

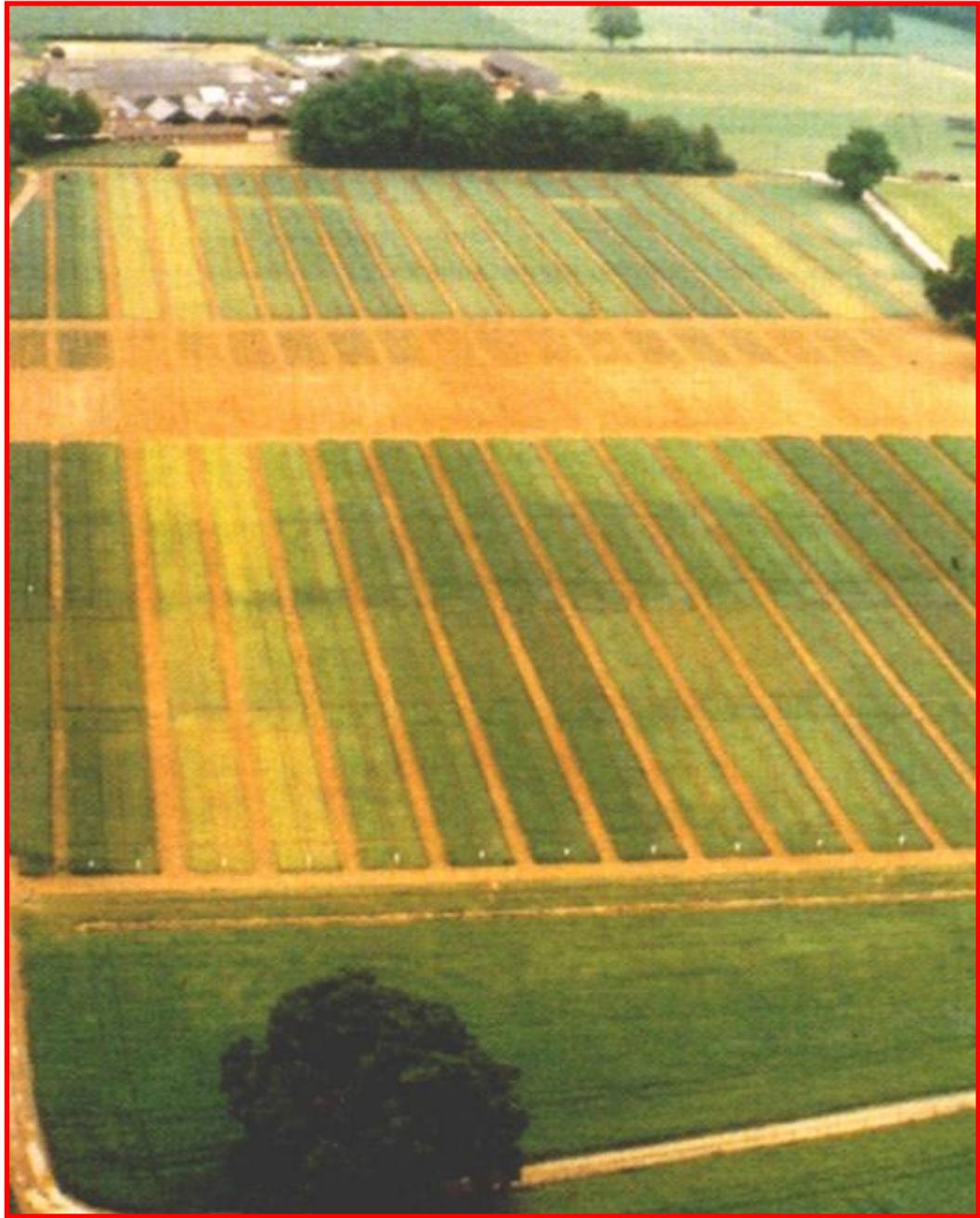


Club of Bologna- EXPO 2015 Milano

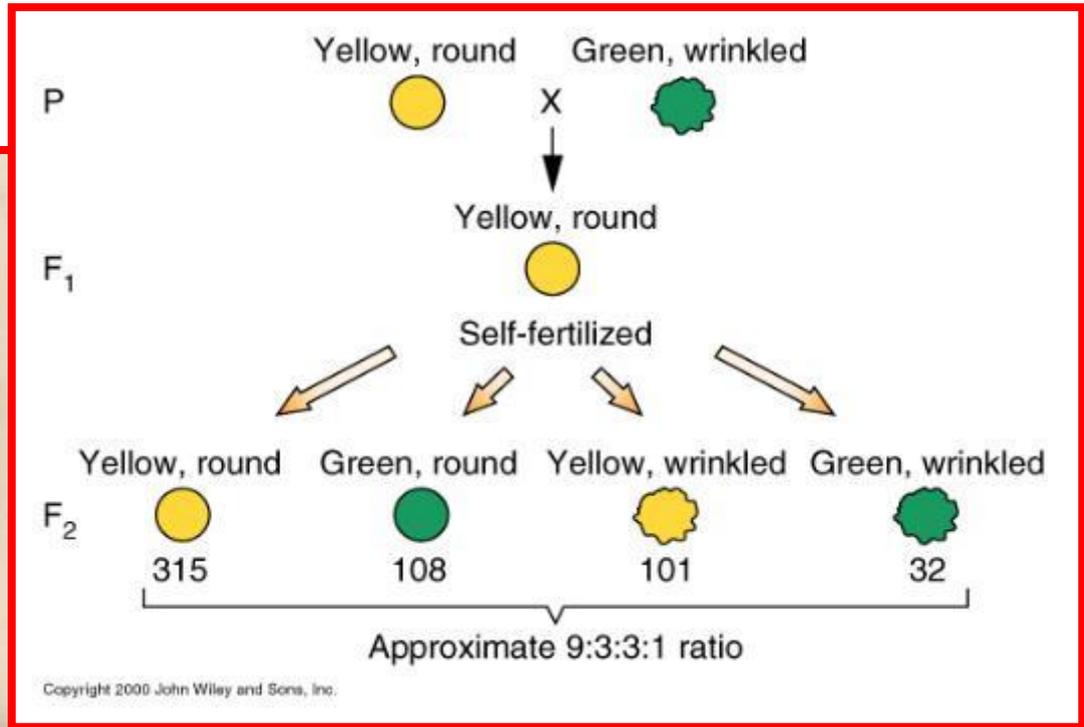
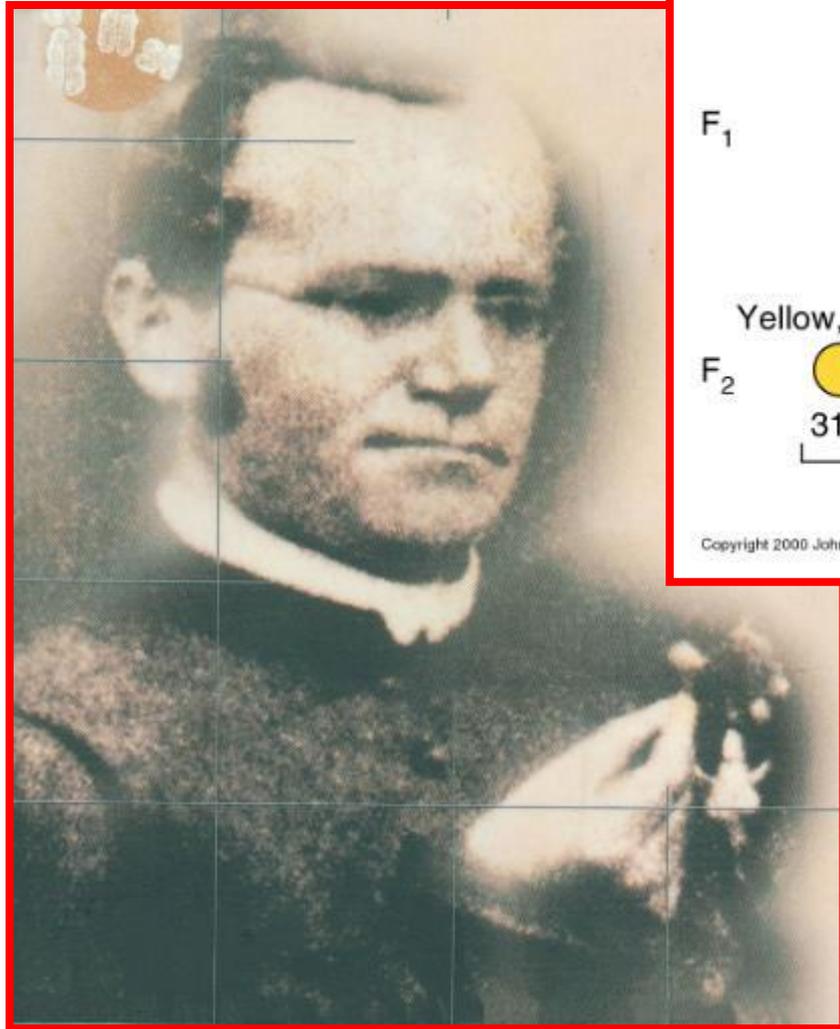
Genetic Improvement of Plant Productivity for Feeding Ten Billion



Michele Stanca President of the "Union of Italian Academies
for Science Applied to Agriculture
Food and Nature -UNASA



