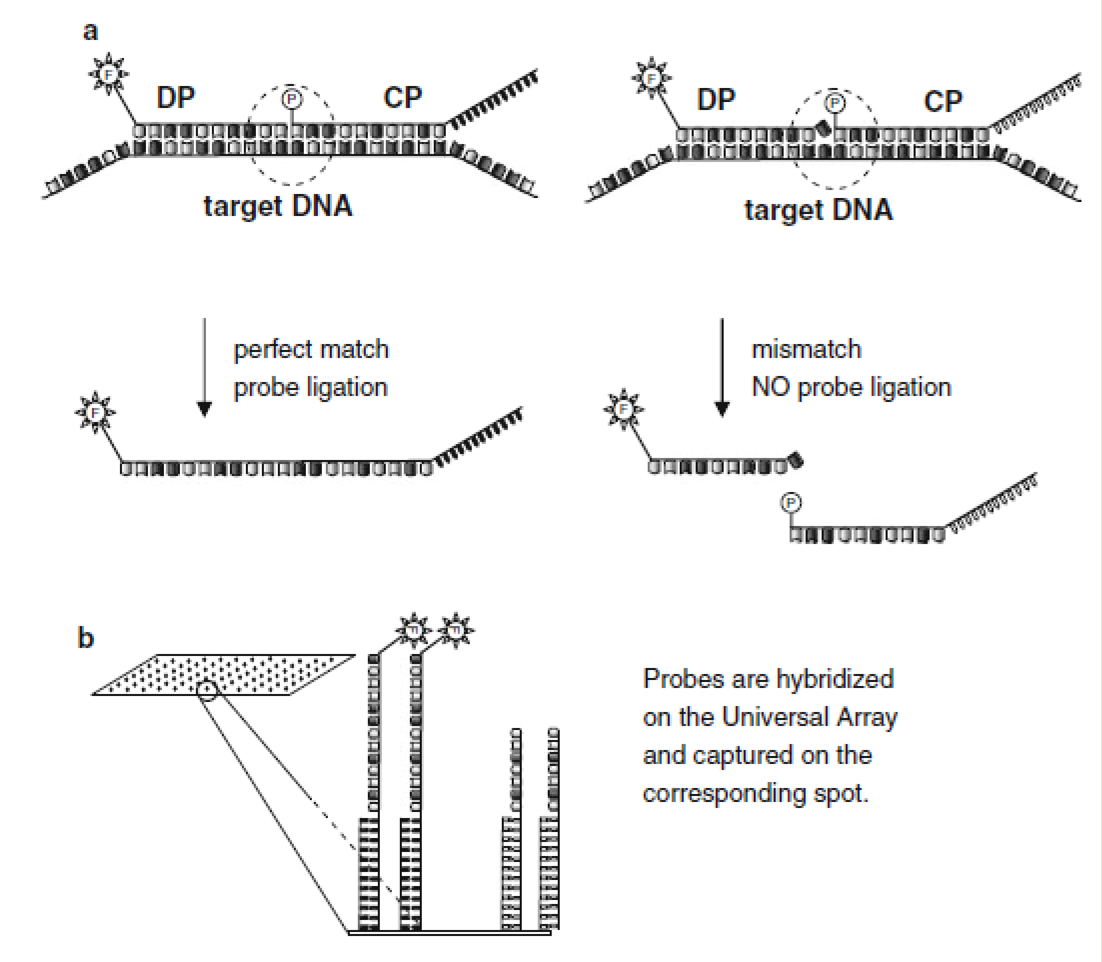


DNA MICROARRAYS

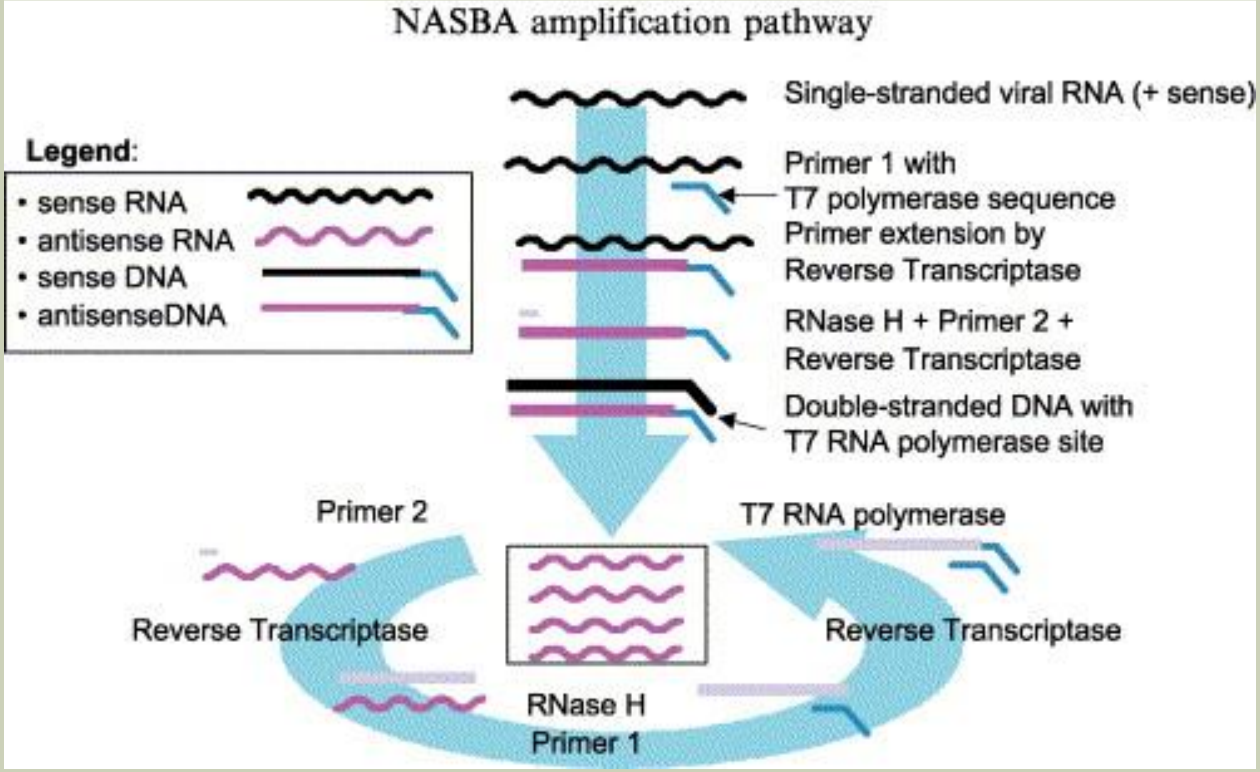


Miller, M.B. and Y.W. Tang Clin Microbiol Rev, 2009. **22**(4): p. 611-33.

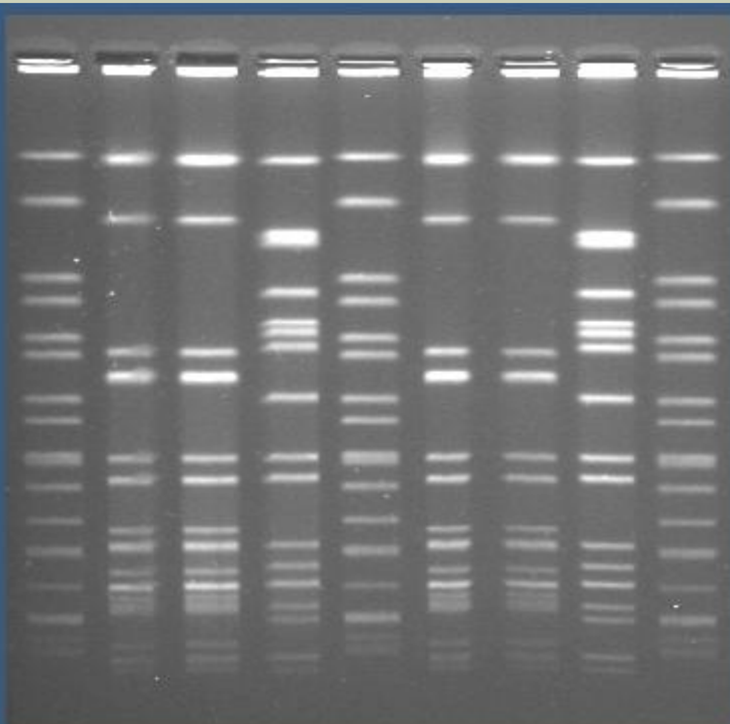
LIGATION DETECTION REACTION-UNIVERSAL ARRAYS (LDR-UA)



NUCLEIC ACID SEQUENCE BASED AMPLIFICATION (NASBA)



