



INNOVPLANT PROTECT

Da genómica à proteómica – ferramentas biotecnológicas para o melhoramento

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CURSO DE VERÃO
BIOTECNOLOGIA DE PLANTAS
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CiB centro de informação de biotecnologia 1 2 9 0 **CENTRE FOR FUNCTIONAL ECOLOGY** SCIENCE FOR PEOPLE & THE PLANET

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Laboratório de Biotecnologia Vegetal

CENTRE FOR FUNCTIONAL ECOLOGY SCIENCE FOR PEOPLE & THE PLANET

drv.uc DEPARTMENT OF LIFE SCIENCES

1 2 9 0 **UNIVERSIDADE D COIMBRA**

FACULTY OF SCIENCES AND TECHNOLOGY
UNIVERSITY OF COIMBRA

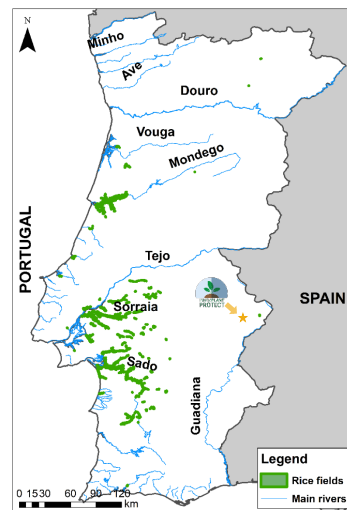
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Associação privada sem fins lucrativos

Sede: Elvas - INIAV, Antiga Estação de Melhoramento de Plantas
Início de atividade em Janeiro de 2020



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Objetivos: Desenvolver soluções de prevenção e de combate para a proteção de plantas (Produtos de base biológica, Soluções Digitais)



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<https://scitechdaily.com/>



Foco na interação planta/organismo com o objetivo principal de aumentar a resistência de plantas a pragas e doenças:



- Encontrando na diversidade existente plantas que apresentem capacidade de resistência.



- Obtendo novas variedades de plantas resistentes ao ataque de doenças, utilizando a tecnologia de edição do genoma.



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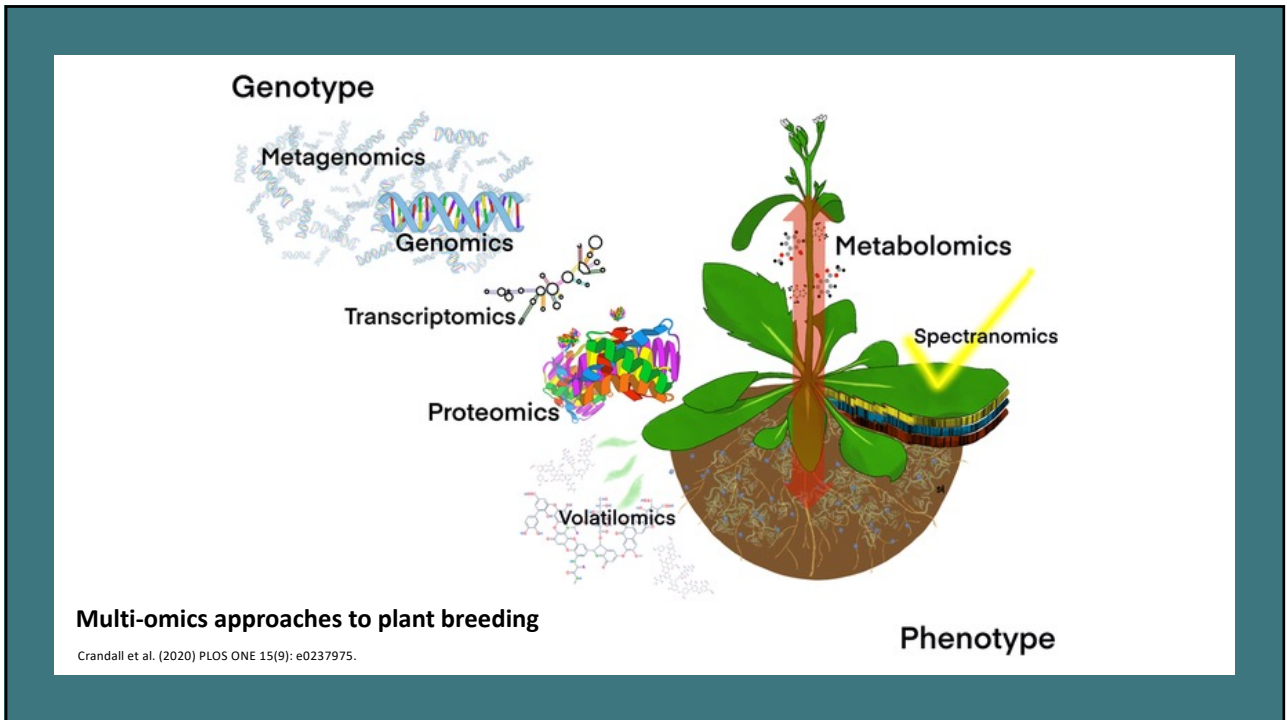
- Identificar genes de resistência de plantas por mapeamento genético e abordagens genómicas.
- Identificar pragas e agentes patogénicos no campo (epidemiologia e diagnóstico).
- Triagem de marcadores moleculares para seleção assistida de cultivares resistentes.
- Desenvolver estratégias de edição de genomas para mutar genes de suscetibilidade de interesse.
- Testar a eficiência de métodos biológicos para proteção de plantas (BCAs, biopesticidas, bioestimulantes).
- Estabelecimento *in vitro* e micropropagação de plantas; ensaios de *screening in vitro*.