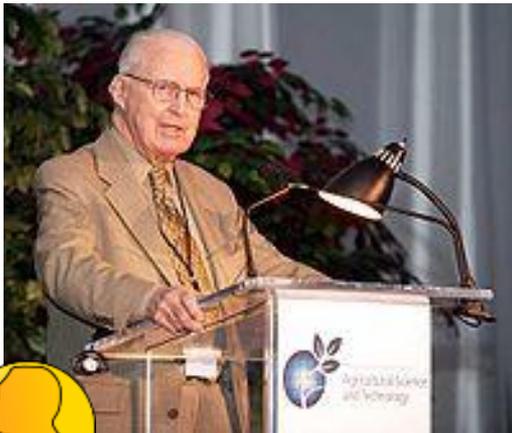




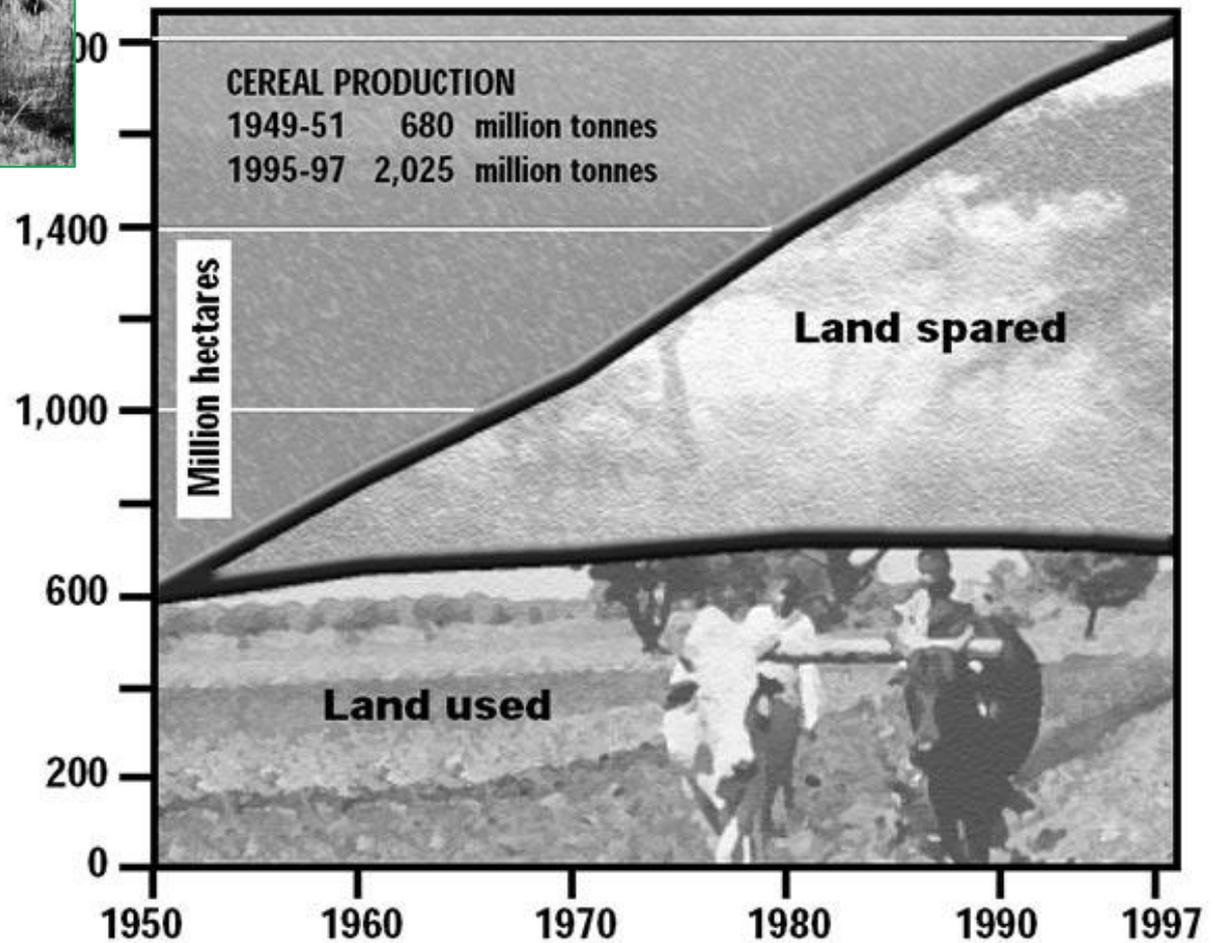
Nazareno Strampelli

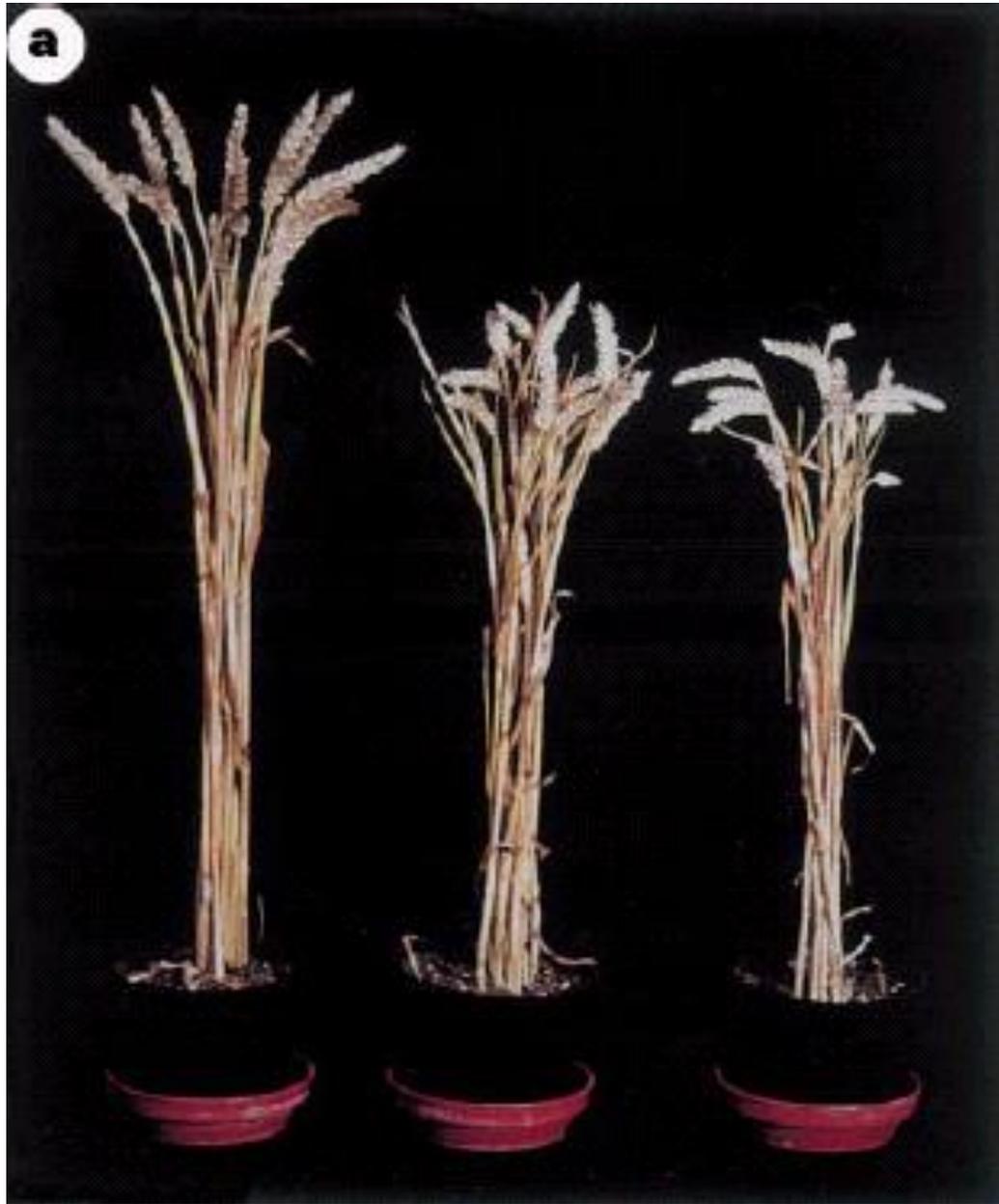


Mendel

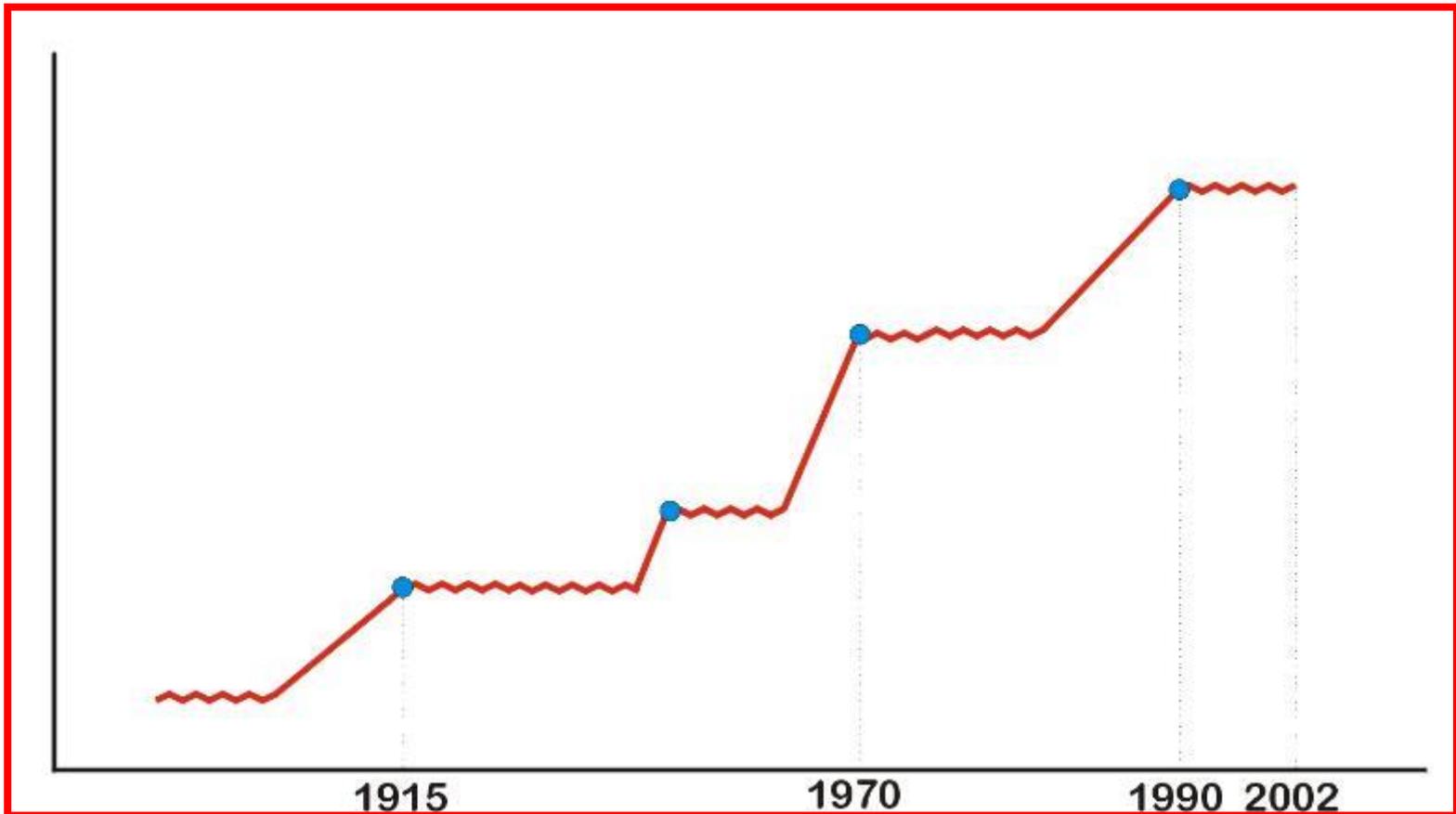


Norman Borlaug



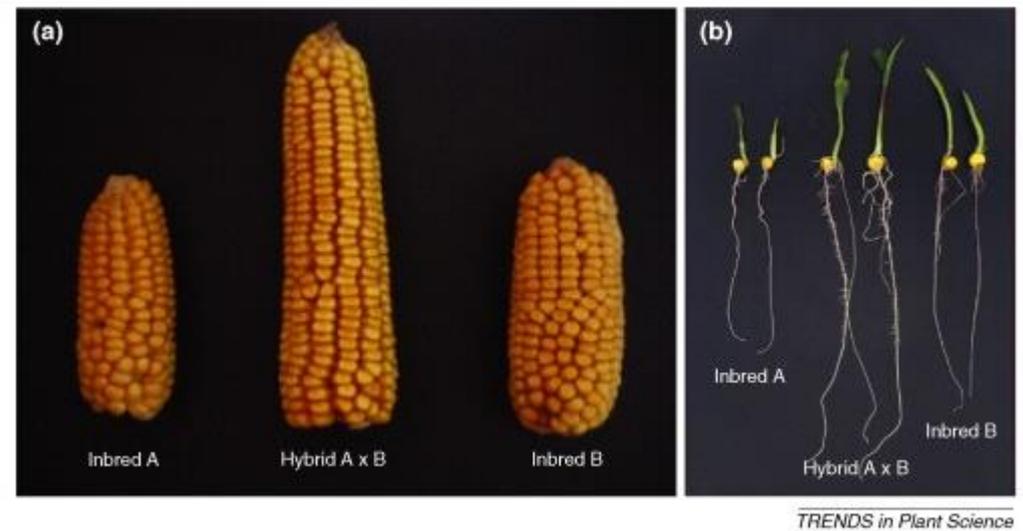


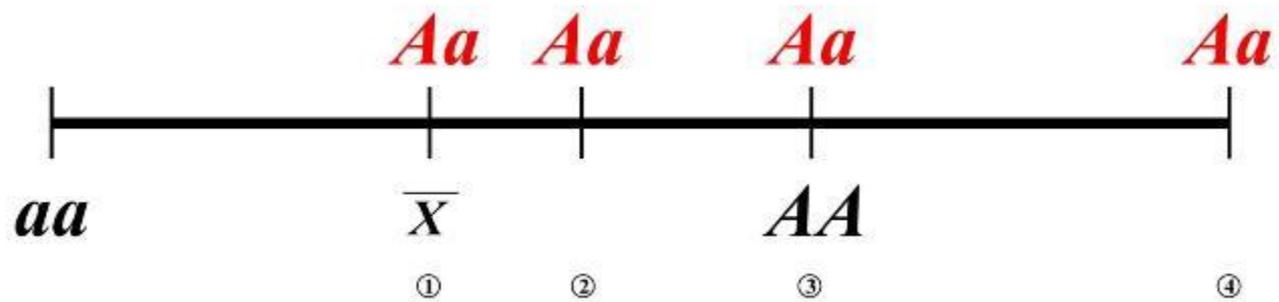
Model of the Breeding progress in the last 100 years



Towards the molecular basis of heterosis.

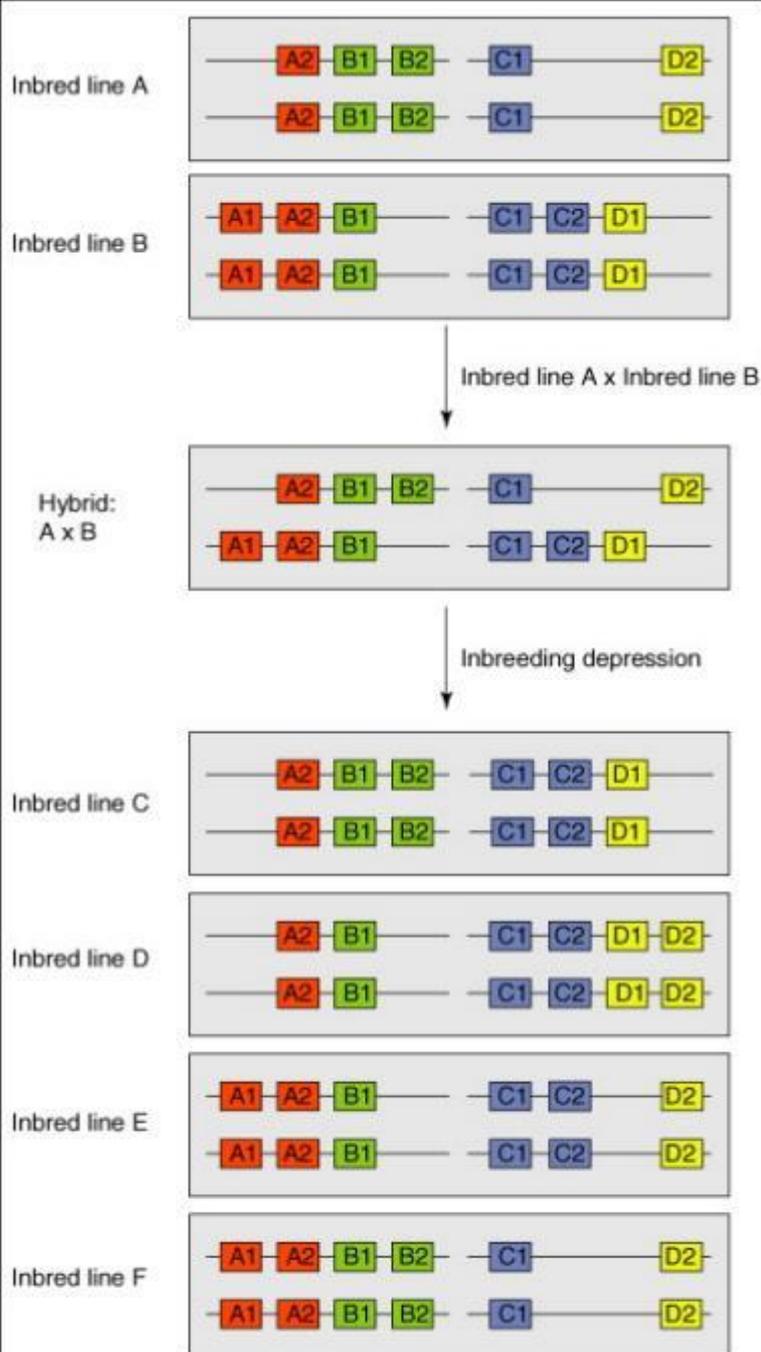
Phenotypic manifestation of heterosis





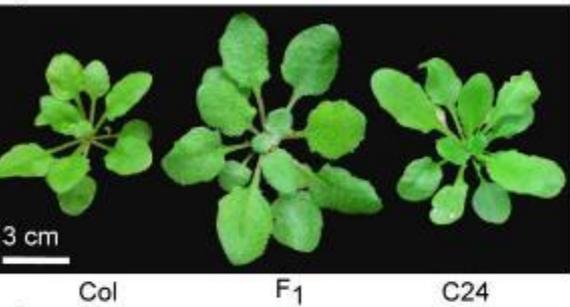
Genetic hypothesis to explain heterosis

Hemizygous complementation in maize hybrids. Different maize inbred lines are characterized by a considerable loss of genetic colinearity, that is, the loss of particular genes. It is hypothesized that gene loss can be partly compensated in hybrids by hemizygous complementation, which also leads to an improved performance of hybrids versus inbred lines. The colored boxes A to D represent different genes. Different members of gene families are indicated by the same colour (e.g. A1 and A2 belong to a gene family). The loss of a member of a gene family can be partly compensated for by the action of other members of this gene family and leads only to minor phenotypic effects in inbred lines. When a hybrid is selfed over several generations inbreeding depression is observed because not all genes present in the hybrid will be maintained. To date, partial loss of colinearity has only been observed in maize. In other species as well as in maize, additional factors might also contribute to heterosis.

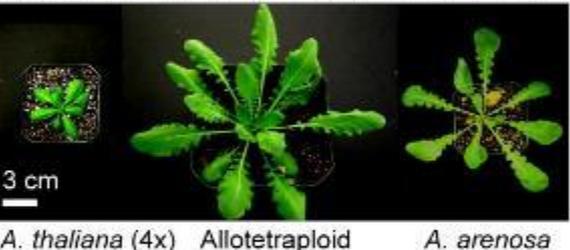


Molecular mechanisms of polyploidy and hybrid vigor.