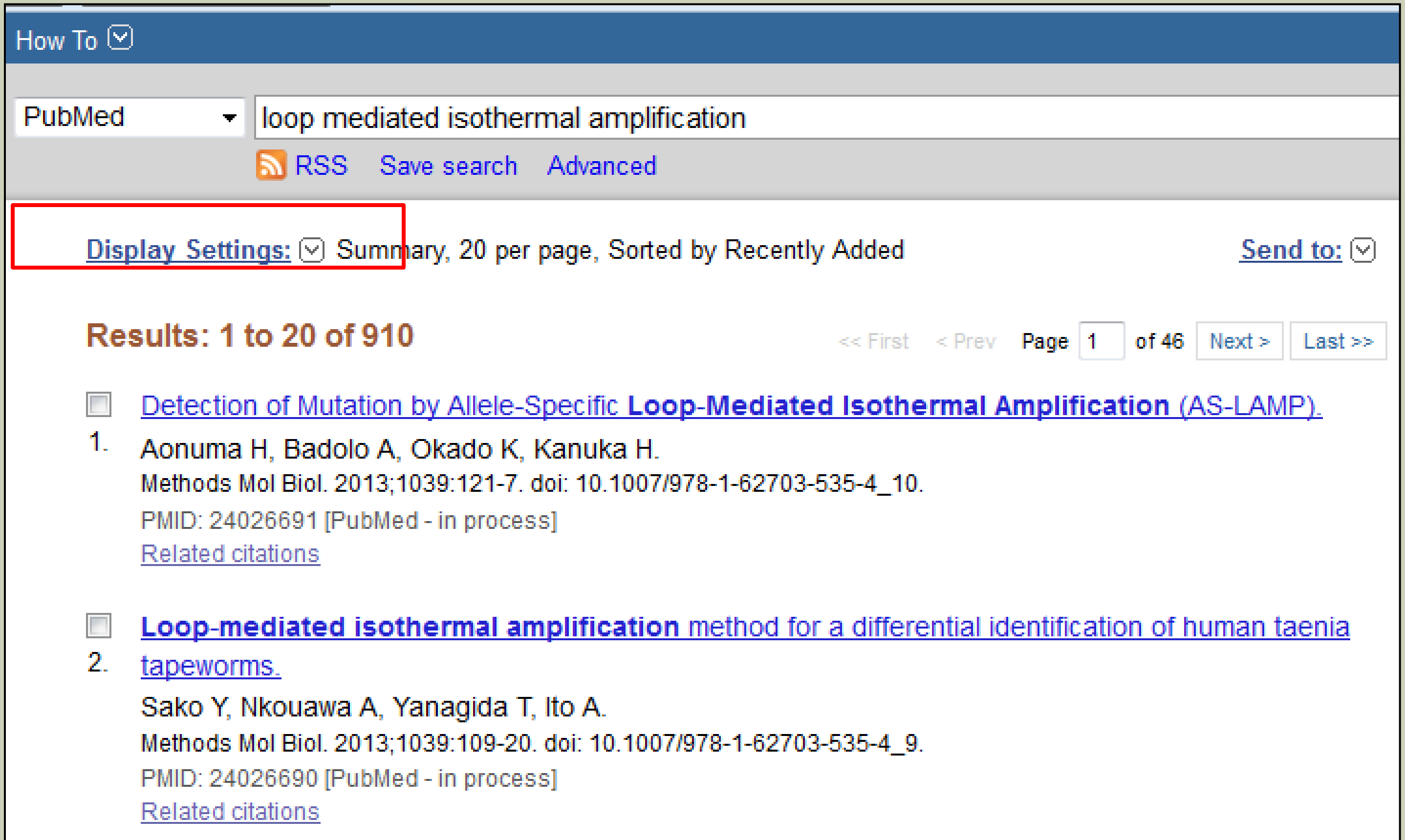
PULSED-FIELD GEL ELECTROPHORESIS (PFGE)



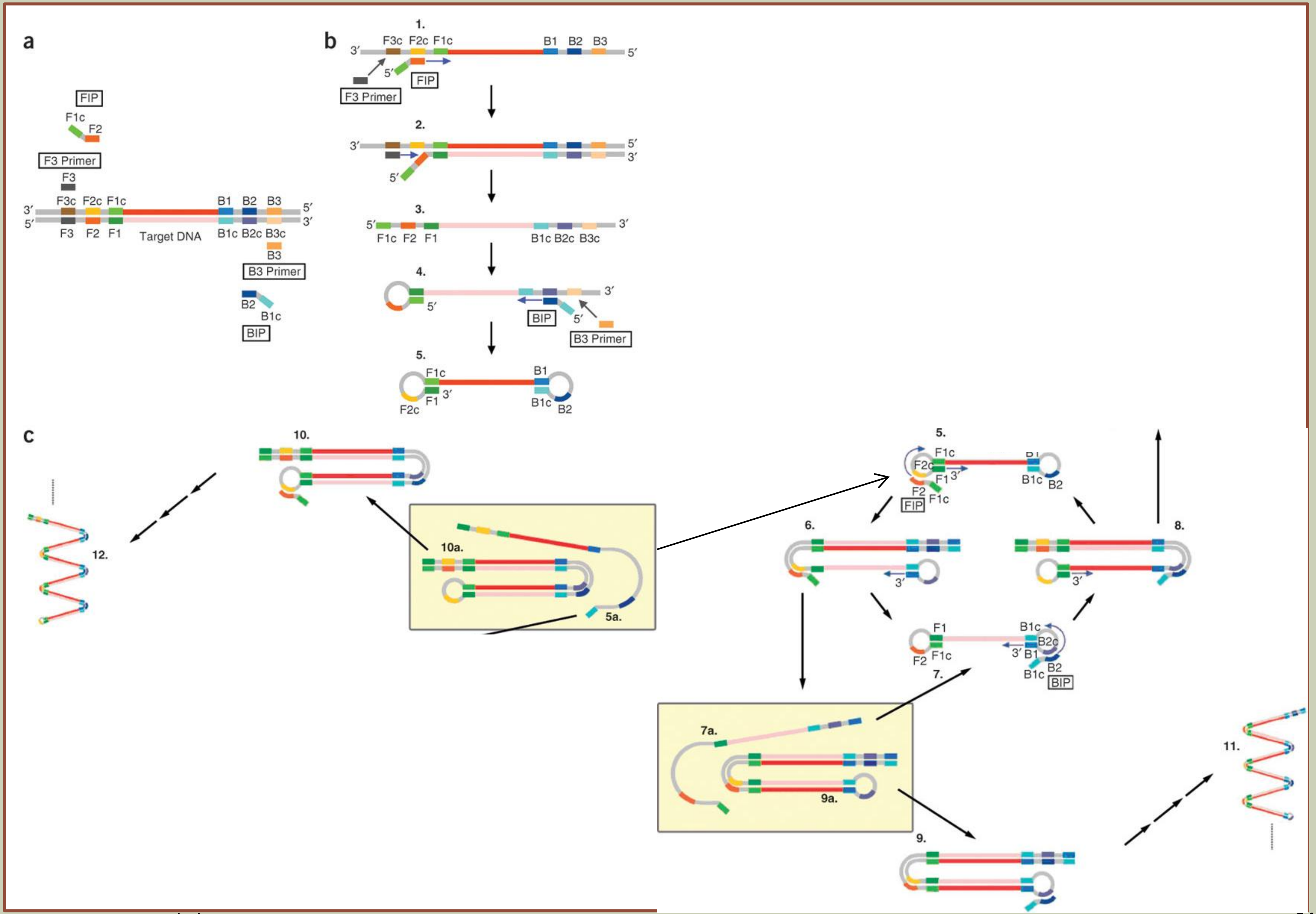
- -Large DNA Fragments
- -“Universal” Technique
- -PulseNet Standardizations
- -Usually Epidemiologically Relevant

time consuming, low discrimination, low sensitivity

LOOP MEDIATED ISOTHERMAL AMPLIFICATION



LOOP MEDIATED ISOTHERMAL AMPLIFICATION



TRACEABILTY OF DOP PRODUCTS

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CERTH

SOUTH EAST EUROPE
Jointly for our common future

INNO-FOOD SEE

DOP Products (Denomination of Origin Protect)