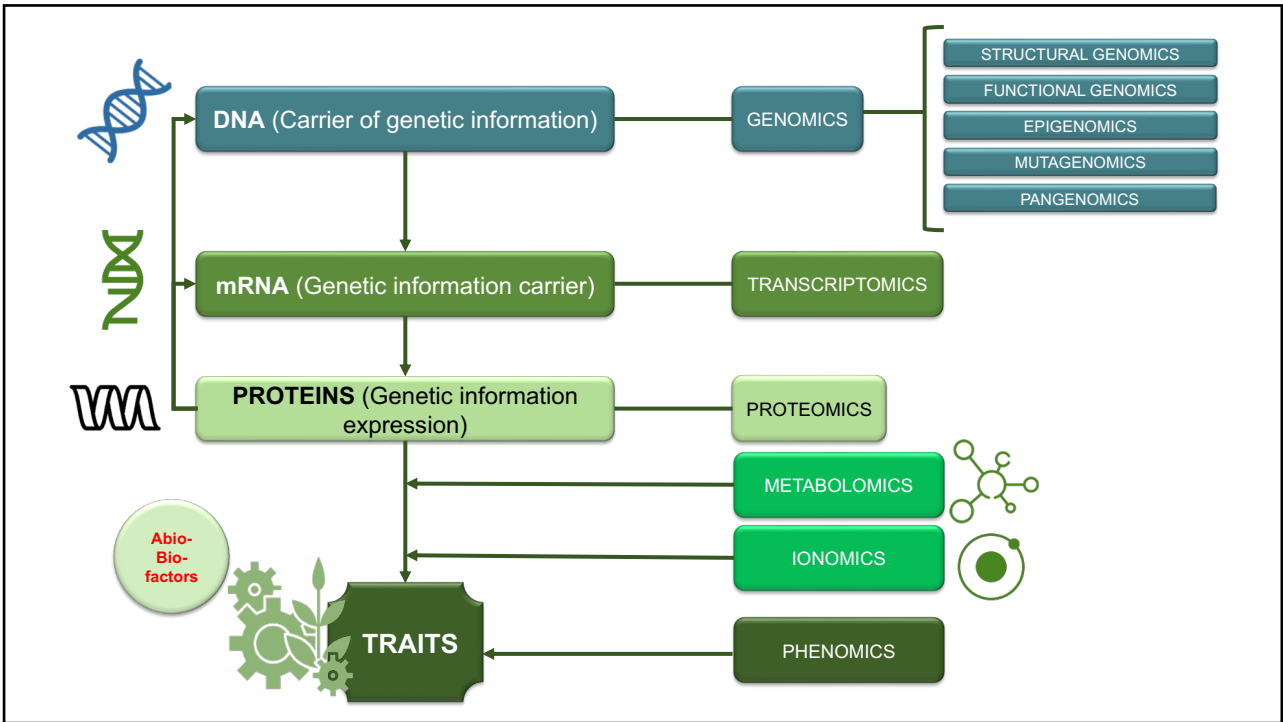
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Da genómica à proteómica – ferramentas biotecnológicas para o melhoramento