(a) A hybrid formed between two ecotypes



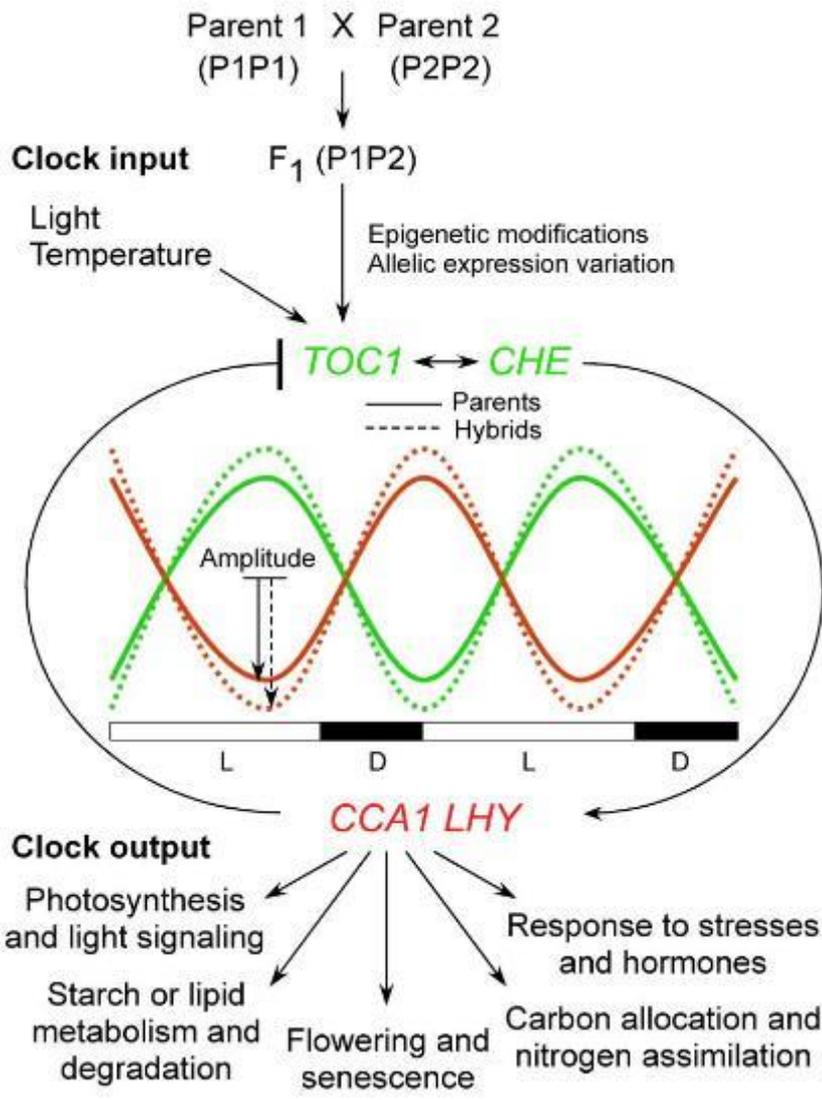
(b) An allotetraploid formed between two species



(c) Flowers



(d) Seeds



A molecular clock model explains the basis of heterosis. In the hybrids, the allelic interactions between parent 1 (P1) and parent 2 (P2) induce epigenetic repression of *CCA1* and *LHY* expression amplitudes (red dashed line) and upregulation of *TOC1* expression amplitudes (green dashed line) relative to the expression values in the parents (solid red and green lines, respectively), whereas the periodicity of the clock remains the same because maintaining clock periodicity and rhythm is important for plant growth and fitness



Modifica dell'architettura della pianta e della capacità di fioritura in *Osteospermum*









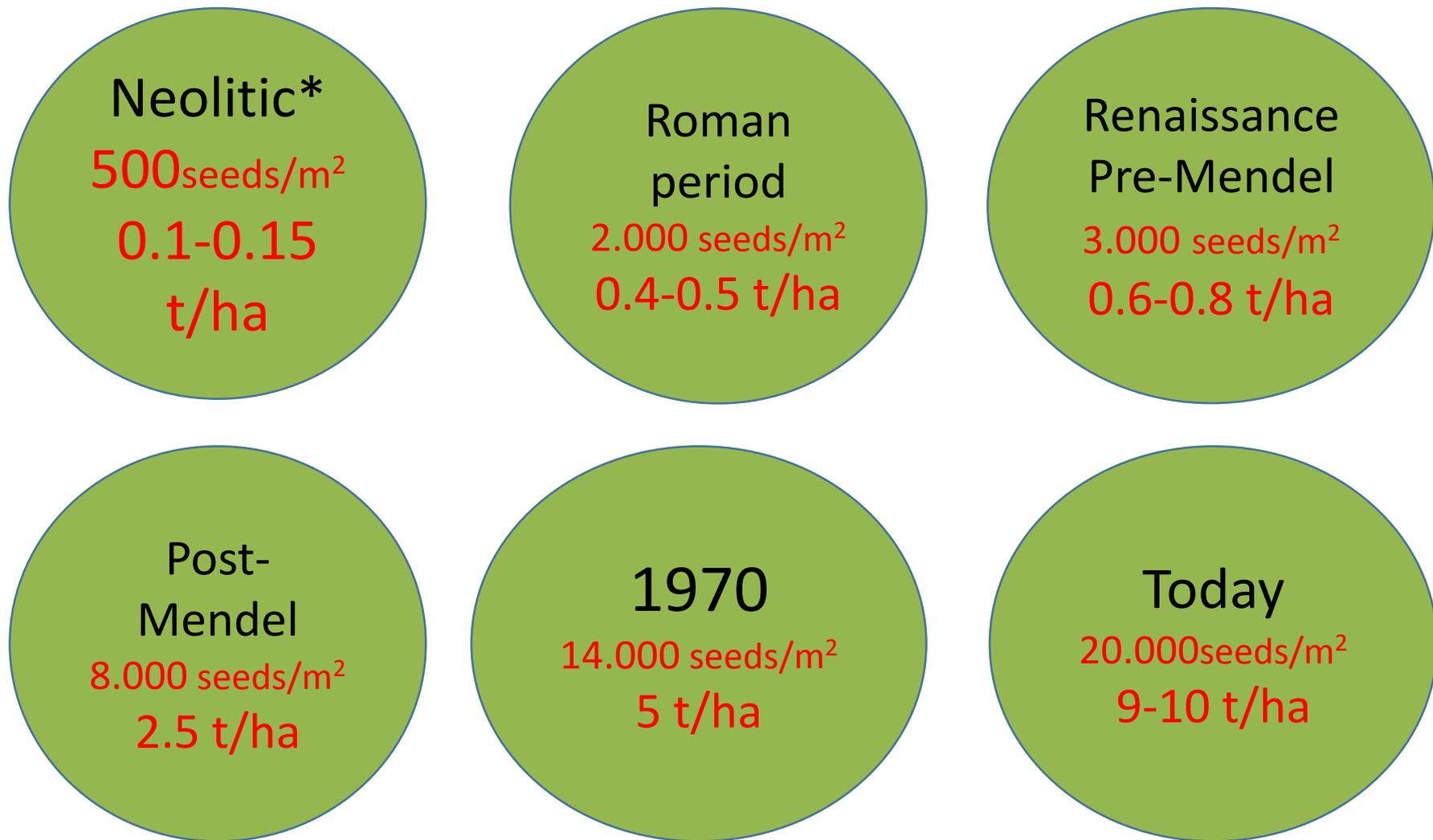


Figure 4



I.S.C.B.

SHORT TERM PROGRAM

“Cross the best to get the best”

- Pedigree and its modification
- Development of recurrent selection programme to increase the frequency of good alleles

MEDIUM-LONG TERM PROGRAM

- a) - Biodiversity analysis for agronomically useful gene (traditional or with molecular assisted selection)
 - resistance to biotic and abiotic stresses
 - improvement of fruit quality for traditional or non traditional uses
- b) - Transferring agronomically useful genes in elite genotypes *via* transformation or by developing **New molecular tools for PreBreeding-Breeding Programme**
- c) - Analysis and use of developmental mutants



GENETICA



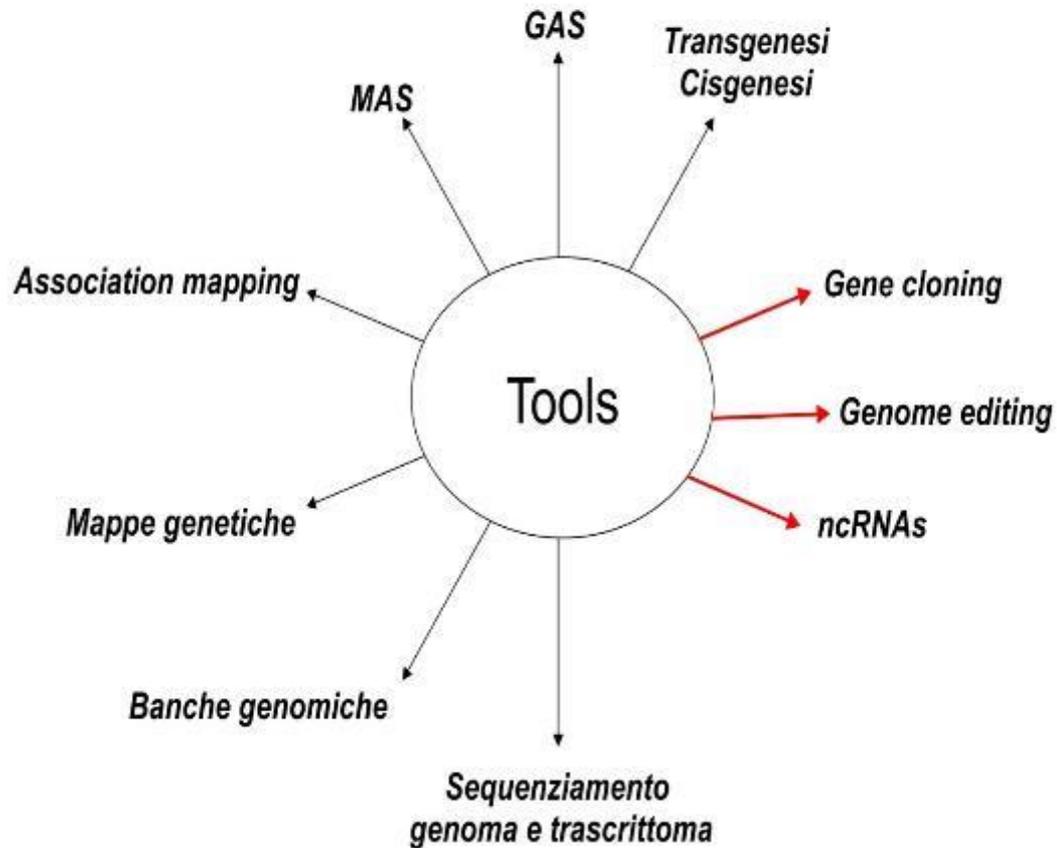
GENOMICA



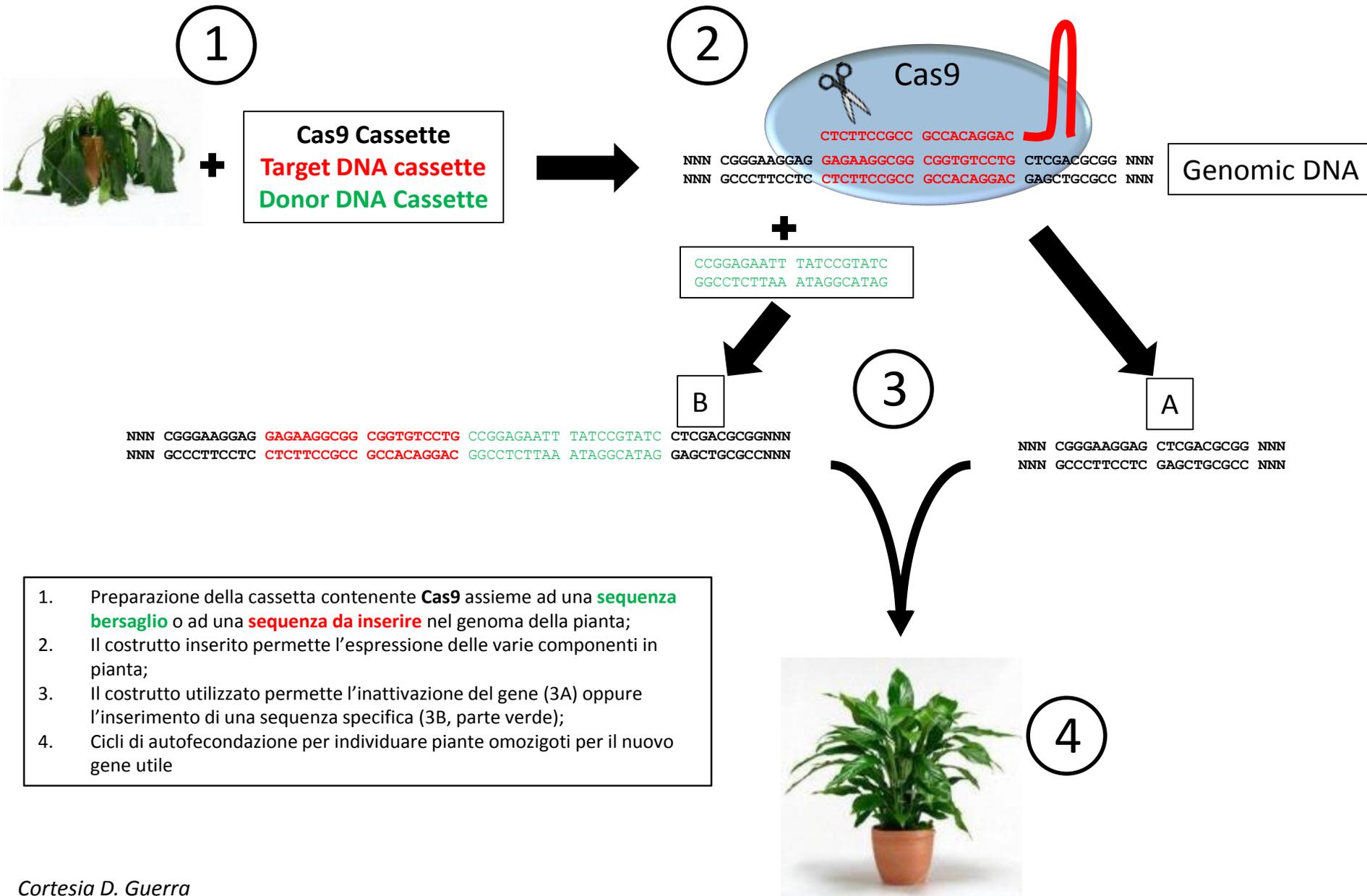
studia il Genoma
(l'intero contenuto di DNA di
una Cellula)