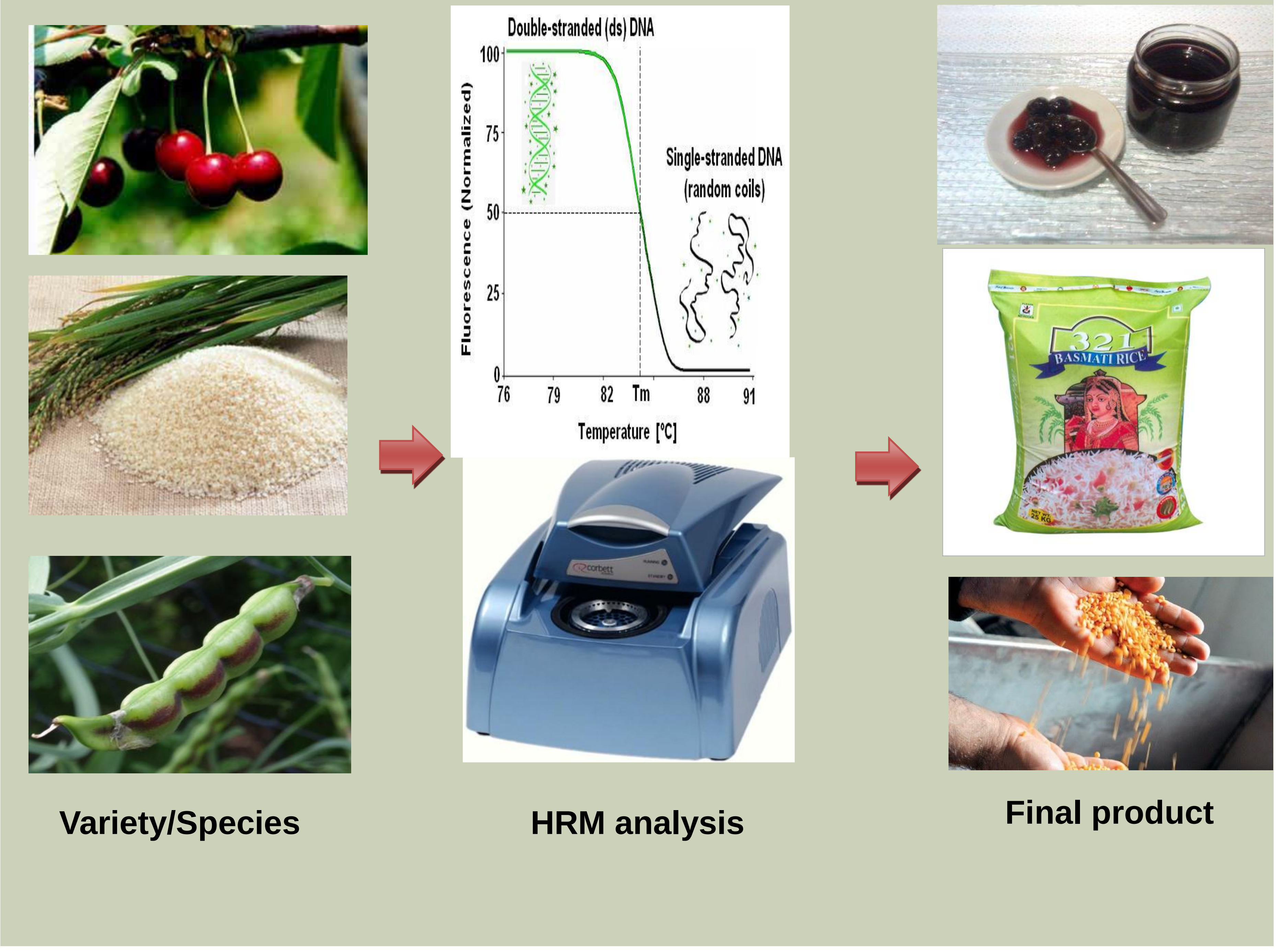


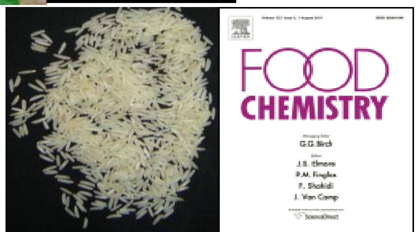


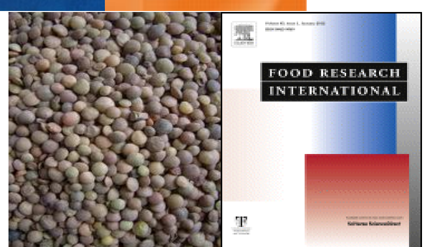
- Product from a particular geographical area
- The quality or characteristics are essentially or exclusively to a particular geographical environment (natural and human factors - climate, soil quality, experience)
- The production, processing and preparation takes place in the defined geographical area

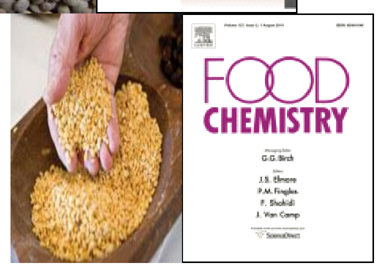
Reasons for introduction:

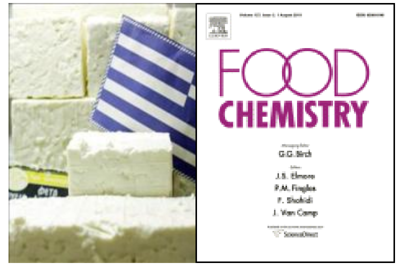
- ❑ Encourage diversified agricultural production
- ❑ Protect names from misuse and imitation
- ❑ Better understanding of the specific nature of the products by consumers

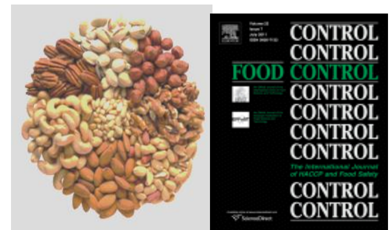

Double-stranded (ds) DNA
Fluorescence (Normalized)
100
75
50
25
0
Single-stranded DNA
(random coils)
76
79
82
Tm
88
91
Temperature [°C]
321
BASMATI RICE
corbett
Variety/Species
HRM analysis
Final product