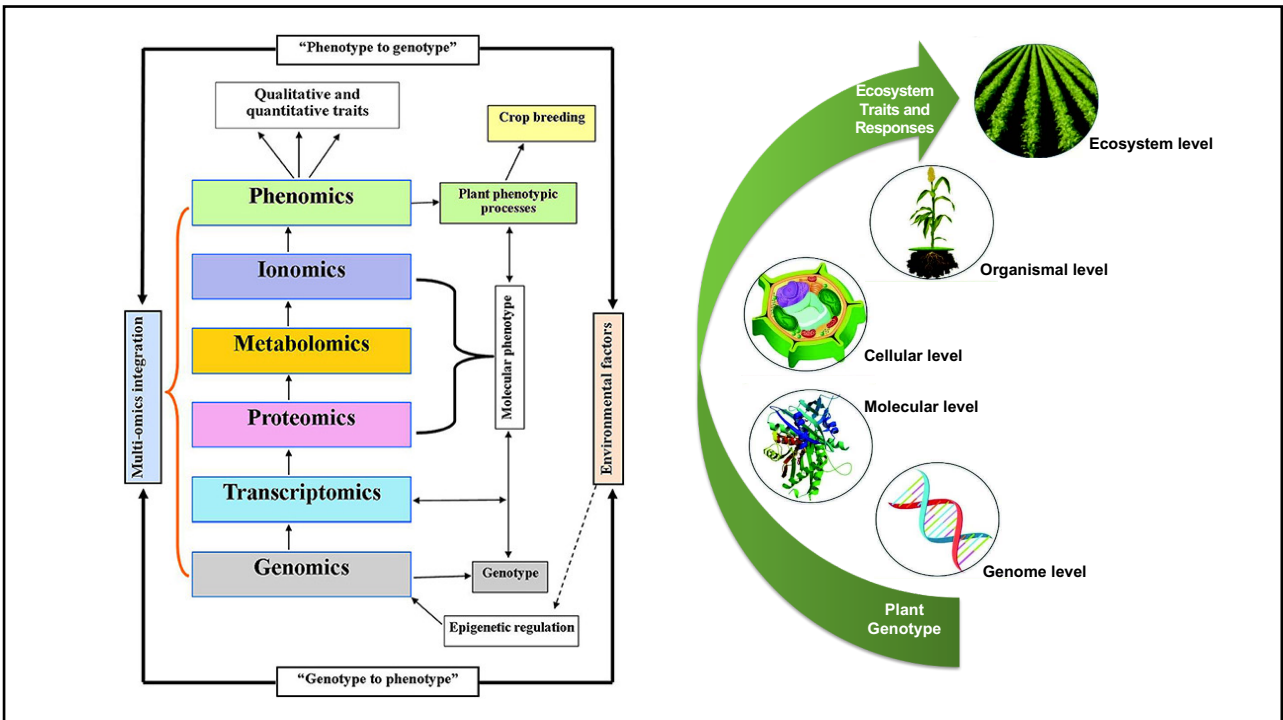
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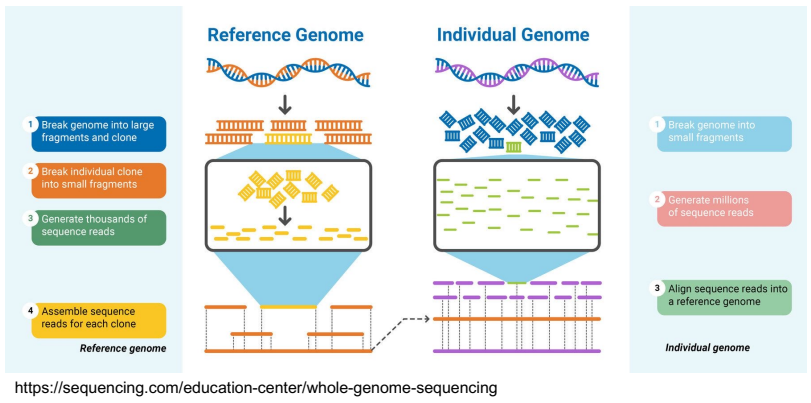
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GENOMICS

- ✓ The comprehensive study of **whole sets of genes** and their **interactions** .
- ✓ It investigates the variation in genes and how it affects protein structure and function throughout the life of a cell.