Genomic Tools

For
Molecular Pre Breeding - Breeding

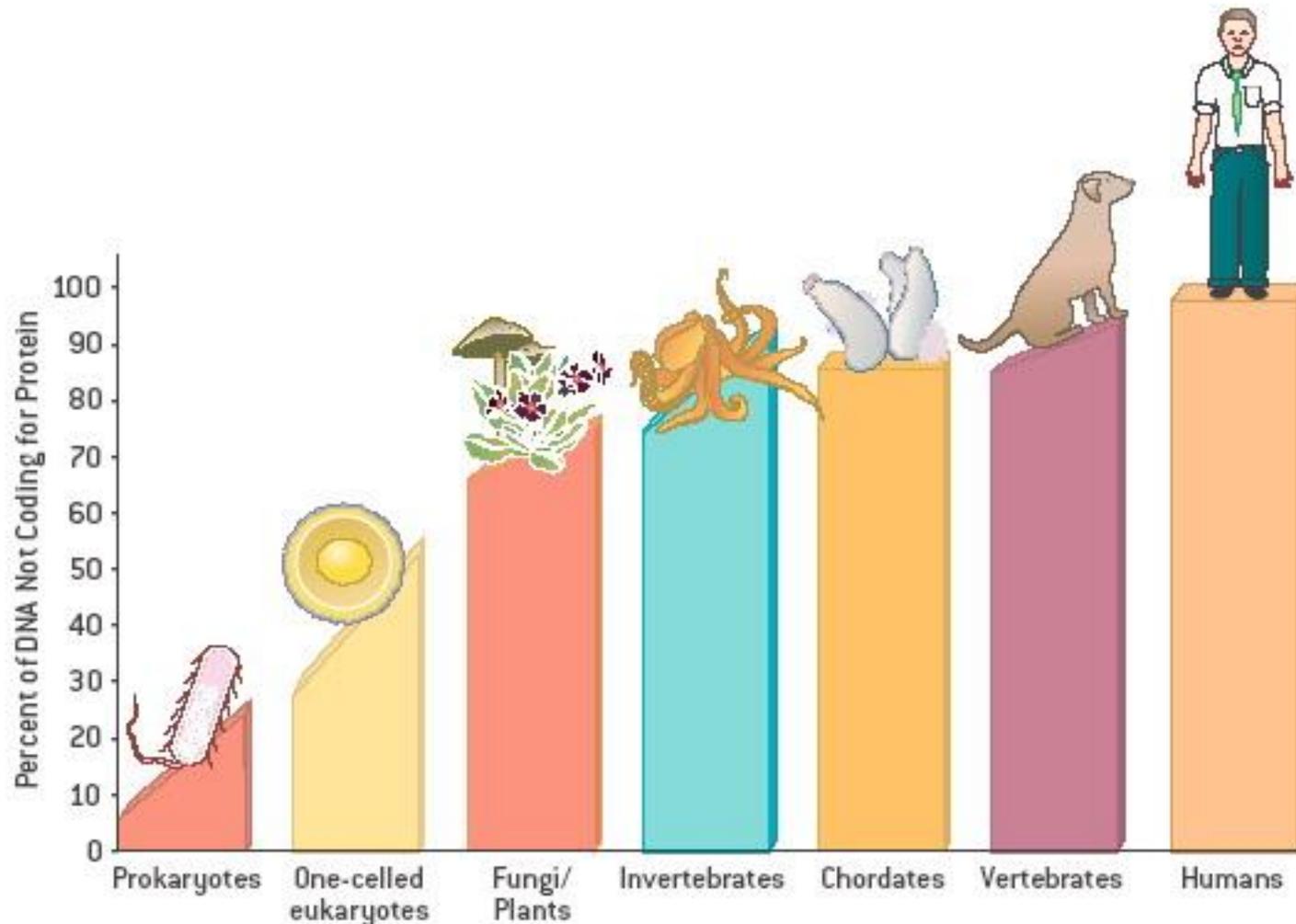


Genome Editing for pre-breeding advancement

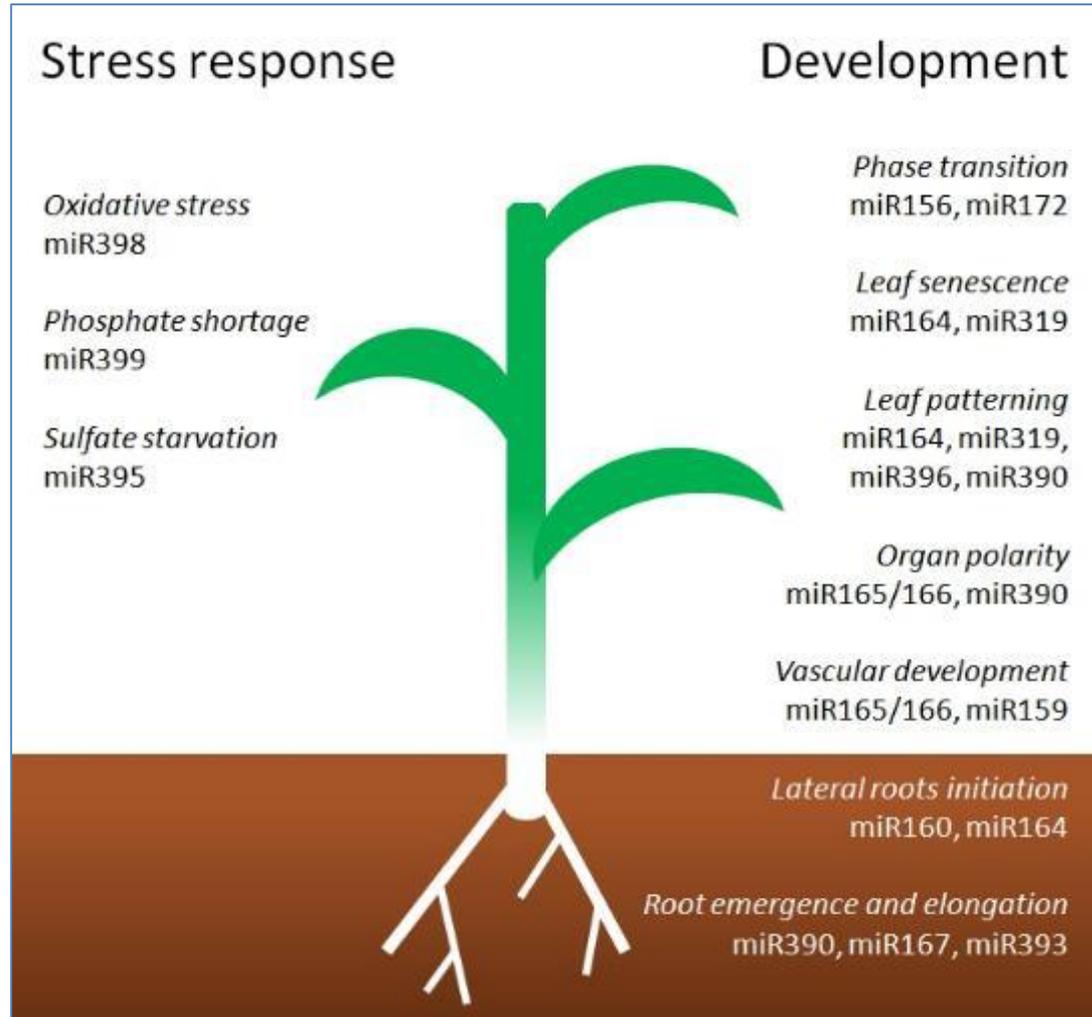


Non-coding RNAs

relative abundance in different organisms



Plant microRNAs

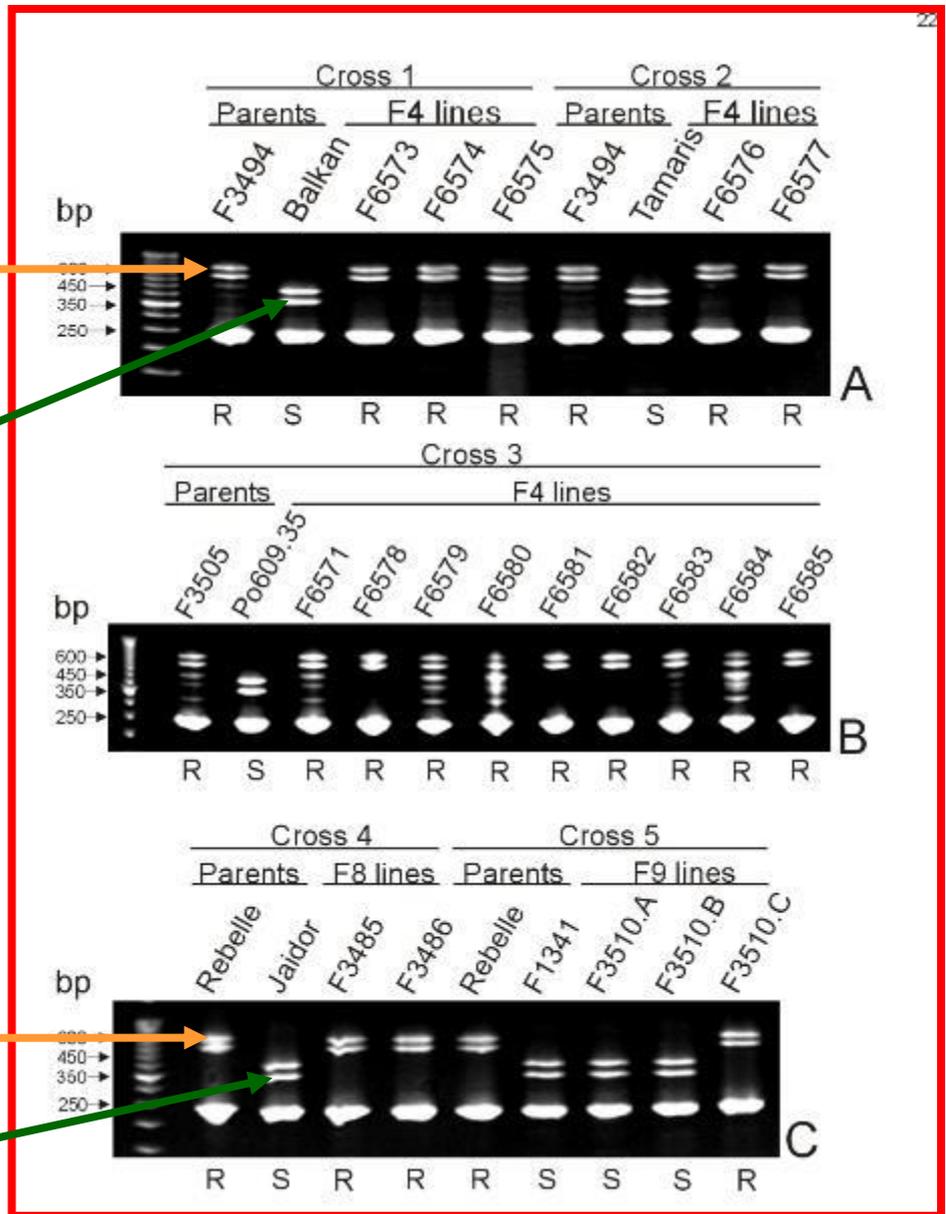


Piante resistenti

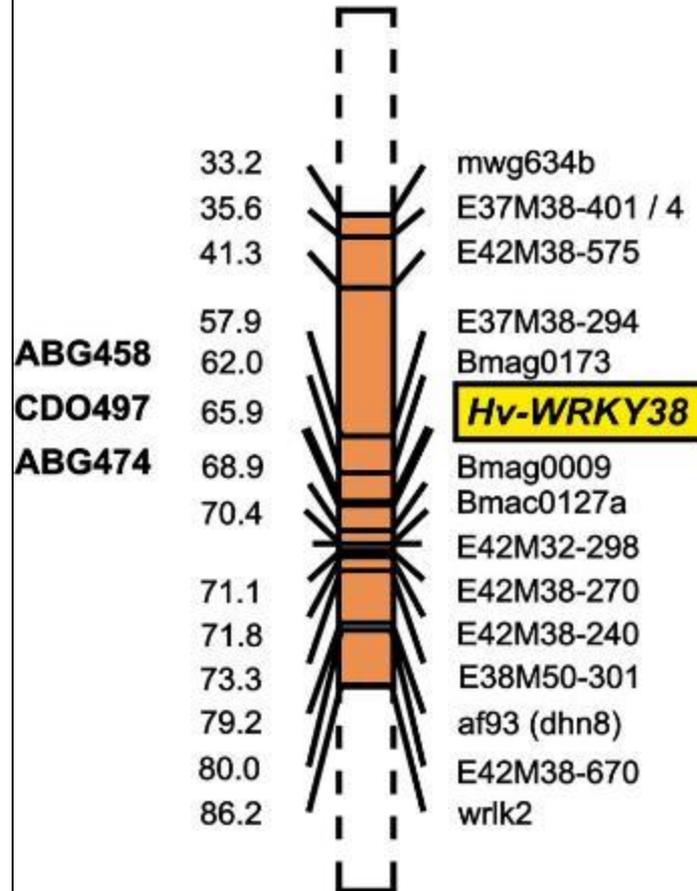
Piante suscettibili

Piante resistenti

Piante suscettibili



6H





1. Prelievo dei campioni

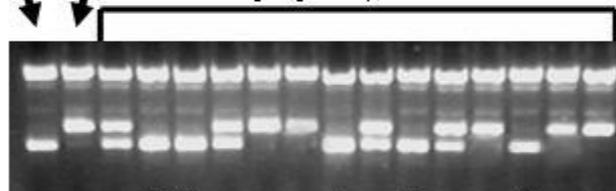


2. Estrazione del DNA dal tessuto

MAS=Molecular Assisted Selection

Controllo Resistente	Controllo Suscettibile
----------------------	------------------------

Piante segreganti per il carattere



4. Selezione delle piante desiderate in base al profilo del DNA

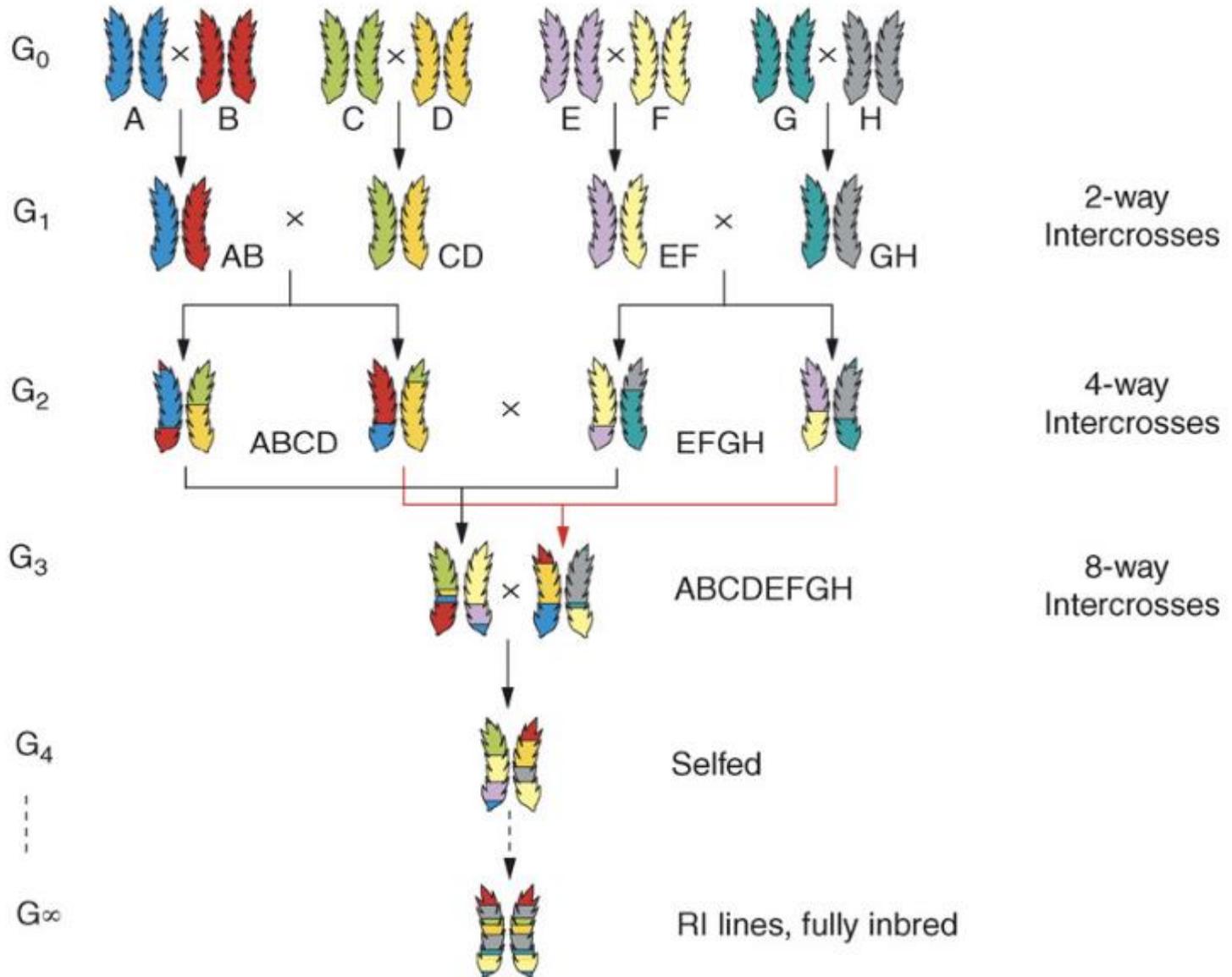


3. Reazione PCR con i marcatori molecolari associati al carattere d'interesse



5. Esecuzione di nuovi incroci "mirati"

Multi-parent Advanced Generation Inter-Cross (MAGIC)