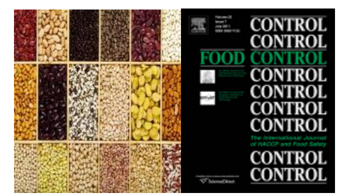






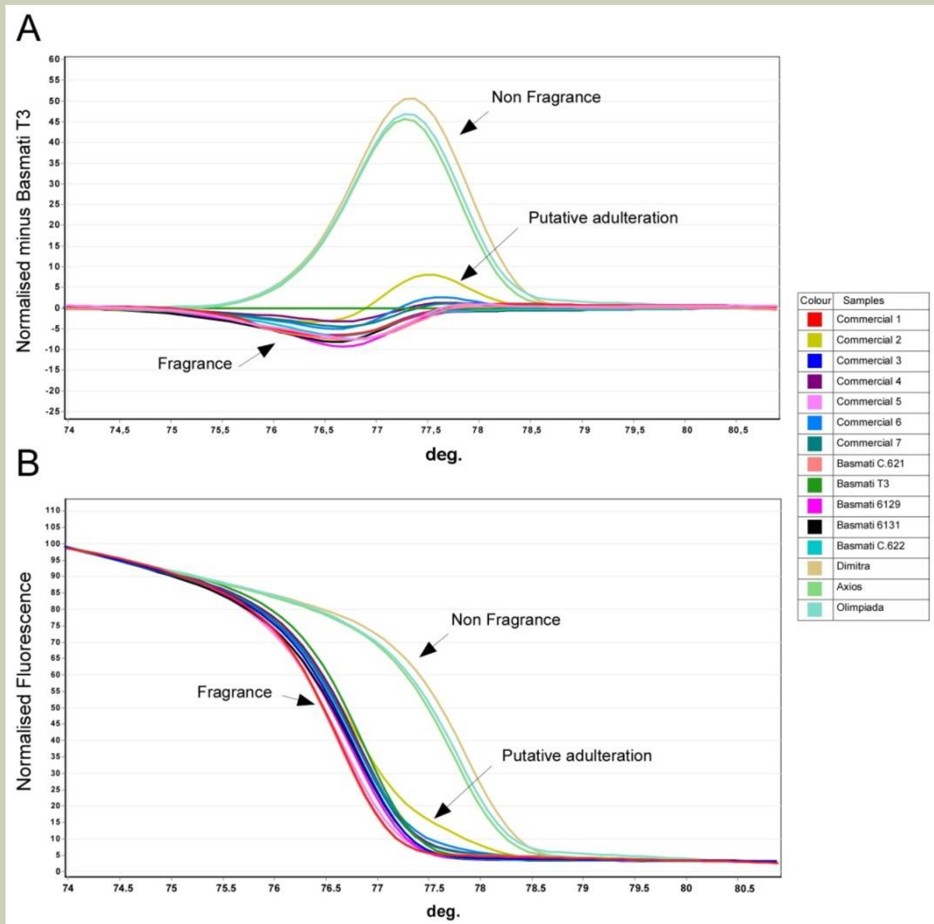




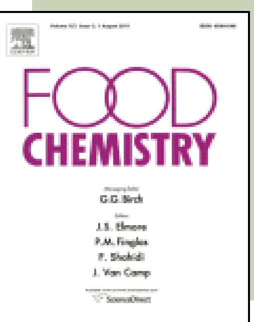


WORK IN PROGRESS

BASMATI AROMATIC RICES



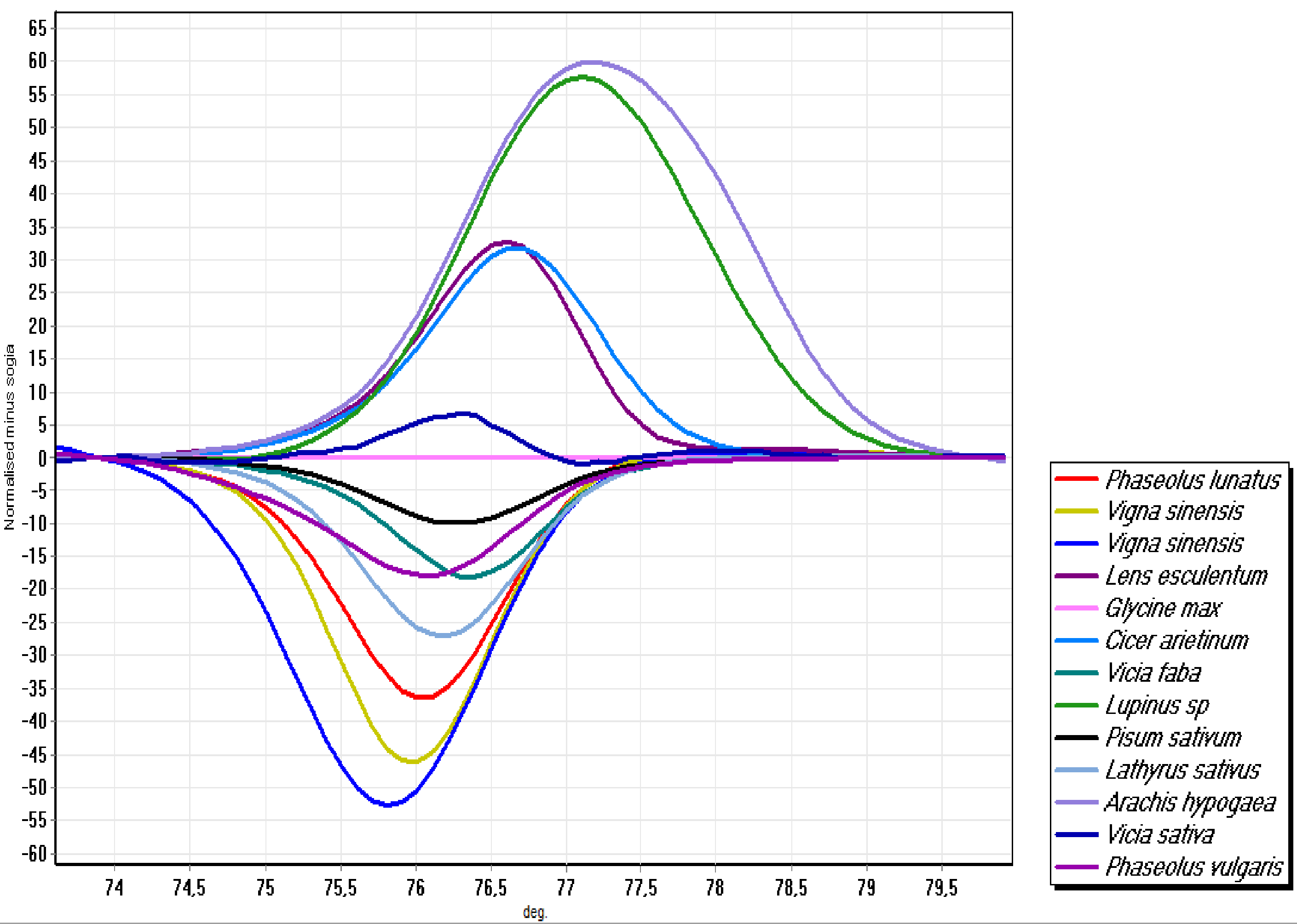
2011



Ganopoulos I., Argiriou, A. and Tsaftaris A.

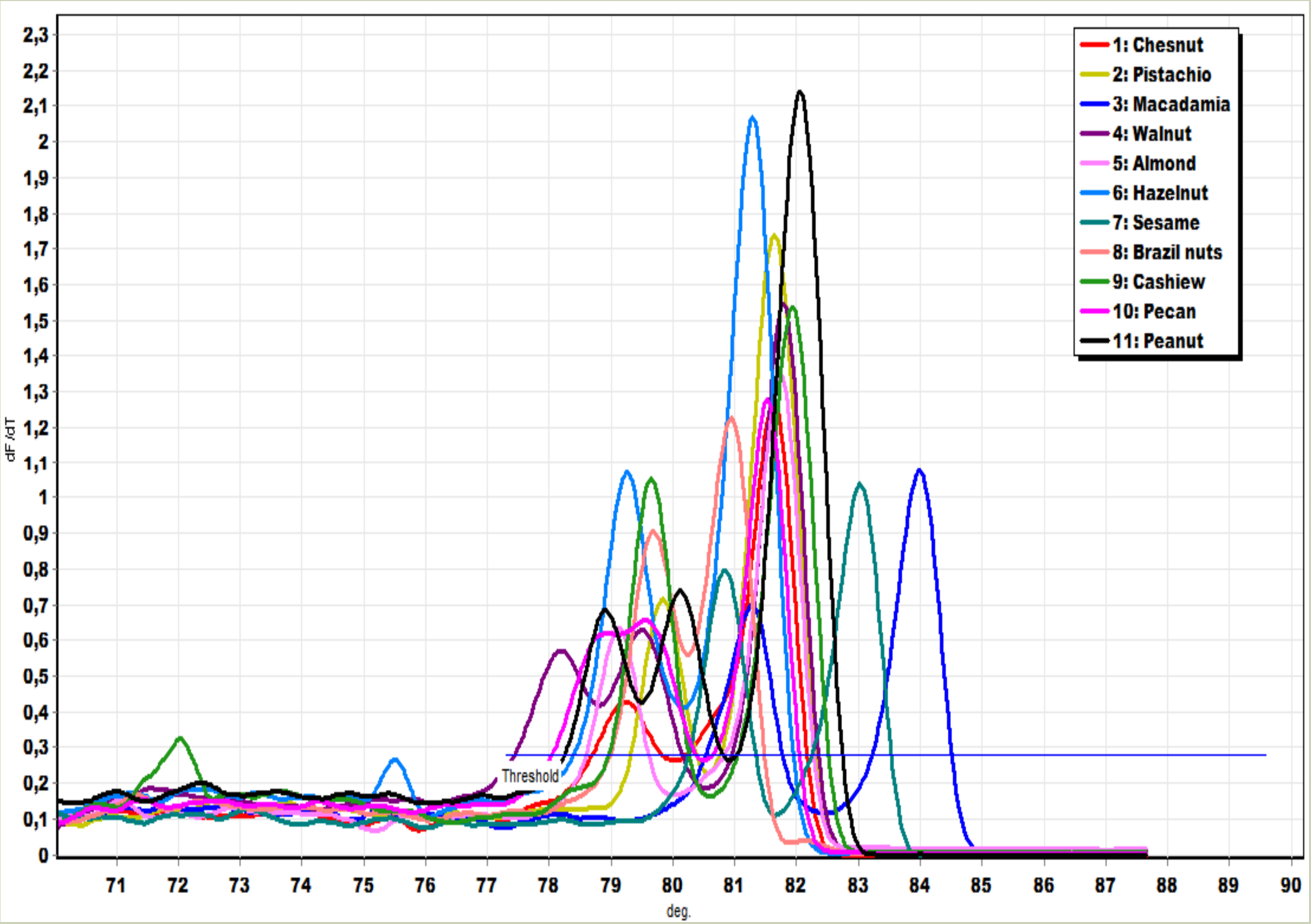
Leguminus

2012



Madesis P., Ganopoulos I., Argiriou A. and Tsaftaris A.

Nuts



2012

Madesis, P., Ganopoulos I., Bosmali I. and Tsaftaris A.

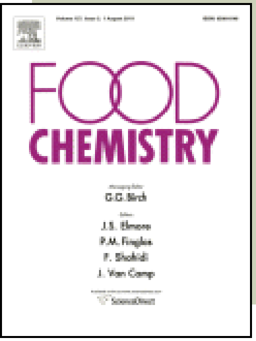
GREEK FETA CHEESE

+Sheep and goat milk.

+ Goat milk till 30% w/w

- Prohibition to use milk from other animal species

2012



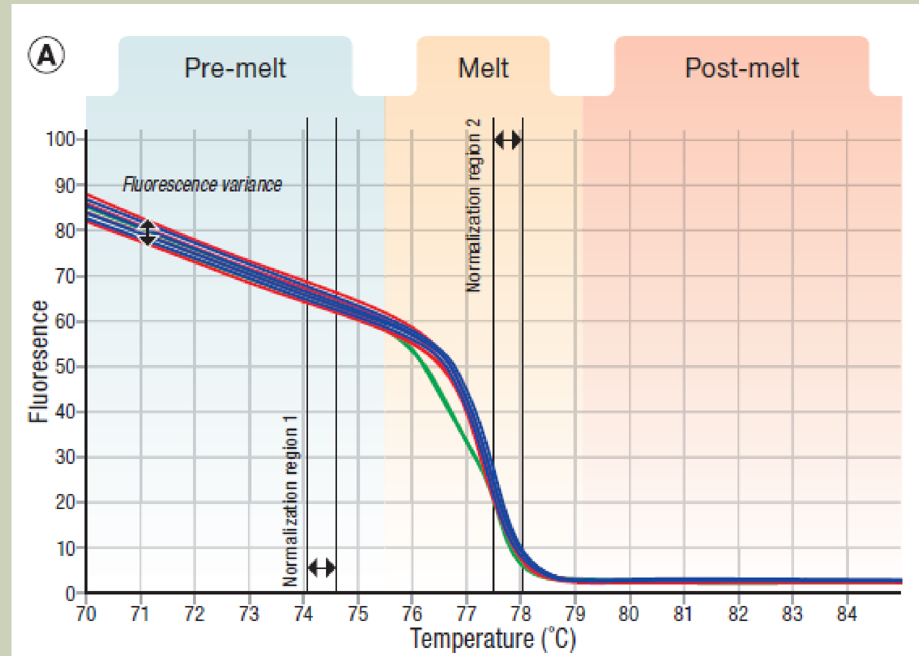
Ganopoulos I., Madesis, P., Sakaridis I., and Tsaftaris A.