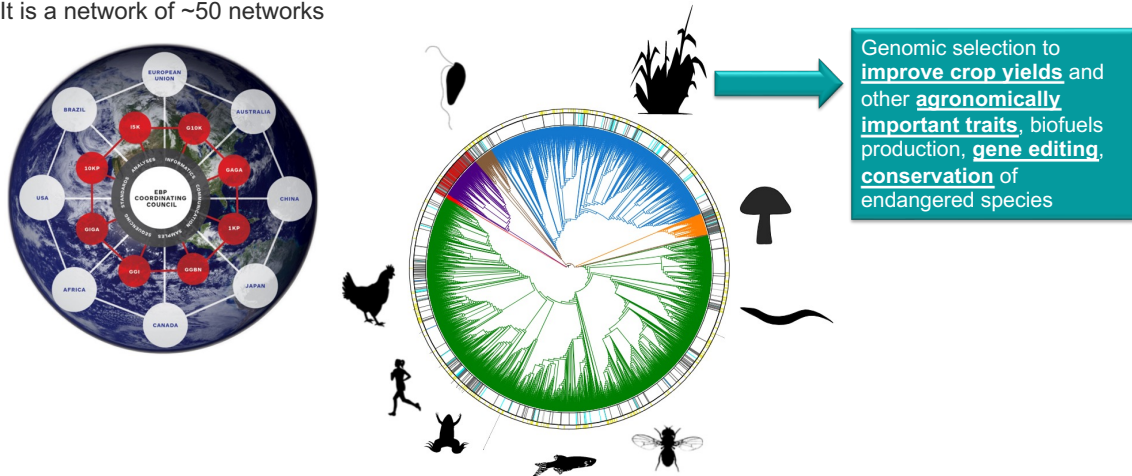
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GENOMICS

Earth BioGenome Project: Sequencing life for the future of life

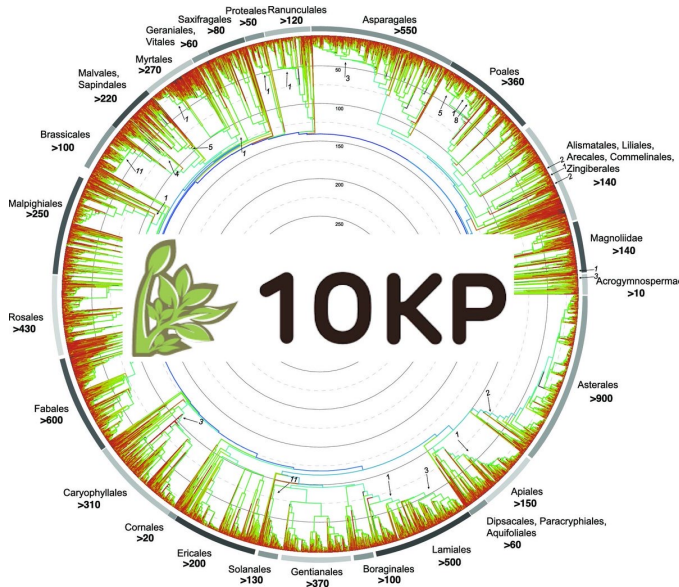
<https://www.pnas.org/doi/epdf/10.1073/pnas.1720115115>

- ✓ Target of developing reference genomes of 1.8 million named species by the year 2030
- ✓ It is a network of ~50 networks



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GENOMICS



The 10,000 plants (tenKP or 10KP) aims to:

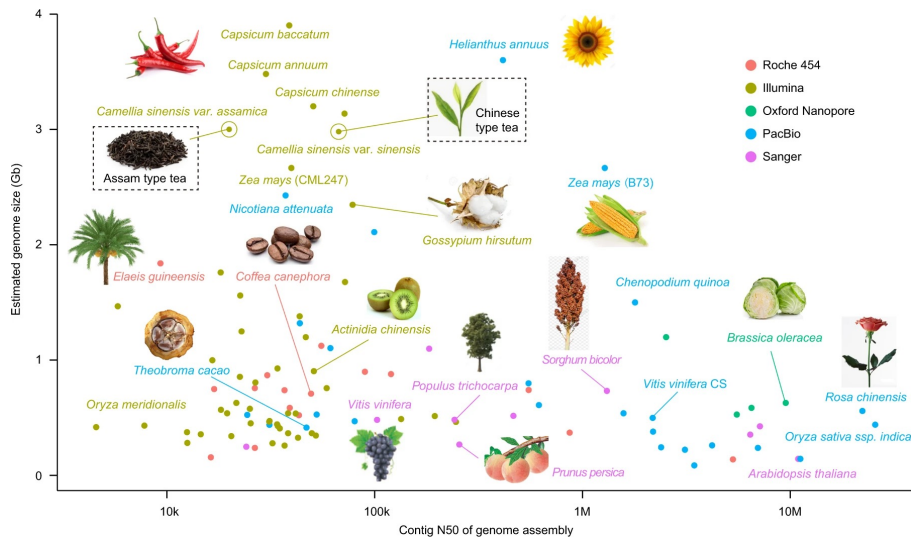
- ✓ Sequence over 10,000 genomes representing every major clade of plants and eukaryotic microbes;
- ✓ Develop new tools for de novo genome sequencing and assembly platforms.

Major supporters:

- ✓ Beijing Genomics Institute in Shenzhen (BGI-Shenzhen)
- ✓ China National Gene Bank (CNGB)

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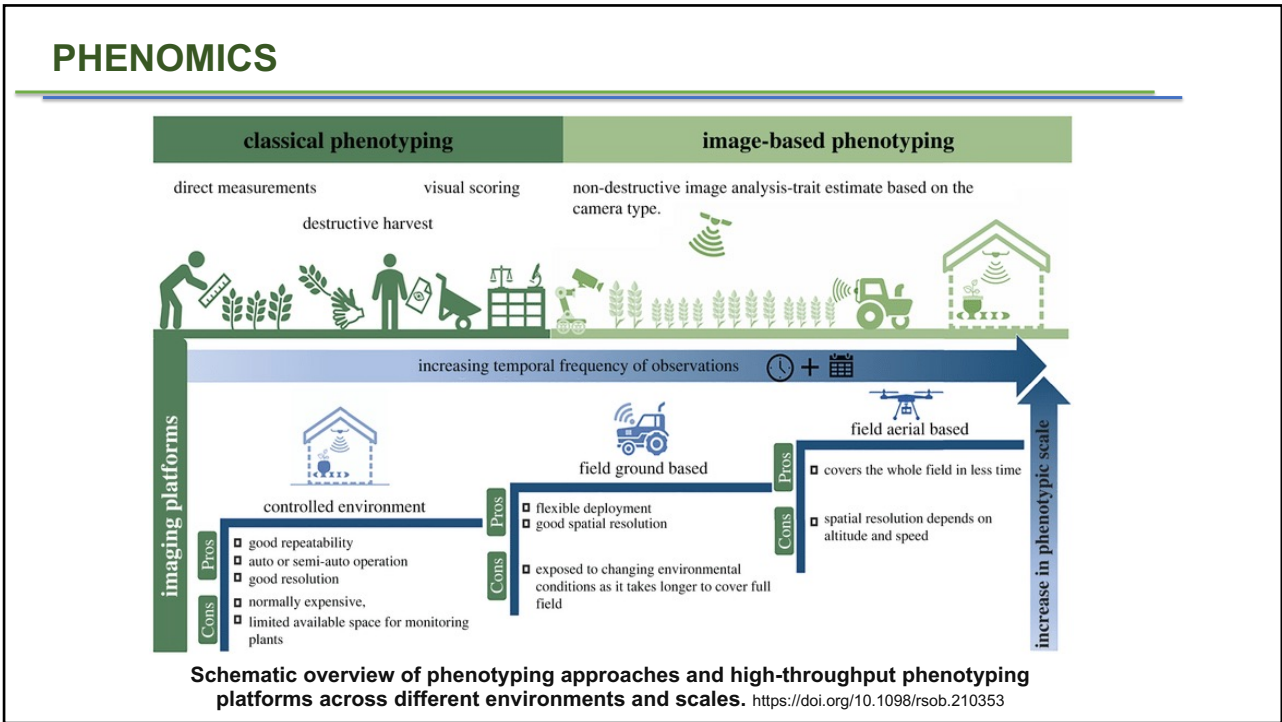
GENOMICS