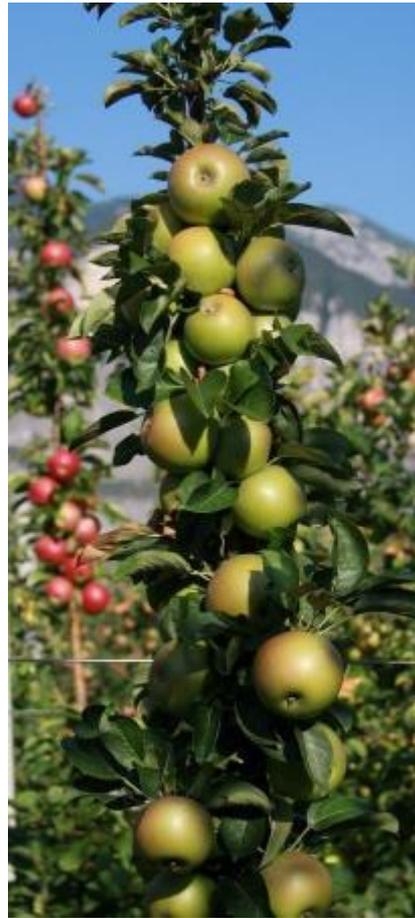


Dell'Acqua.....Frascaroli.....PE'

Genetic properties of the MAGIC maize population: a new platform for high definition QTL mapping in *Zea mays*

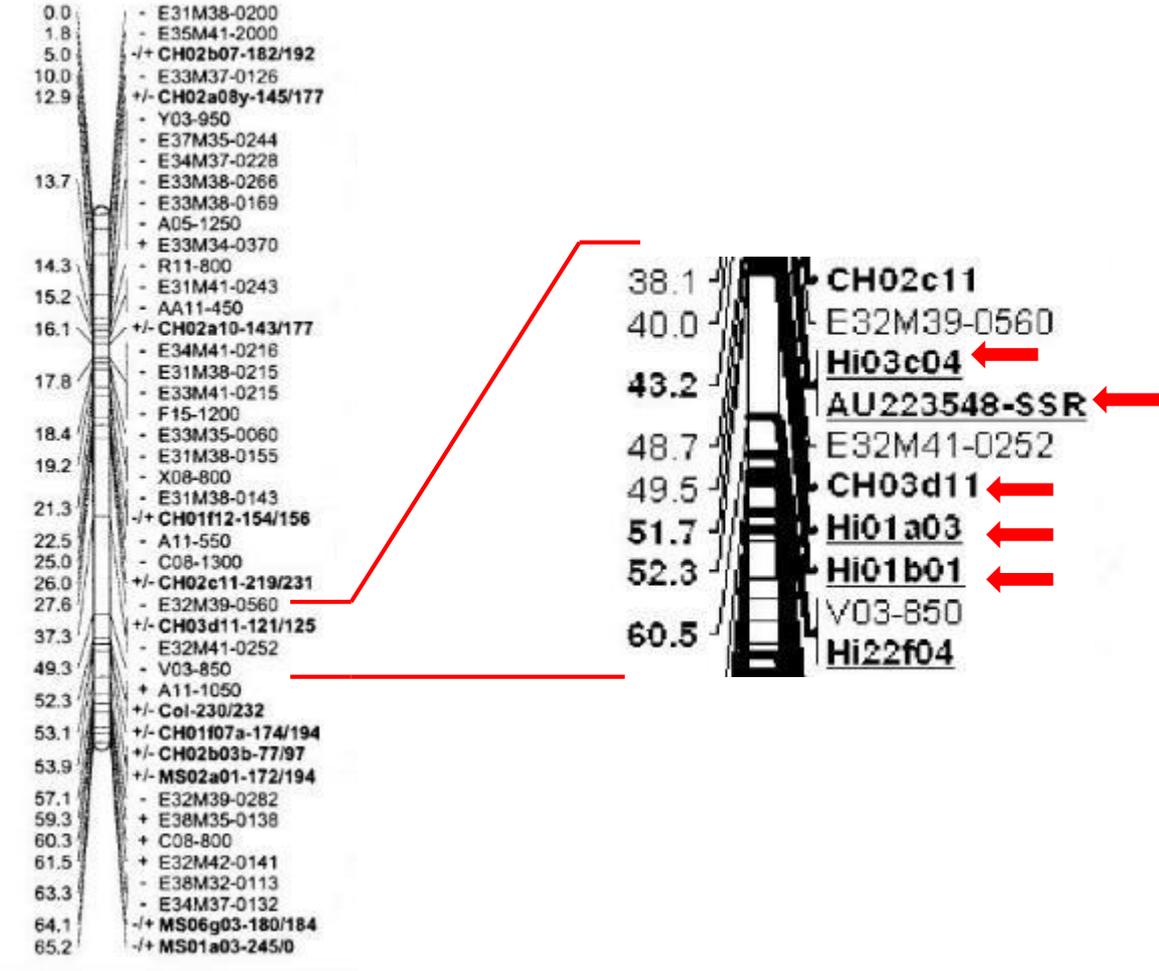
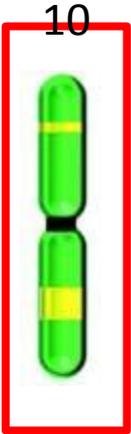
Genome Biology 2015, **16**:167

Apple Columnar Phenotype

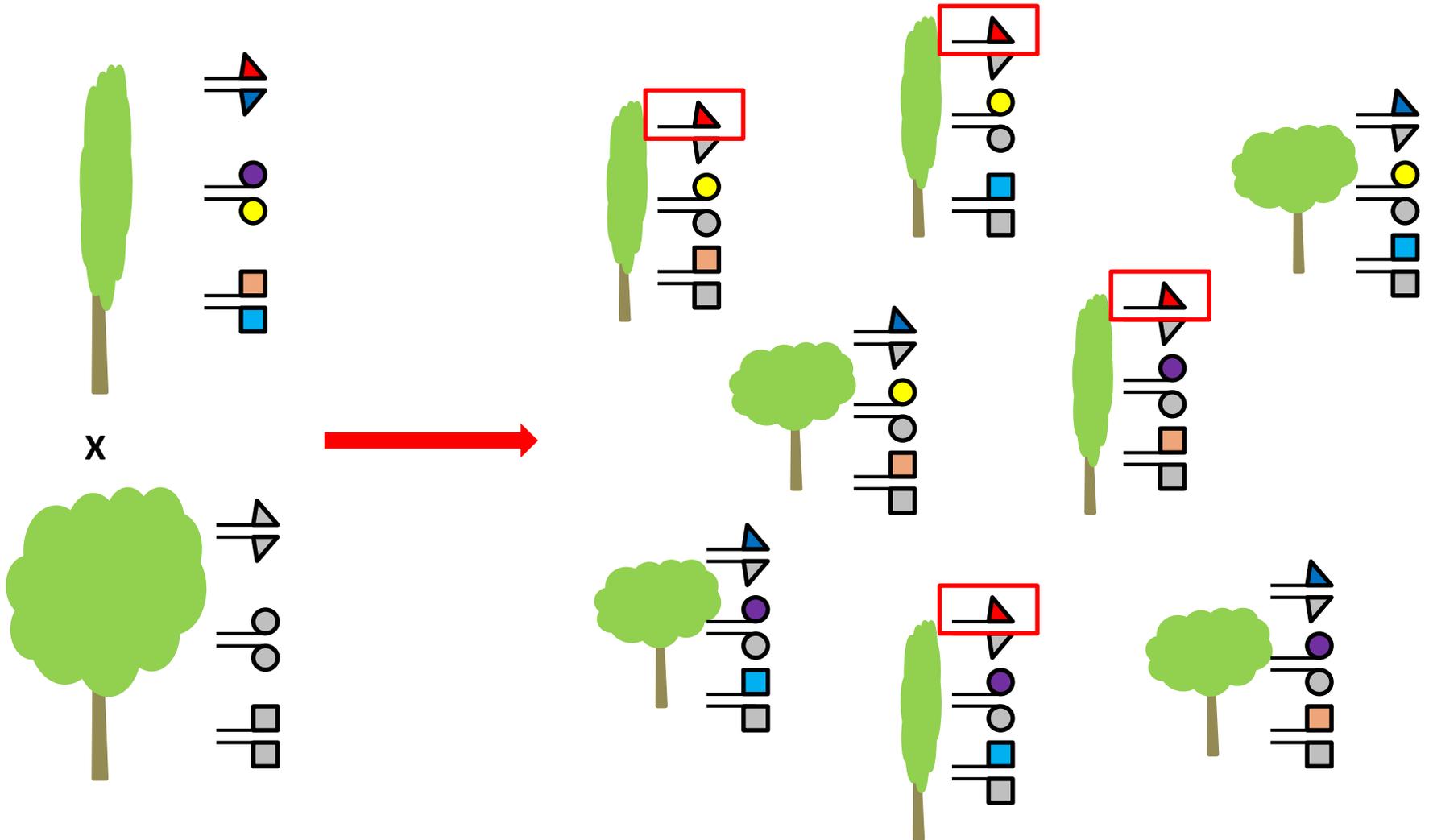


- The columnar growth habit in apple was discovered in 1970 as a natural mutation of the cultivar McIntosh. It seems to be controlled by a single, dominant gene and it is characterized by short internodes a thick stem

Columnar (Co) State of the Art



Phenotype – Genotype Association



Phenotypic Plasticity in *Vitis vinifera*

Vitis vinifera spp is one of the most plastic plants known: a single genotype is able to produce berries with different quality, thus different wine qualities, depending on the micro-environment where it is cultivated.

Berry plasticity is very high

Individual berries

Among berries within a cluster

Between clusters on a vine

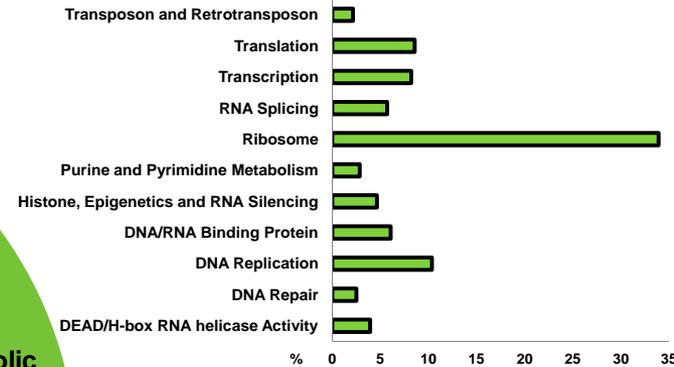
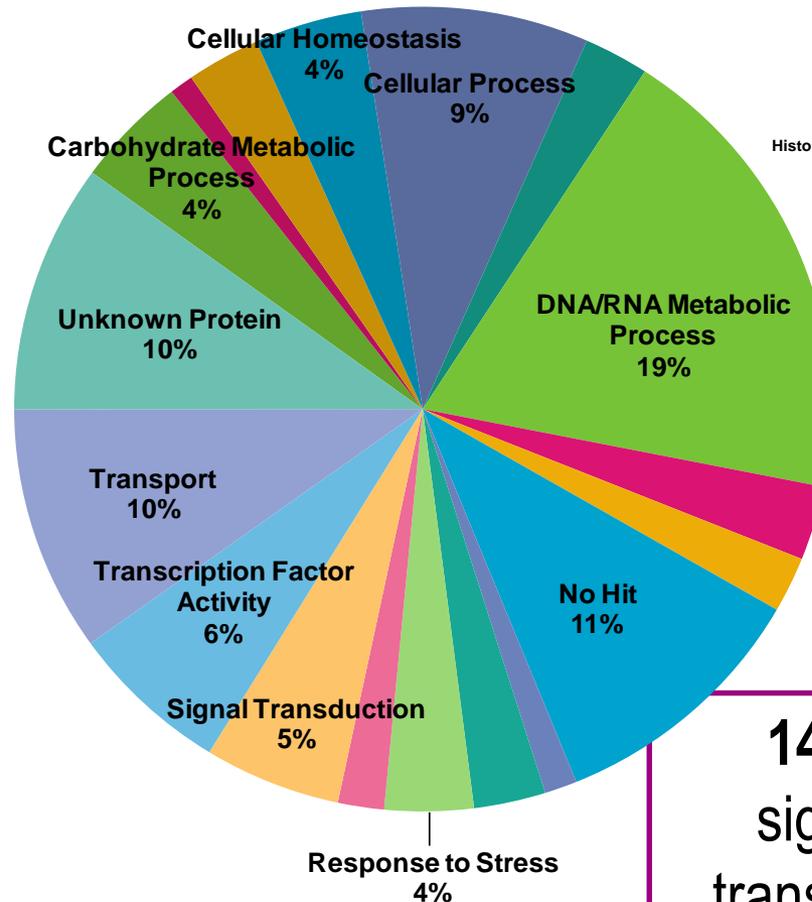
Among vines in the vineyard