Olive Oil

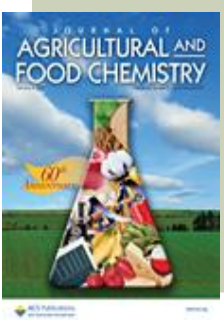
DNA Isolation

Analysis

Genotyping using chloroplastic markers



2012



Ganopoulos I., Madesis, P., Kalaitzis P. and Tsaftaris A.

ASSESSING THE LOCAL BIODIVERSITY

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INNO-FOOD SEE

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European Food Research & Technology
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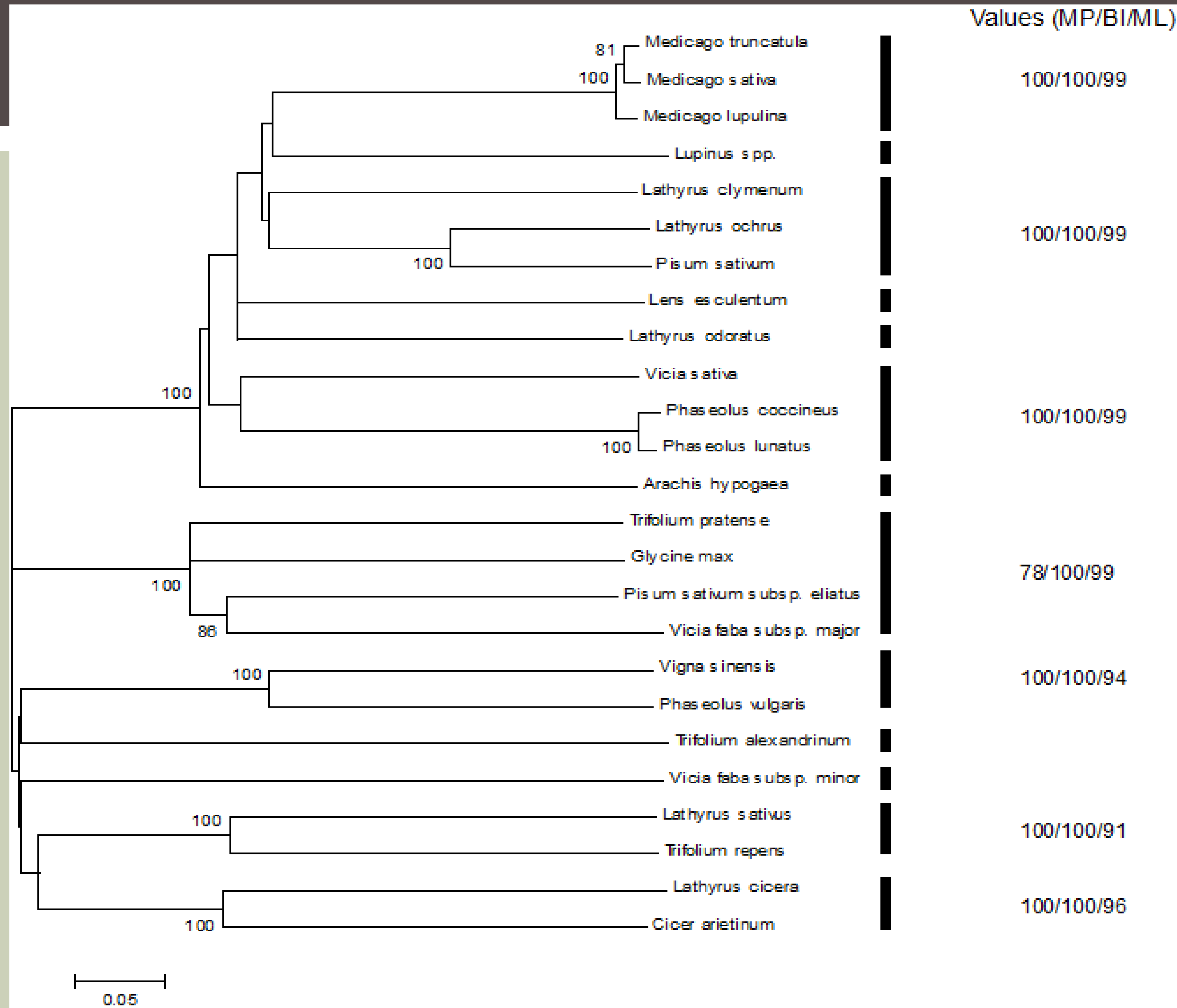
PLoS BIOLOGY
PLoS one
PLoS GENETICS
PLoS NEGLECTED TROPICAL DISEASES
PLoS PATHOGENS
PLoS COMPUTATIONAL BIOLOGY
FOOD RESEARCH INTERNATIONAL
Wood Science and Technology
Tree Genetics & Genomes
PLANT MOLECULAR BIOLOGY REPORTER
plant disease


WORK IN PROGRESS

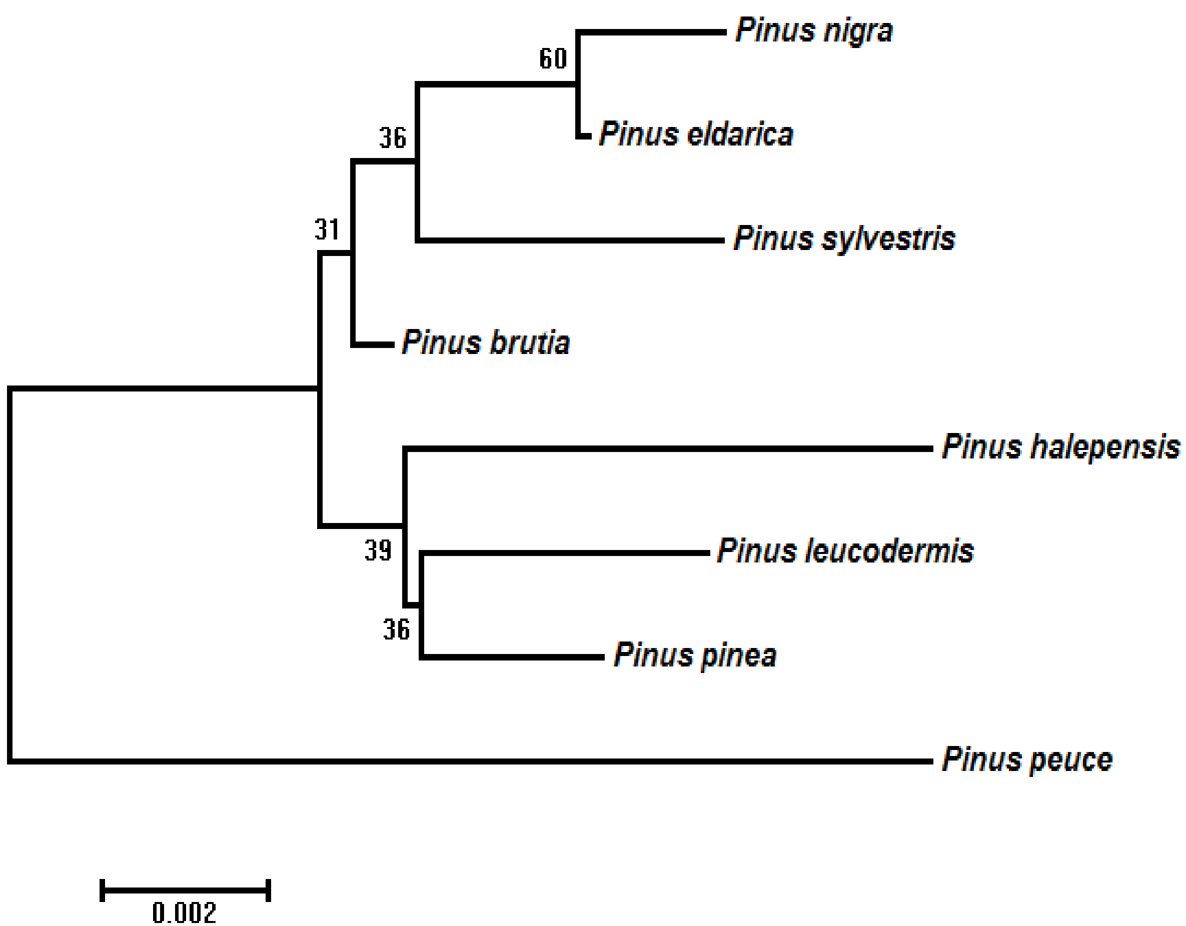
Leguminous species



2012

Madesis, P., Ganopoulos I., Ralli, P. and Tsaftaris A.