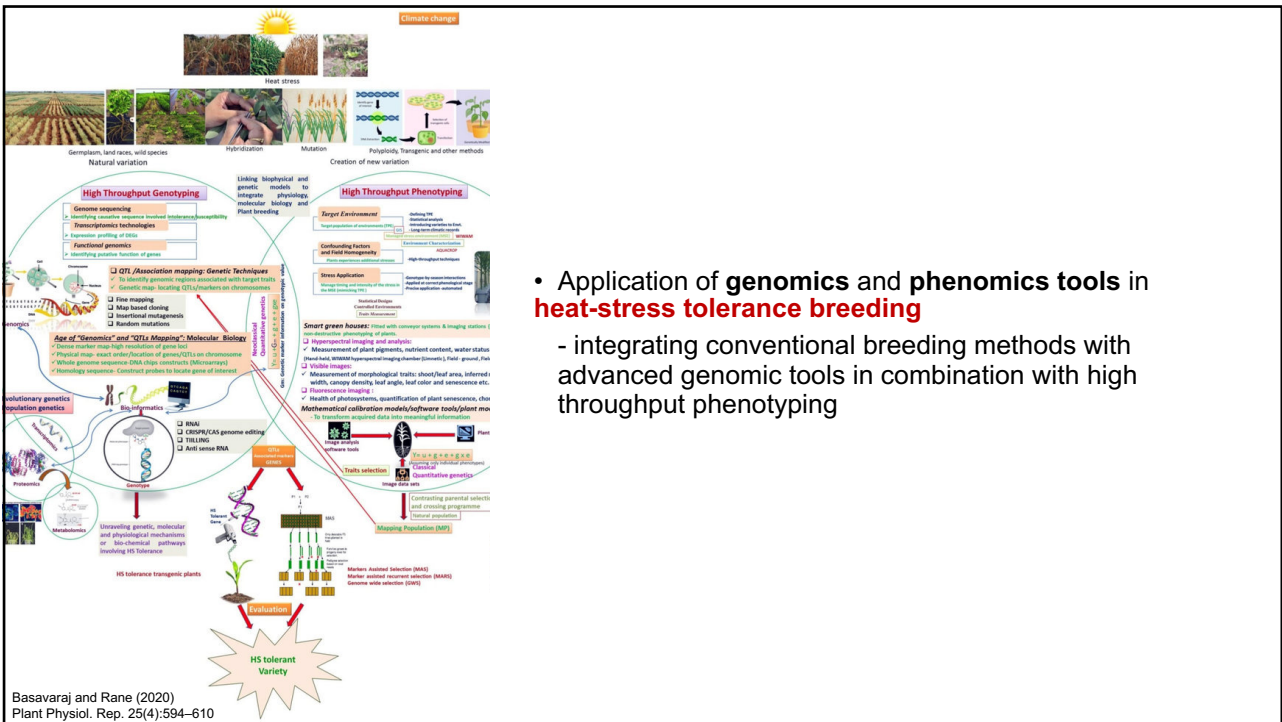
Current genome sequencing progress in several plants