Transcriptome Plasticity during Berry Development

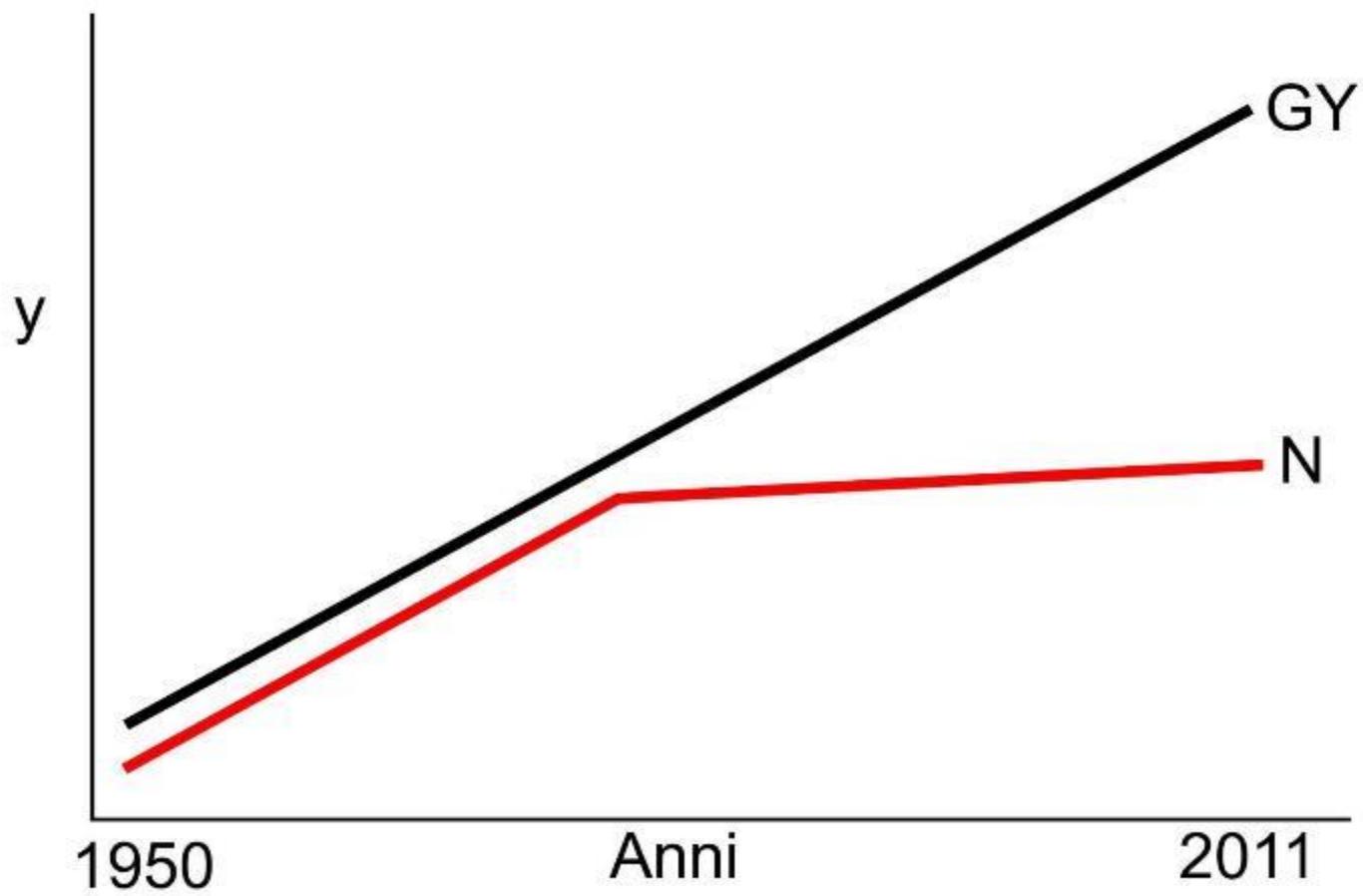
Samples from **2008** harvested in **11** Vineyards in **3** developmental stages

- Carbohydrate Metabolic Process
- Cell Wall Metabolism
- Cellular Amino Acids and Derivative Metabolic Process
- Cellular Homeostasis
- Cellular Process
- Developmental Process
- DNA/RNA Metabolic Process
- Generation of Energy
- Lipid Metabolic Process
- No Hit
- Pentatricopeptide (PPR) repeat-containing protein
- Response to Hormone Stimulus
- Response to Stress
- Secondary Metabolic Process
- Signal Transduction
- Transcription Factor Activity
- Transport
- Unknown Protein



1478 genes showed a significant difference in transcription among the 11 vineyards, during berry development

SPECIE PERENNANTI?



SCIENTIFIC AMERICAN

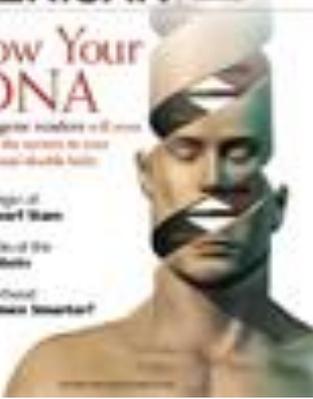
Know Your DNA

Discover gene insights and more
about the science of your
personal health facts.

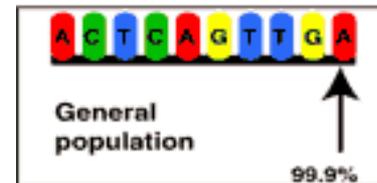
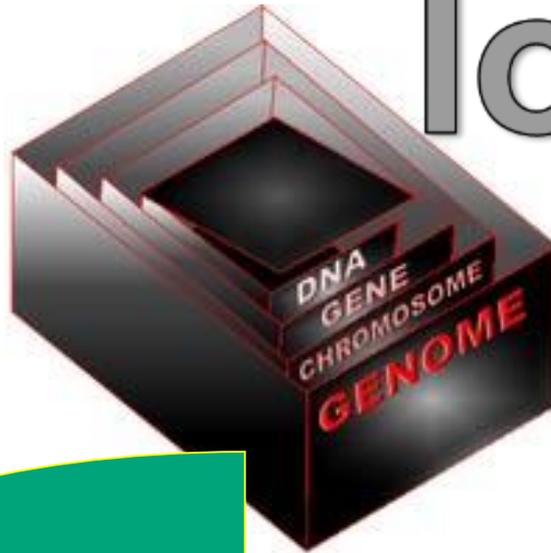
The New Origin of
Brown-Eyed Men

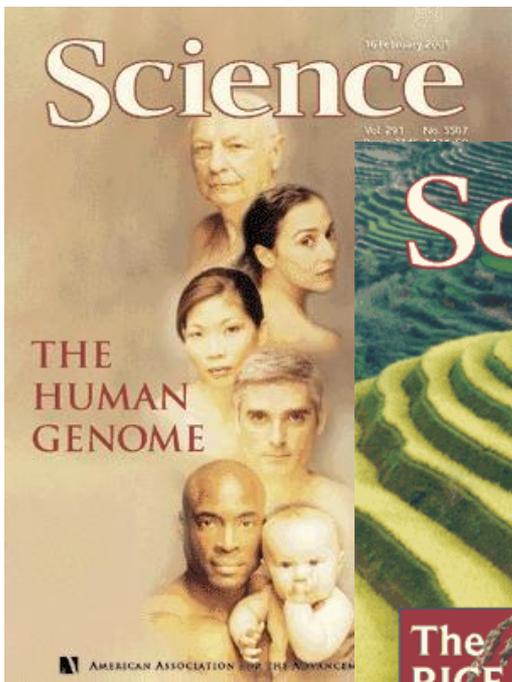
Worry: Ticks of the
Living Robots

Does Motherhood
Make Women Smarter?



Genomi low cost





2001



2002



2007



2009



2009

Nature

ISSN 0950-0804



THE TOMATO GENOME

Sequencing the cultured vegetable to reveal wild relatives from South America

Genetics
THE GREAT
ESCAPE

How a wild potato
genotype escaped
domestication

Genetics
WASTE OF
SPRING

How a mutation
in a gene for
flowering time

Genetics
REPAIRING
THE HEART

How a mutation
in a gene for
heart development

Evolution
THE GREAT
ESCAPE



The elusive dream of
regenerating the heart p. 252

Summer selections for your
reading pleasure p. 266

Mesoscale eddies help drive
ocean circulation p. 322

Science

\$30
18 JULY 2014
sciencemag.org

AAAS

Slicing the wheat genome

Sequencing illuminates bread wheat evolution
and breeding potential p. 285

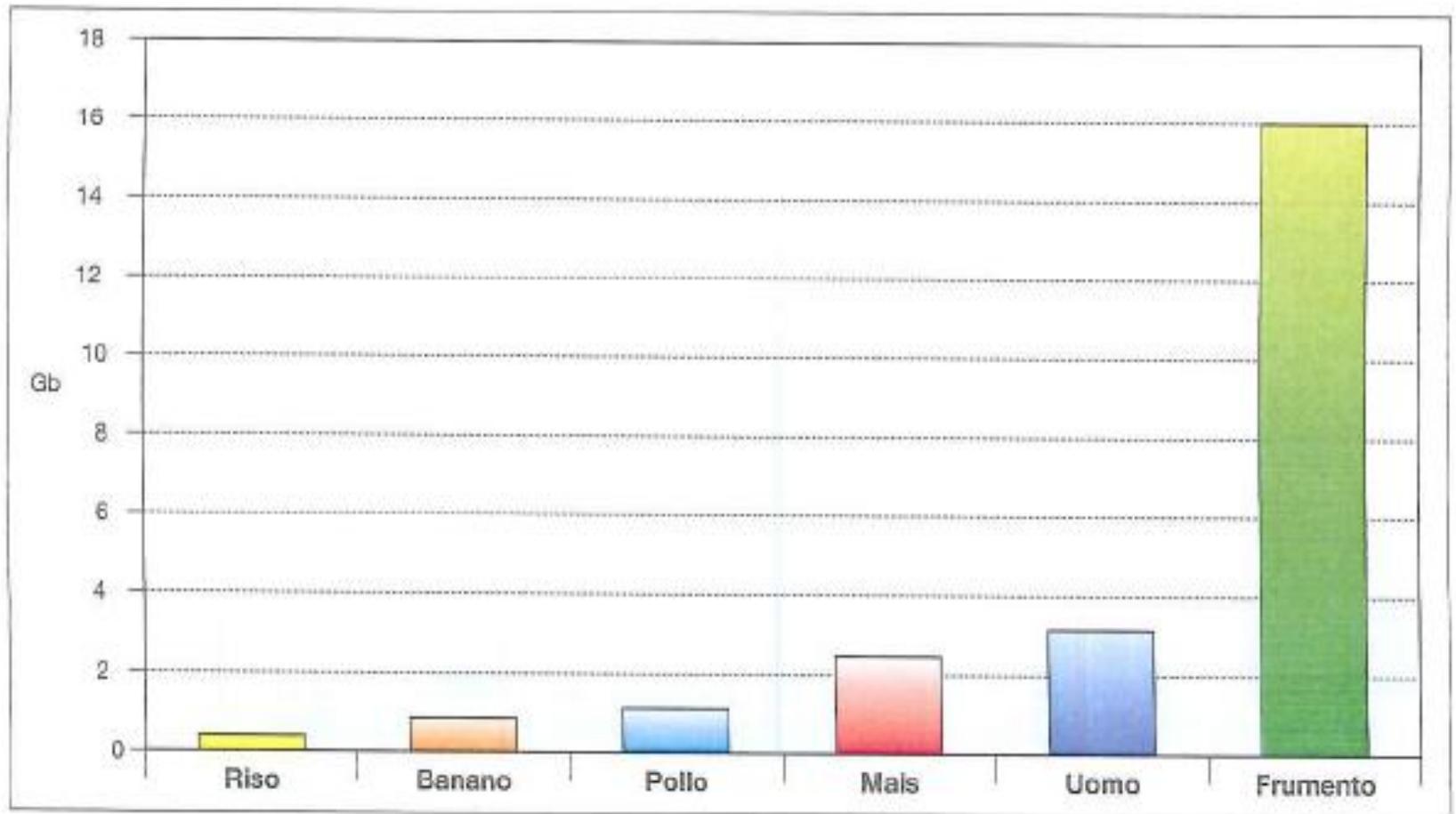
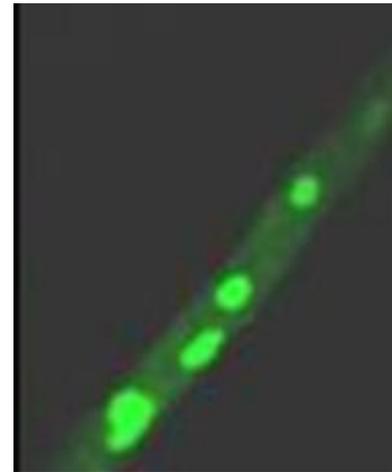
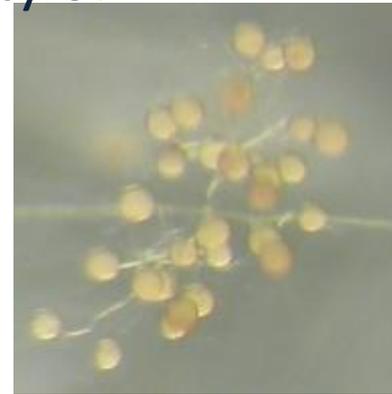
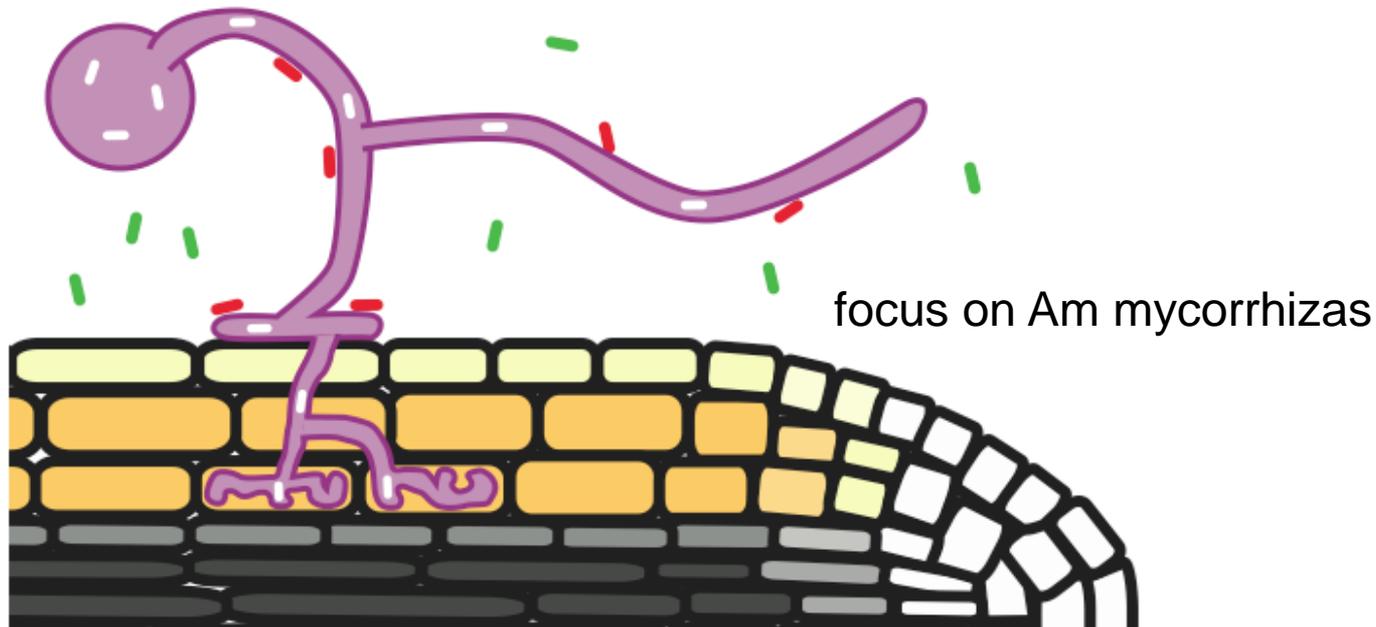


Figura 9.8 Comparazione della dimensione di diversi genomi. Gb: gigabasi, miliardi di paia di basi nucleotidiche.