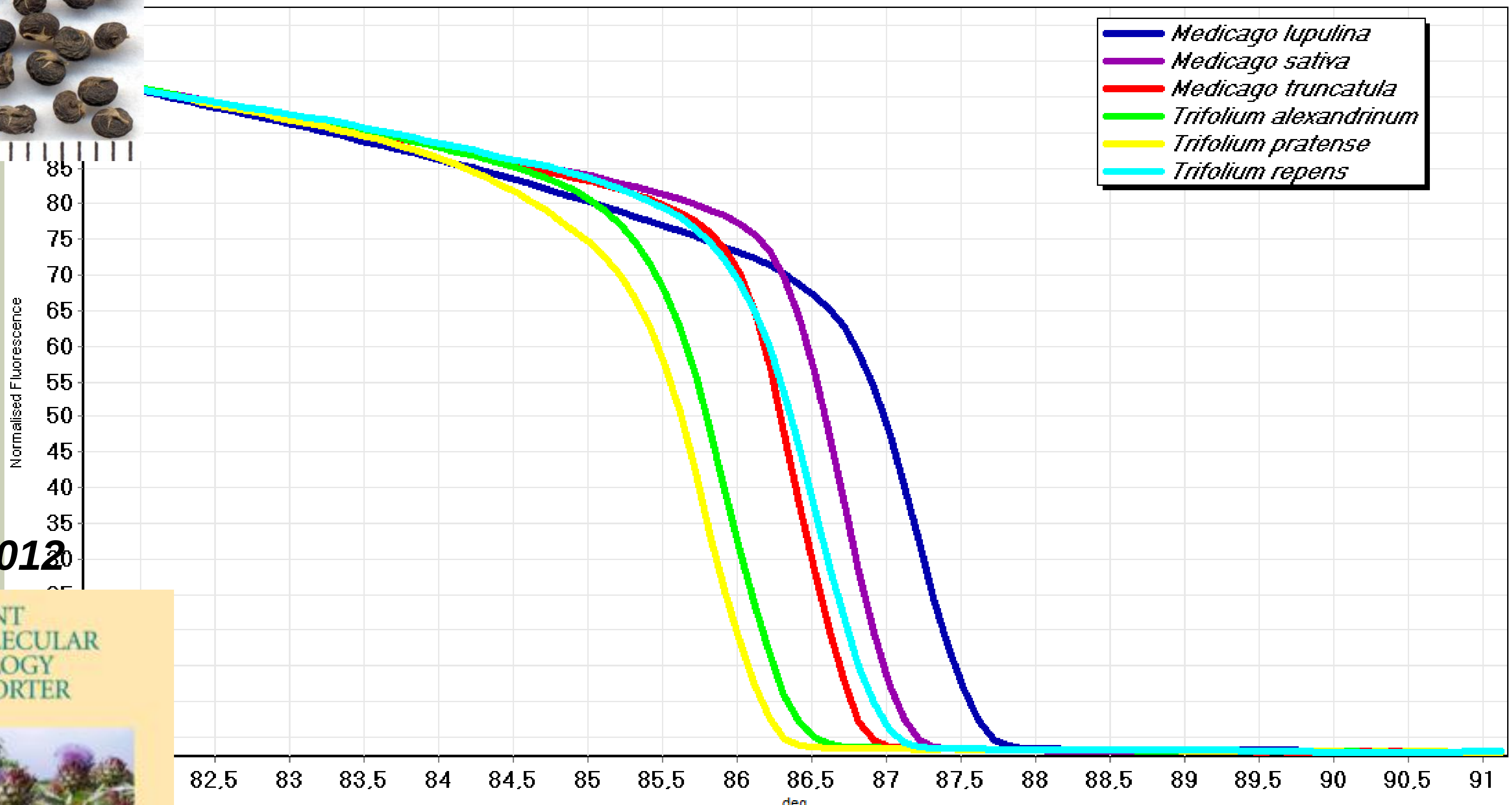
MEDITERRANEAN PINUS SPECIES



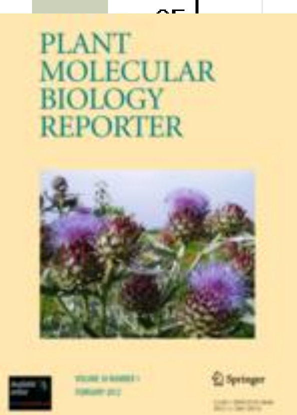
2012

Ganopoulos I., Aravanopoulos F., Madesis, P., Bosmali I., and Tsaftaris A.

PLANTS FOR ANIMAL FORAGE



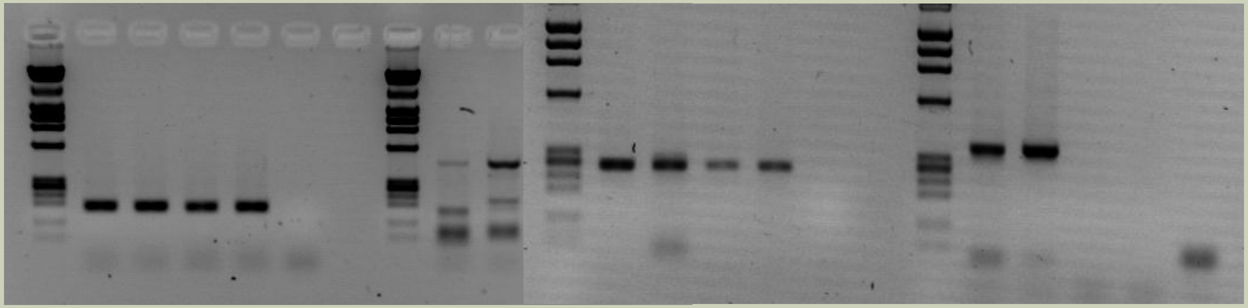
2012



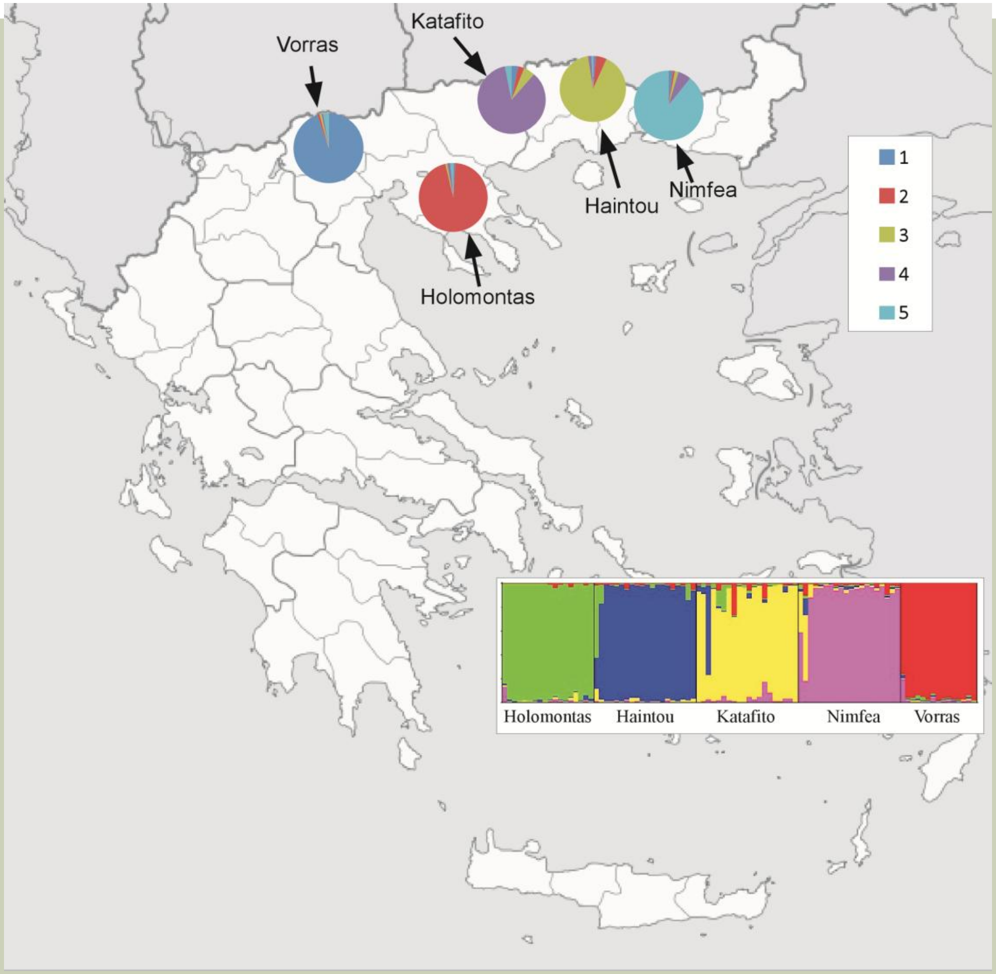
Ganopoulos I., Madesis, P. and Tsaftaris A.