Xia et al. *Hortic Res* 7, 7 (2020). <https://doi.org/10.1038/s41438-019-0225-4>

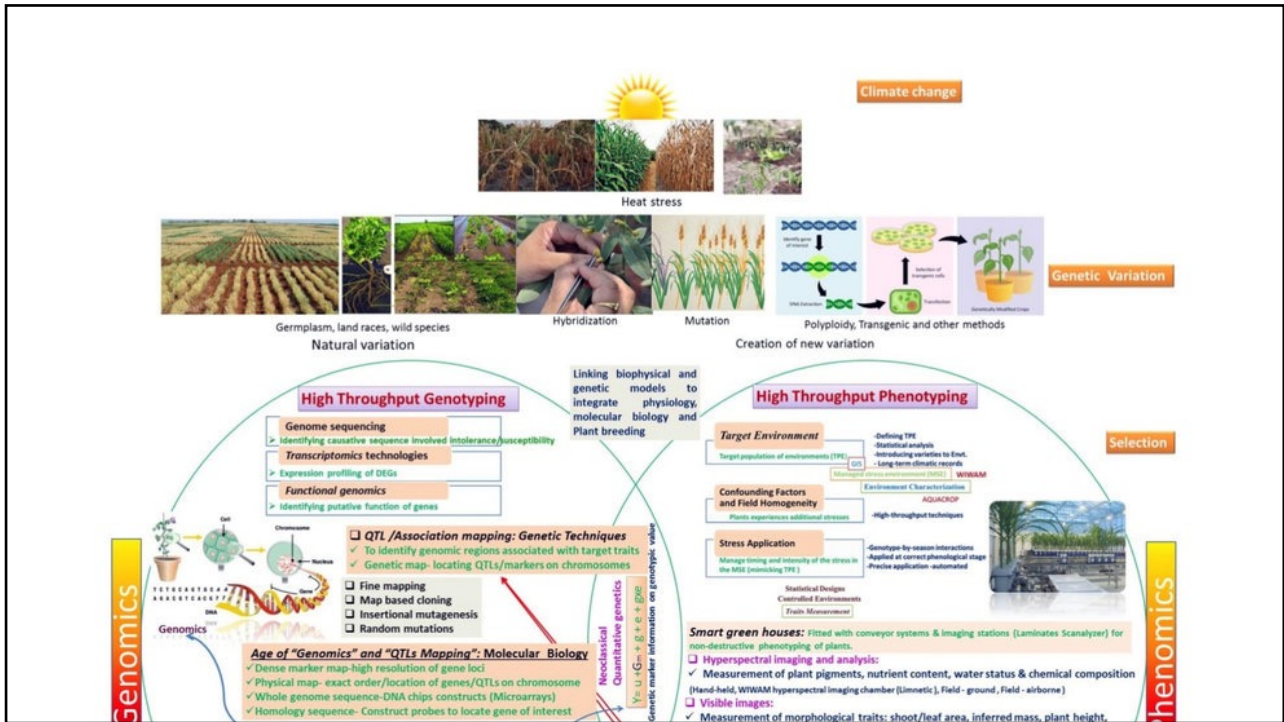
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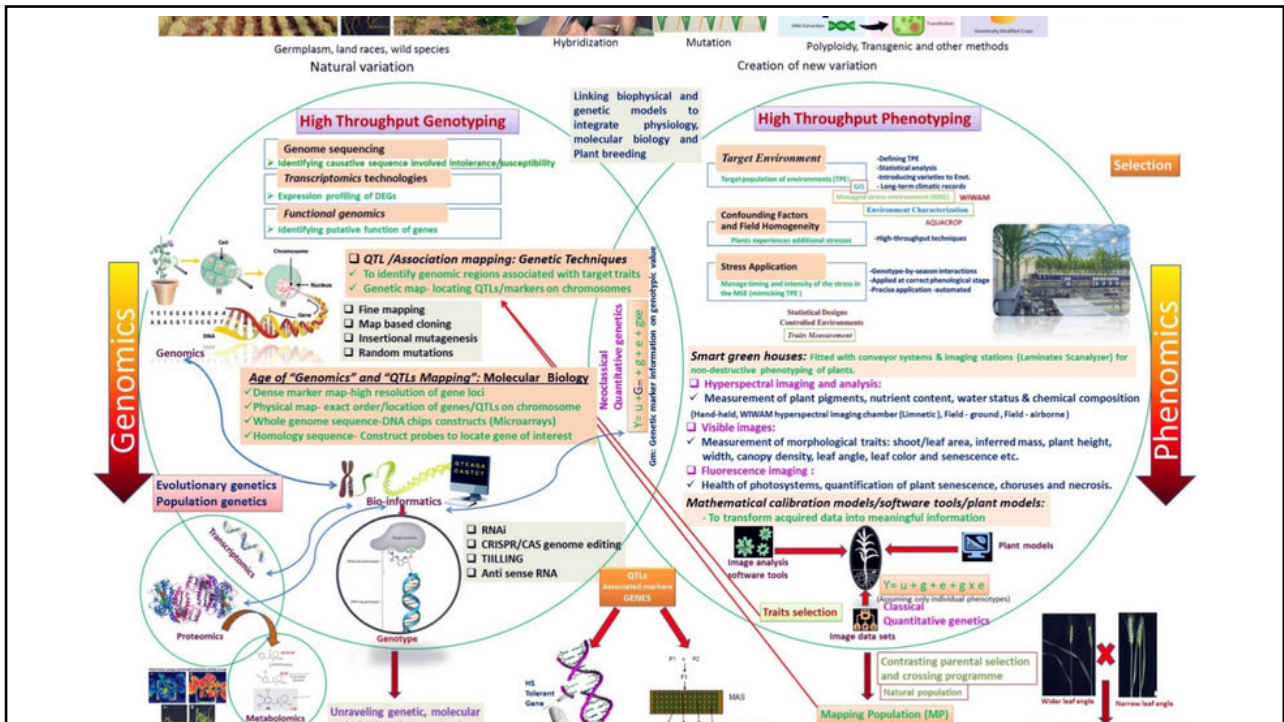