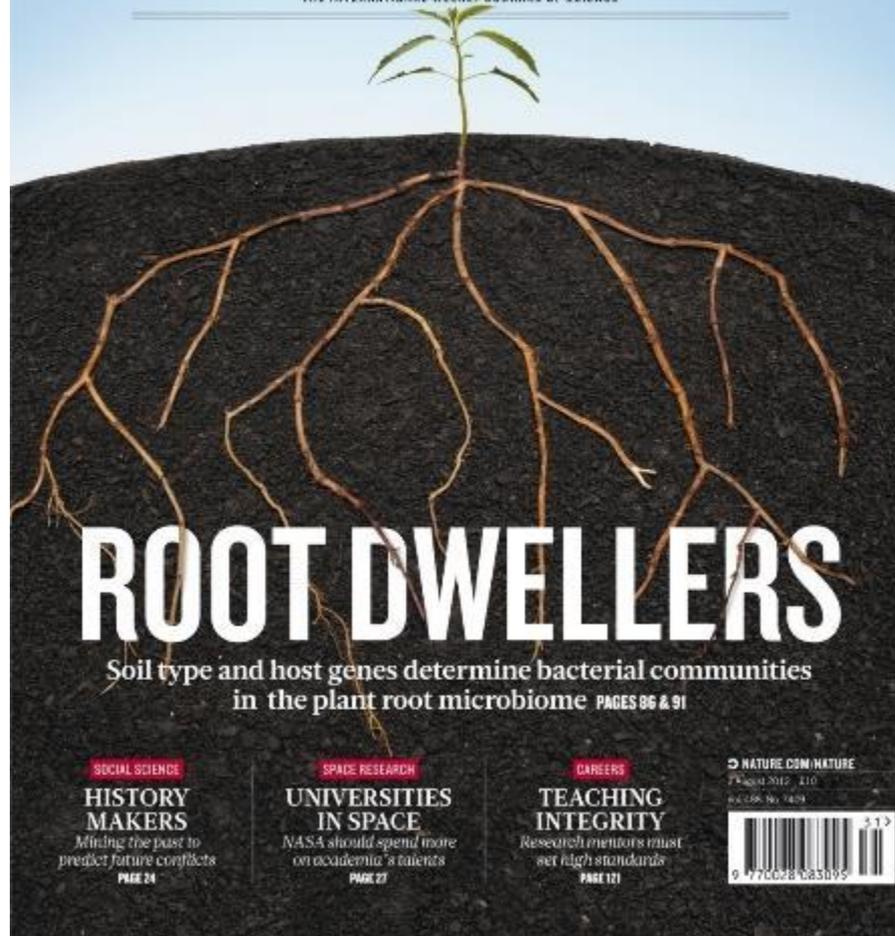
Plant-microbe interaction

Beneath the surface of the earth, an influential community of microbes mingles with plant roots



nature

THE INTERNATIONAL WEEKLY JOURNAL OF SCIENCE



ROOT DWELLERS

Soil type and host genes determine bacterial communities
in the plant root microbiome **PAGES 86 & 91**

SOCIAL SCIENCE

HISTORY MAKERS

*Mining the past to
predict future conflicts*

PAGE 24

SPACE RESEARCH

UNIVERSITIES IN SPACE

*NASA should spend more
on academia's talents*

PAGE 27

CAREERS

TEACHING INTEGRITY

*Research mentors must
set high standards*

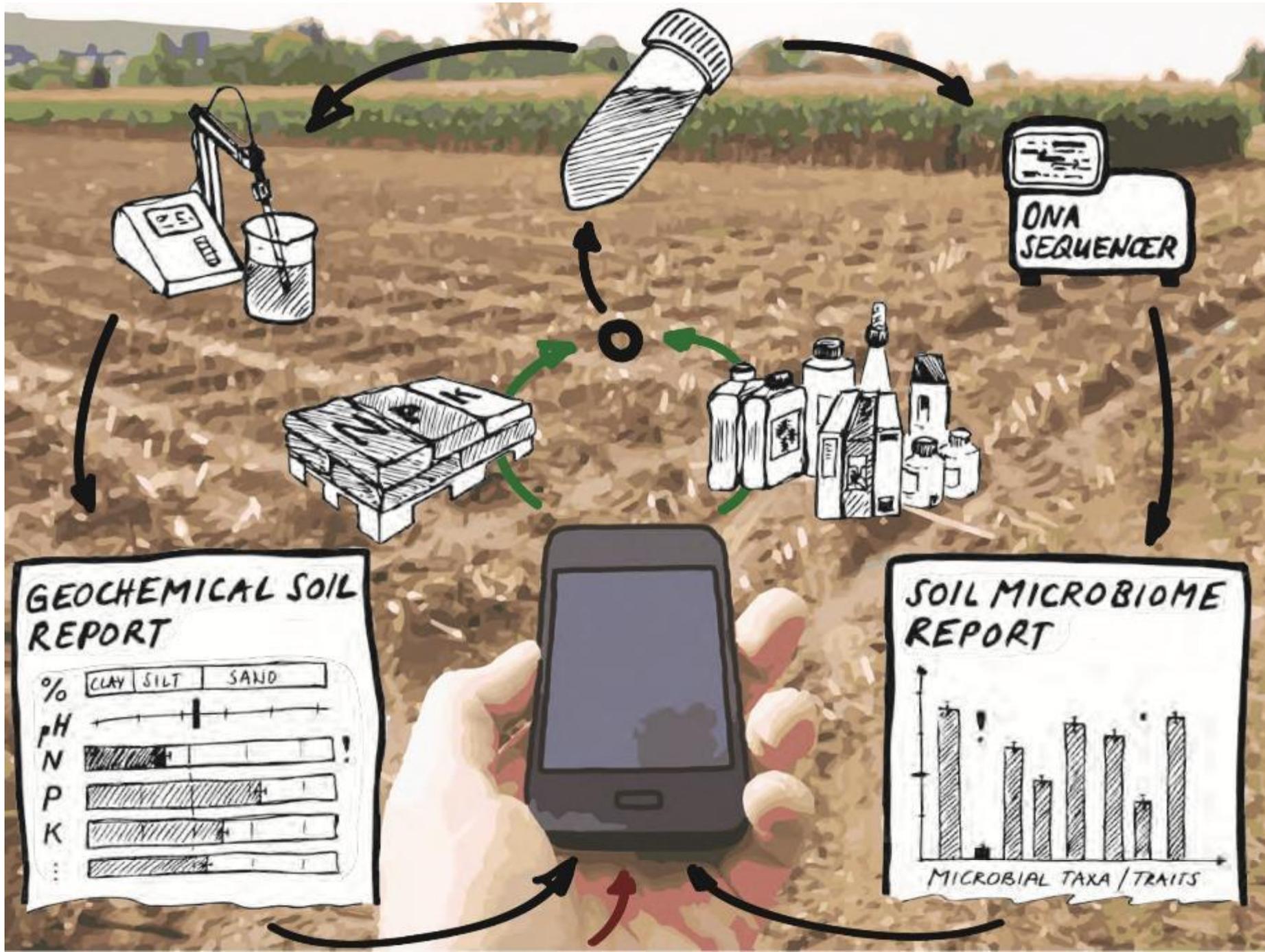
PAGE 121

NATURE.COM/NATURE

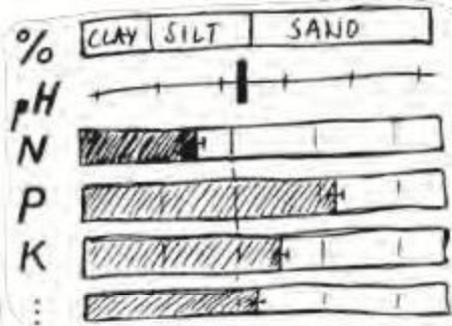
7 August 2012 £10

ISSN 0950-8688 No. 1459

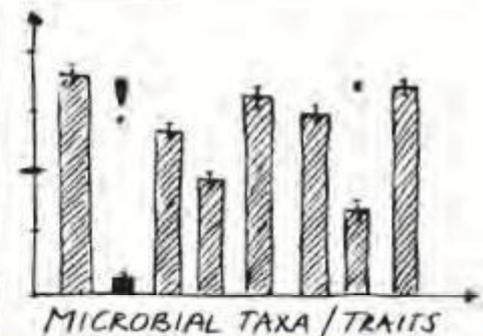




GEOCHEMICAL SOIL REPORT



SOIL MICROBIOME REPORT

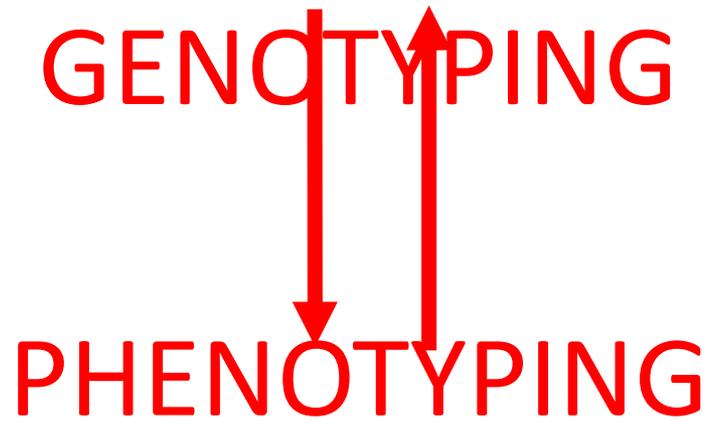


The Plant Microbiome at Work

Klaus Schlaeppi and Davide Bulgarelli

MPMI 2015

Fig. 1. Towards next-generation agriculture. Field soil samples are analyzed geochemically (left part) and are examined for the soil microbiome employing sequencing technology (right part). The availability of plant nutrients and the occurrence of one or both soil biota and their microbial traits (e.g., N fixation, phosphorus solubilization, pathogen protection) are reported to the farmer. The smart integration of available geochemical, microbiome, and other relevant information (red arrow) presents the basis for the rational intervention (green arrows) combining field applications of conventional inputs such as mineral fertilizers (left) and agricultural biologicals, including microbial inoculants (right).



FACE-Free-Air CO₂ Enrichment- is considered the most advanced technology to investigate experimentally the impact of rising atmospheric CO₂ on terrestrial ecosystems



The container of CO₂ and the system of heating and vaporization



the control unit of a ring of the FACE facility



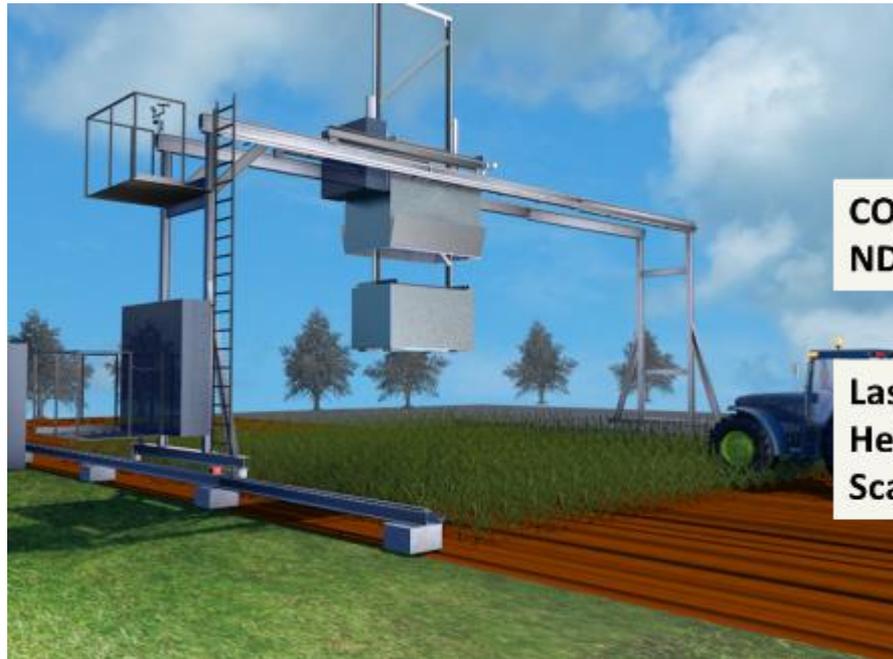
Effect of elevated CO₂ on yield and quality traits?
WHAT ABOUT SOIL Microbioma?

A rings of the FACE facility installed in Fiorenzuola d'Arda with its control unit