CROCUS SPECIES

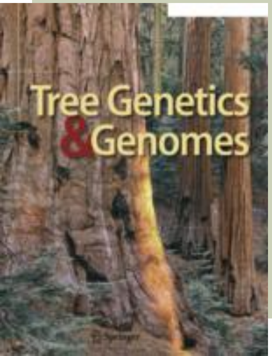
Marker 1 Marker 2 Marker 3



WILD CHERRY

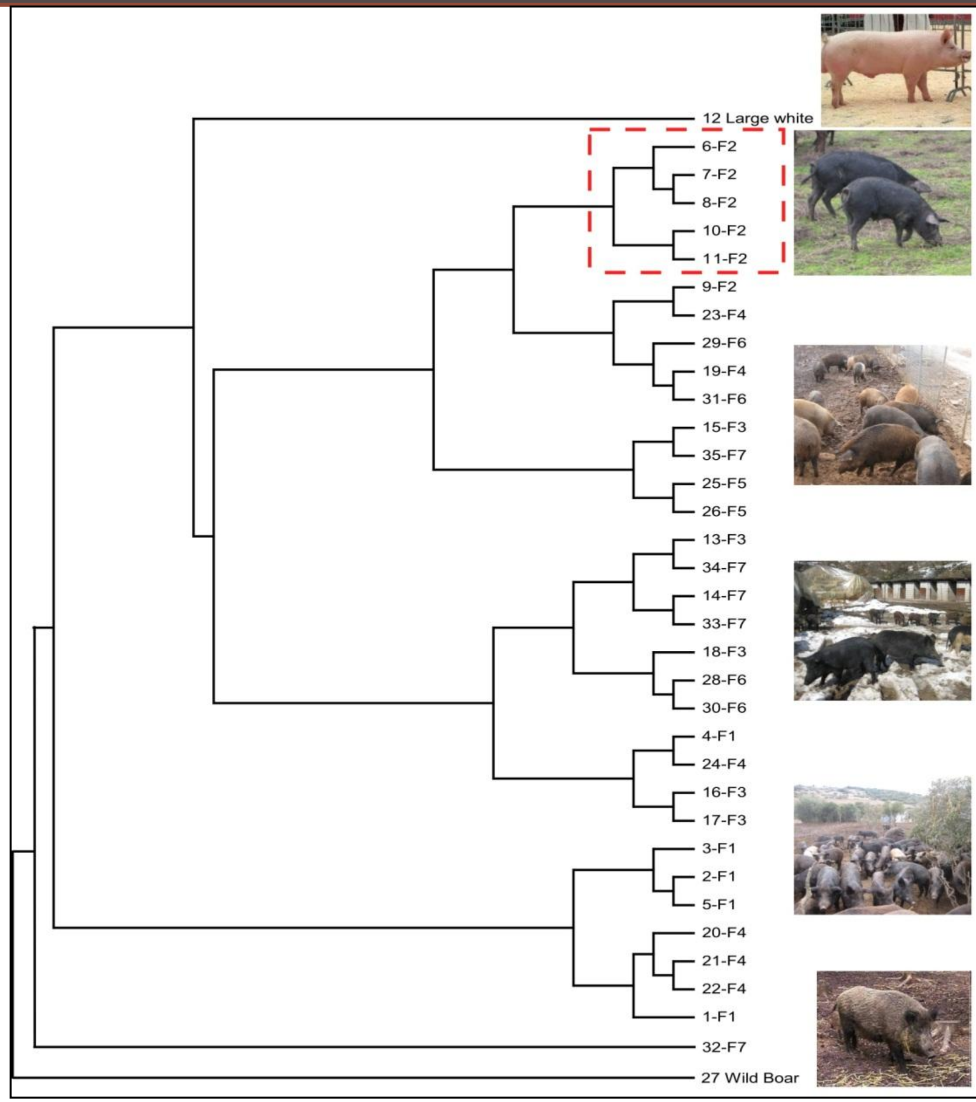


2011



Ganopoulos I., Aravanopoulos F., Argiriou A., Kalivas A. and Tsaftaris A.

GREEK AUTOCHTHONOUS PIG RACES



IDENTIFICATION OF MICROBES IN FOOD PRODUCTS, ANIMAL AND PLANT SPECIES

SOUTH EAST EUROPE
Jointly for our common future

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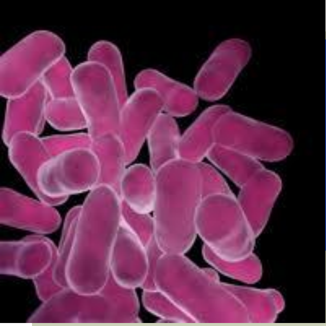
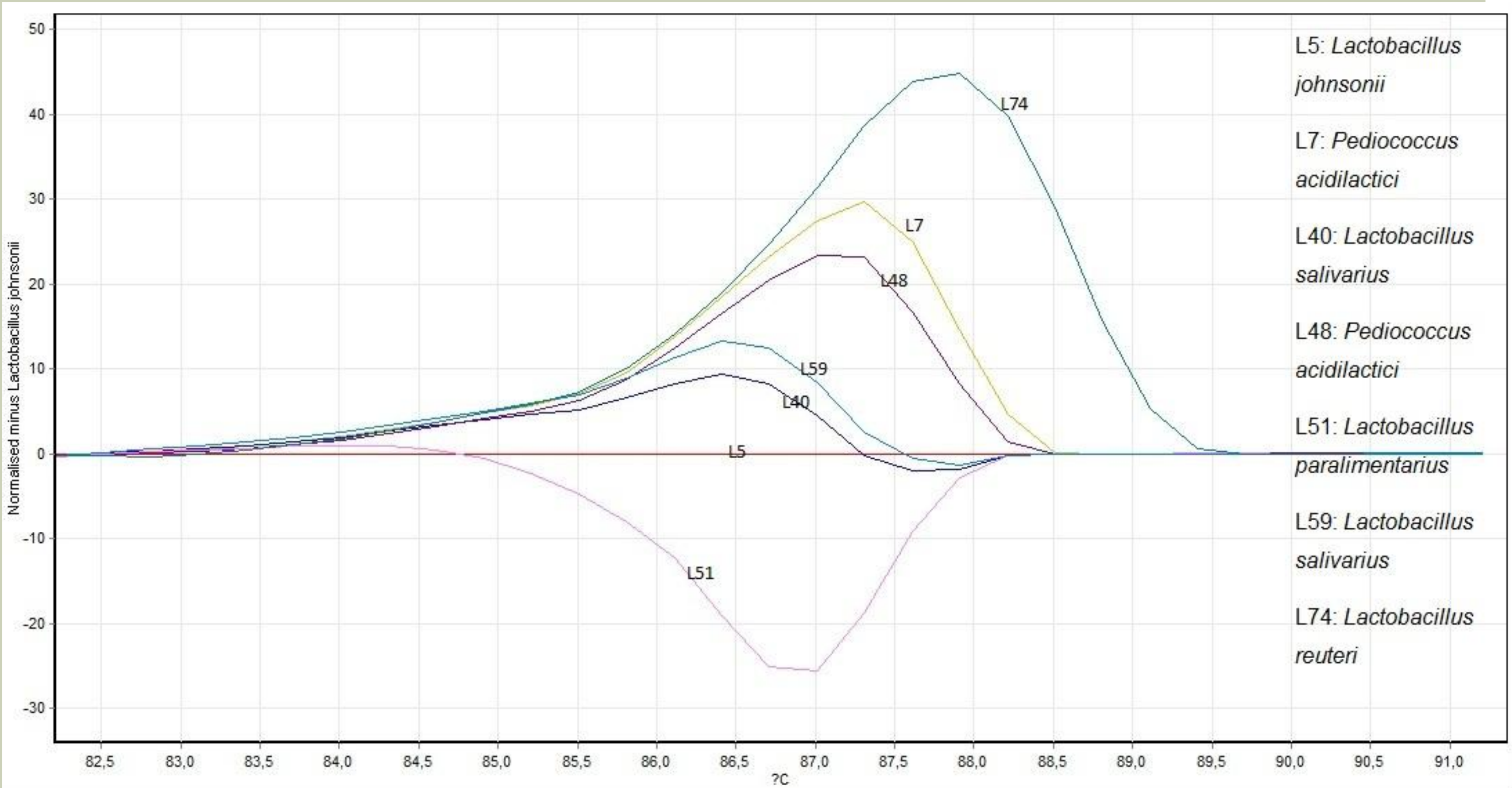