Intensive field HTP phenotyping



ROTHAMSTED
RESEARCH

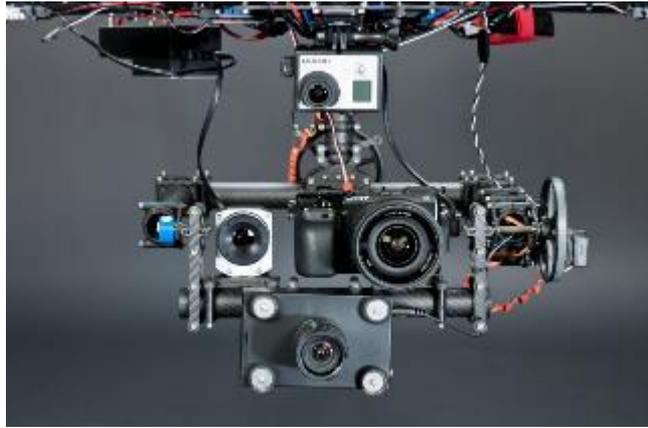


CO₂ and
NDVI

Laser
Height
Scanner

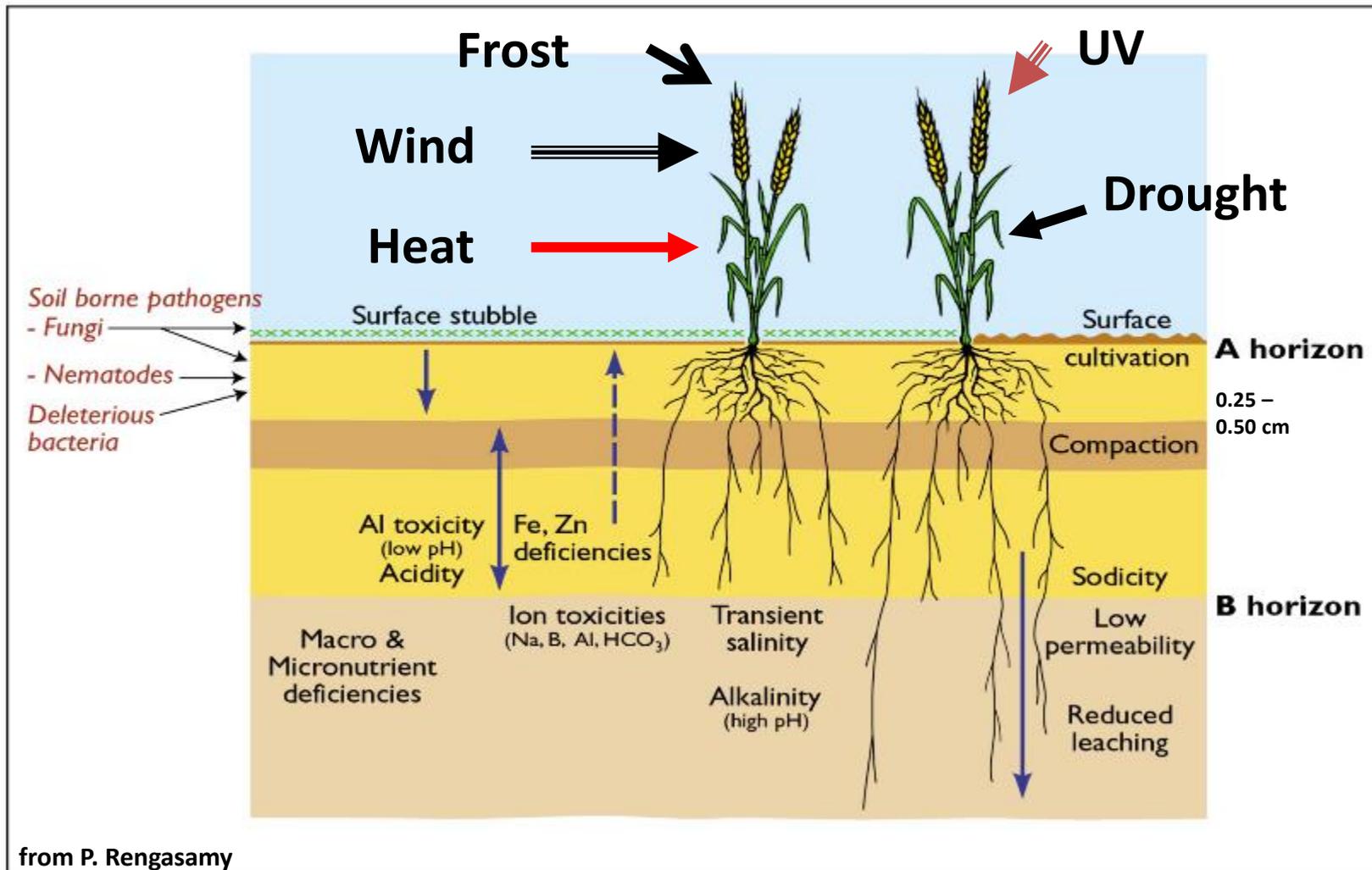


Phenotyping from the air

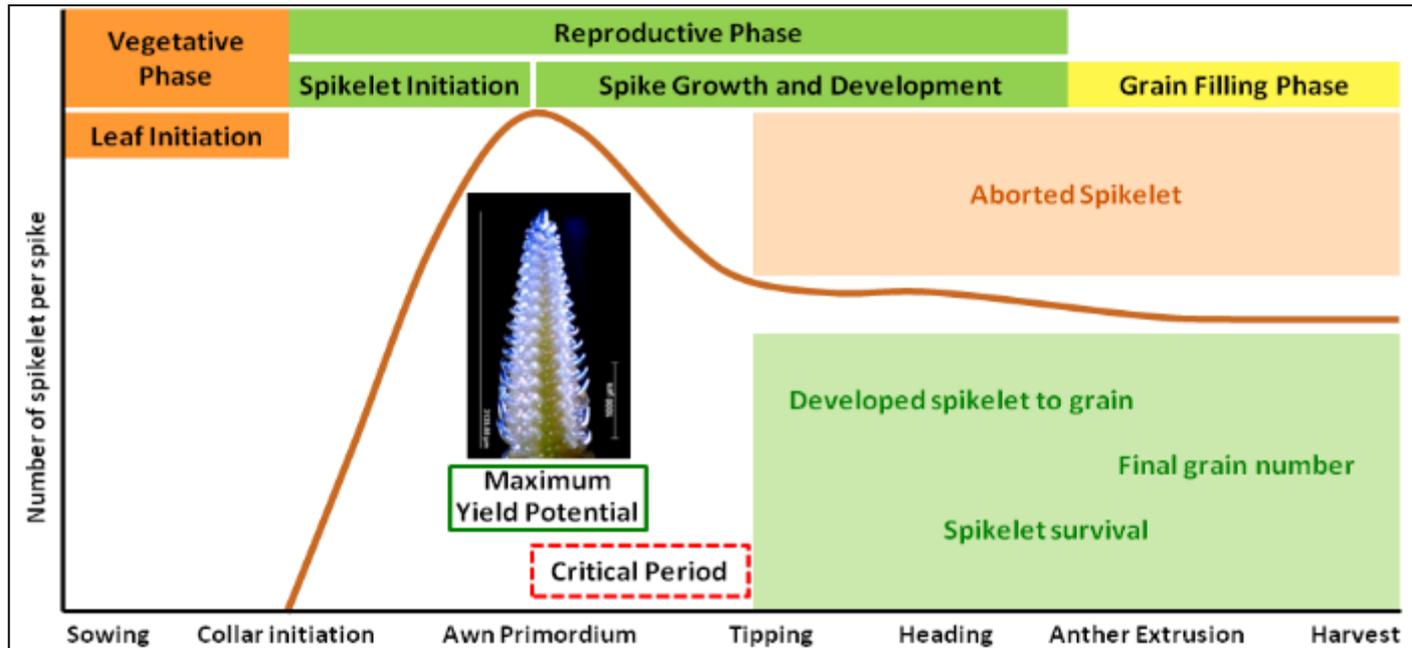


FEEDING TEN BILLION

Factors limiting productivity in low yielding environments



The importance of Pre-Anthesis Phases



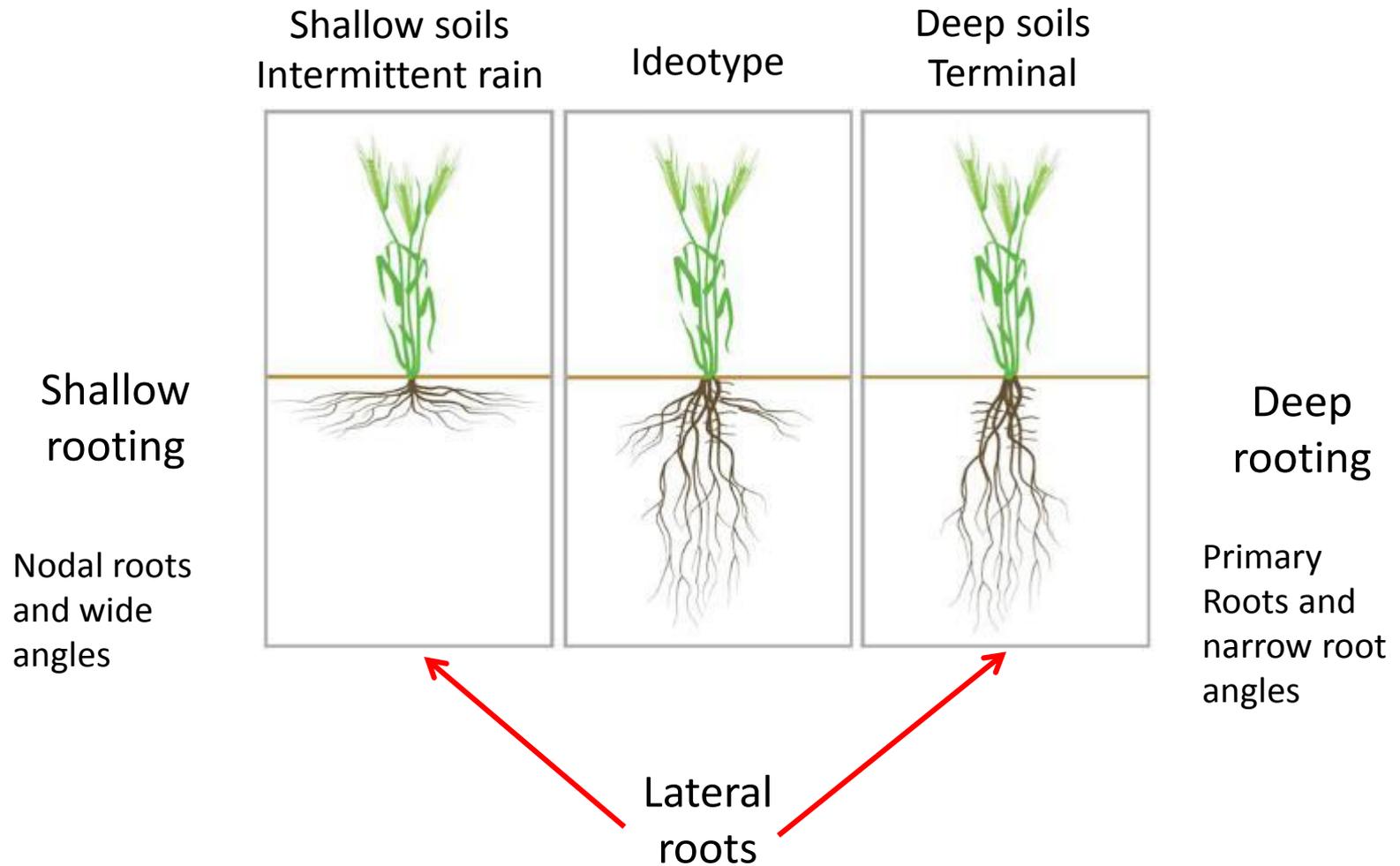
Duration between Awn Primordium to Tipping is highly associated with Grain Number and Spikelet Survival

≥70% of spikelet abortion is happening during this phase

32 accession under field and greenhouse conditions.

Alqudah and Schnurbusch (2014) Funct. Plant Biol. 41: 424-436.

Morphology: root system architecture





Major challenges:

Increase yield potential whilst maintaining quality

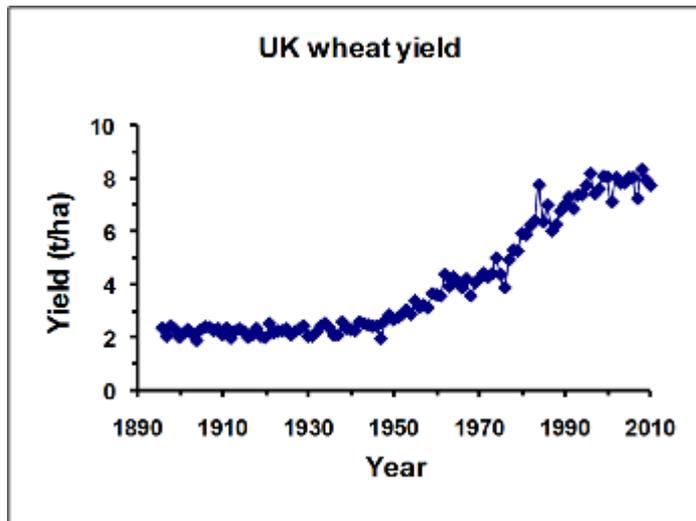
Minimise gap between yield potential & actual farmers yield

Maximise efficiency of input use for sustainability

All involve NUE



20:20 Wheat[®]



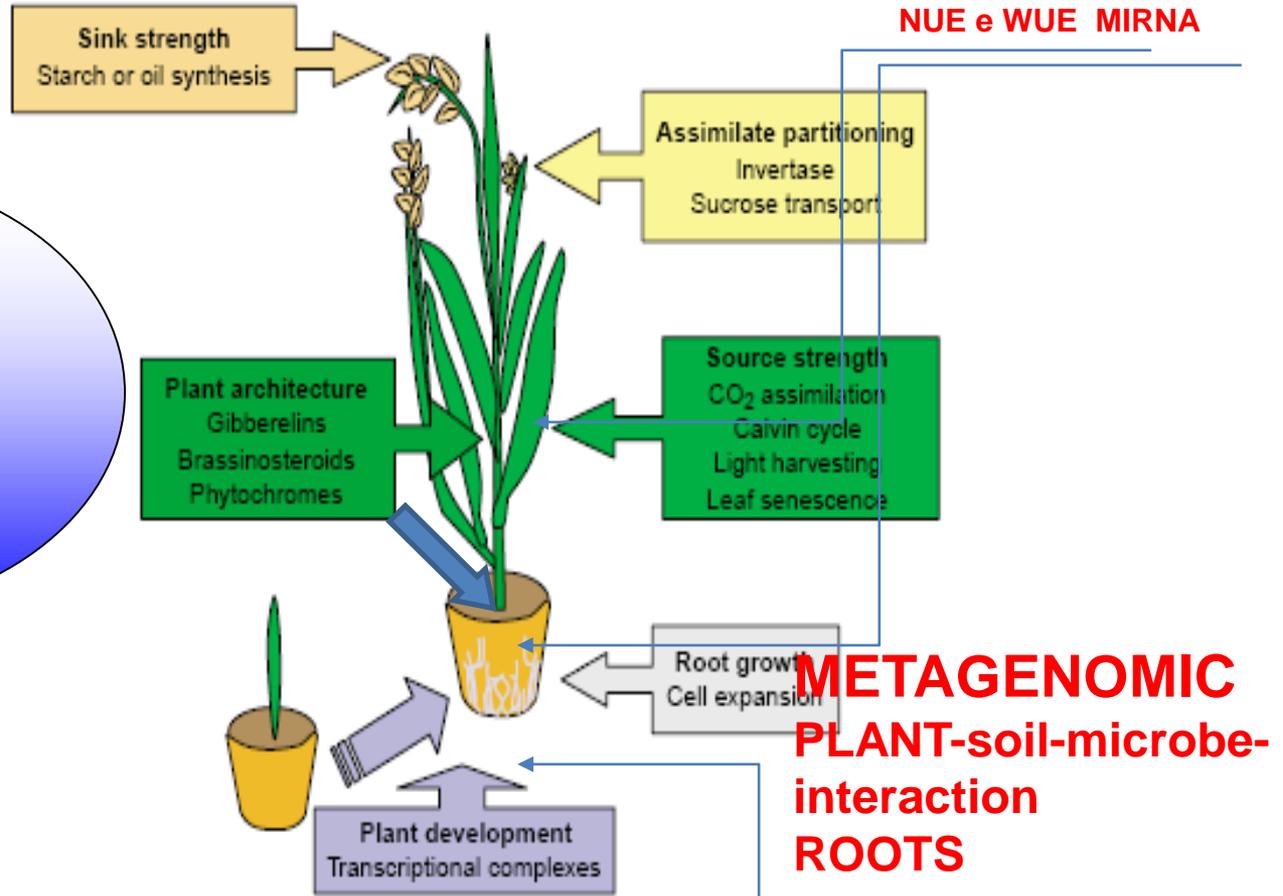
20:20 Wheat[®] aims to provide the knowledge base and tools to increase wheat yield potential (in the UK) to **20 t.ha⁻¹** within the next **20 years**

PLANT for the Future



**Potenzialità
e Stabilità**

**25-30000 semi/m²
120-130q/ha**



Cappelli 2012

CO2
normale



Alta CO2





FEEDING TEN BILLION

Neolitico

500

semi/m²

1-1.5 q/ha

Periodo
Romano

2.000

semi/m²

4-5 q/ha

Rinasciment
Pre-Mendel

3.000

semi/m²

6-8 q/ha

Post-
Mendel

8.000

semi/m²

25 q/ha

1970

14.000

semi/m²

50 q/ha

Oggi

20.000

semi/m²

90-100 q/ha

Phenotypic Plasticity in *Vitis vinifera*

Vitis vinifera spp is one of the most plastic plants known: a single genotype is able to produce berries with different quality, thus different wine qualities, depending on the micro-environment where it is cultivated.



Berry plasticity is very high

Individual berries

Among berries within a cluster

Between clusters on a vine

Among vines in the vineyard