Identification of Lactic Acid Bacteria



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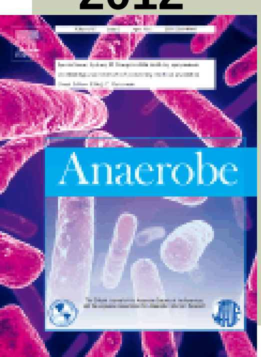
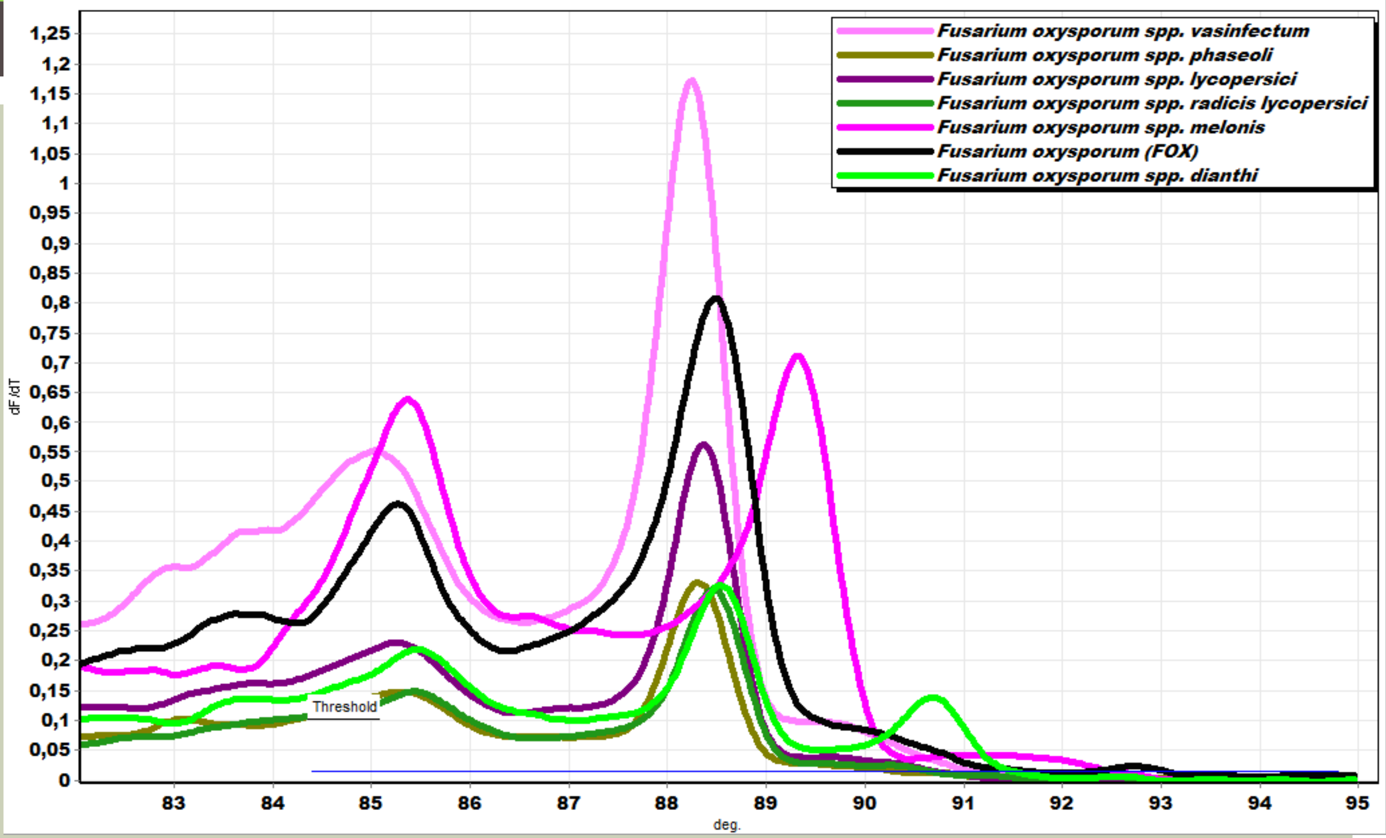


Sakaridis I., Ganopoulos I., Soultos N., and Tsaftaris A.

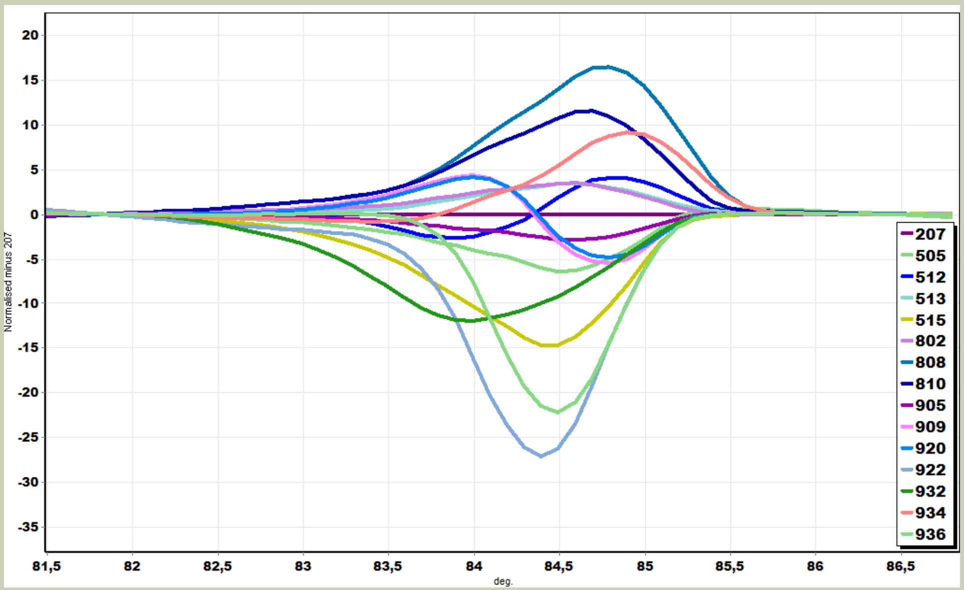
FUSARIUM OXYSPORUM

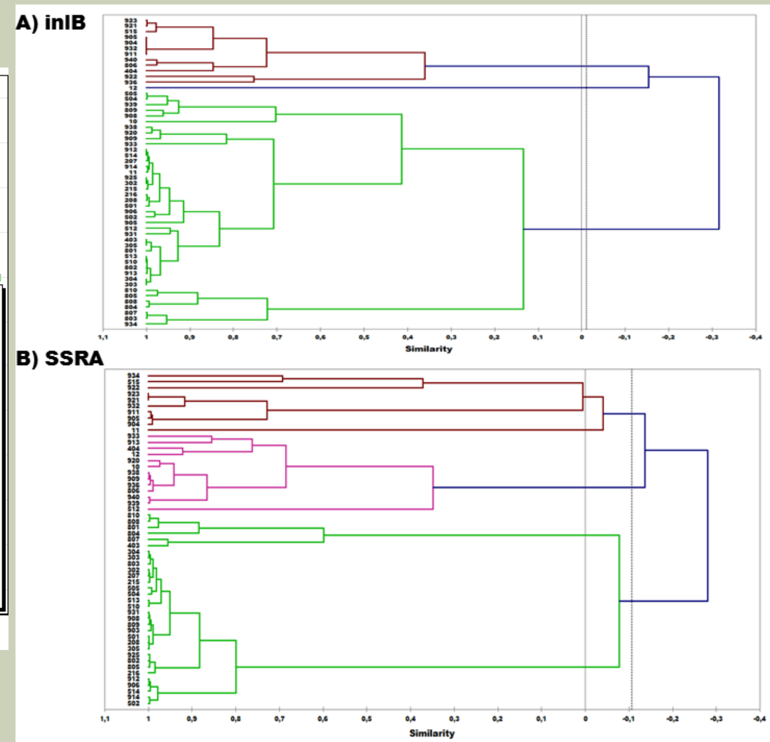


2012

Ganopoulos I., Madesis, P., Zambounis A., and Tsaftaris A.

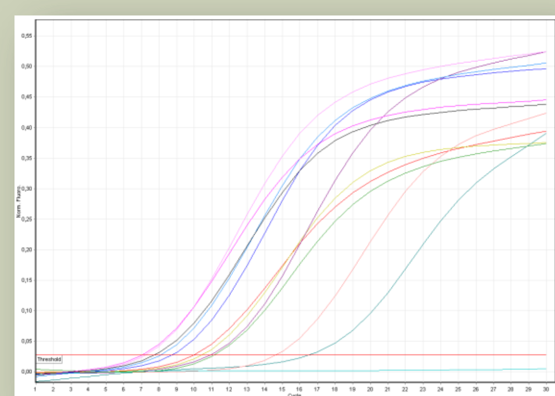
GENOTYPING LISTERIA STRAINS USING HRM

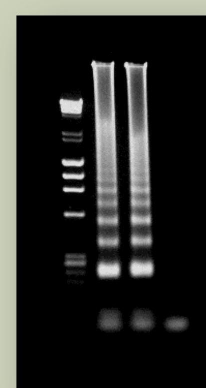


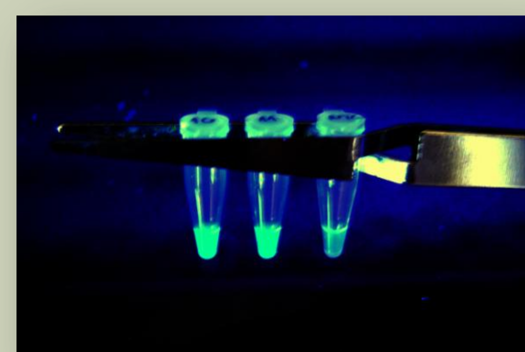


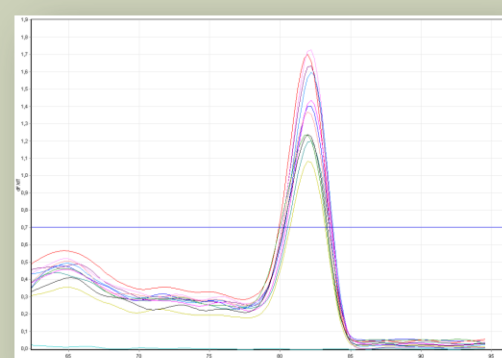
Genotyping of *Listeria monocytogenes* isolates from poultry carcasses using High Resolution Melting (HRM) analysis
Sakaridis, Ganopoulos, Madesis, Tsaftaris and Argiriou
Biotechnology and Biotechnological Equipment, 2013

DETECTION OF *LISTERIA MONOCYTOGENES* USING LAMP









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