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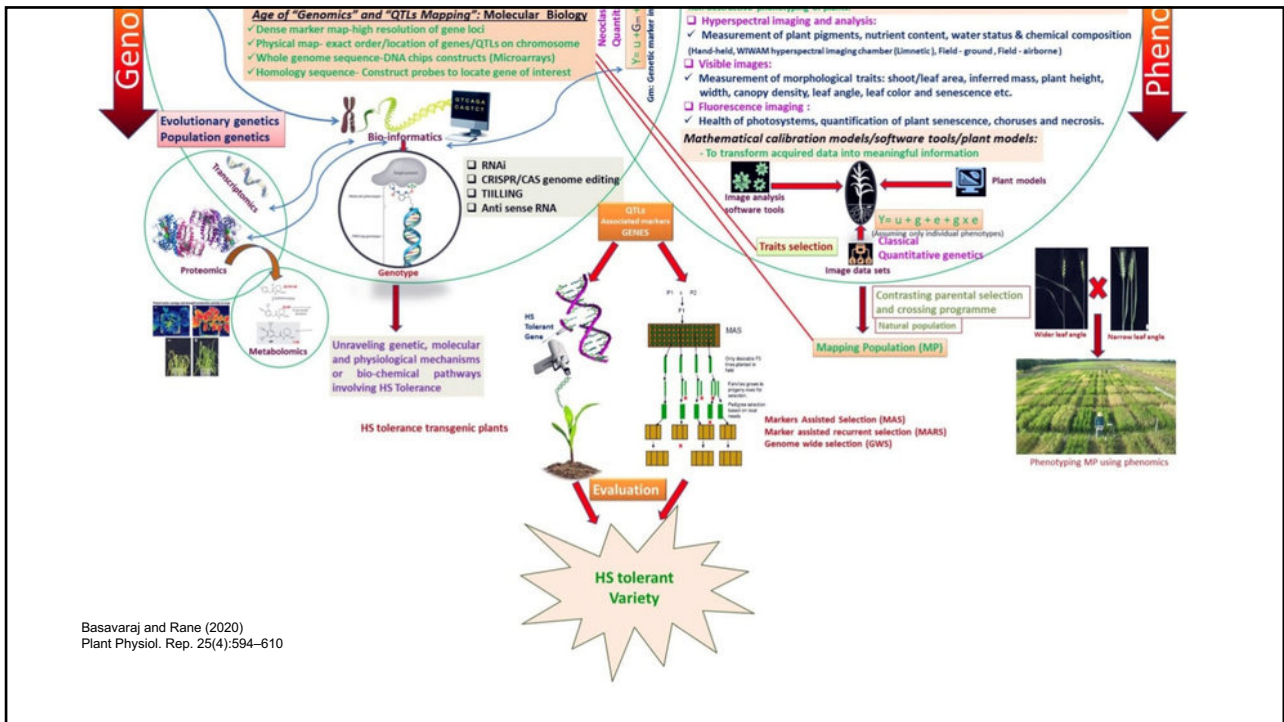
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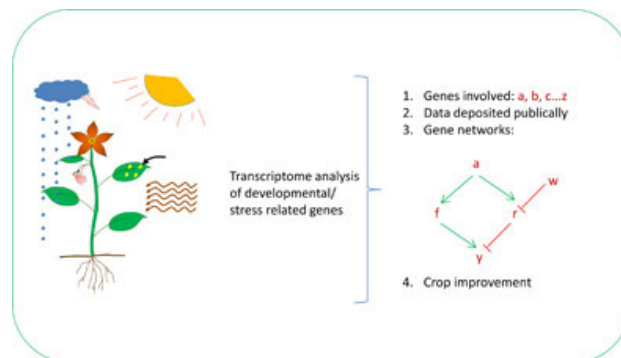
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TRANSCRIPTOMICS

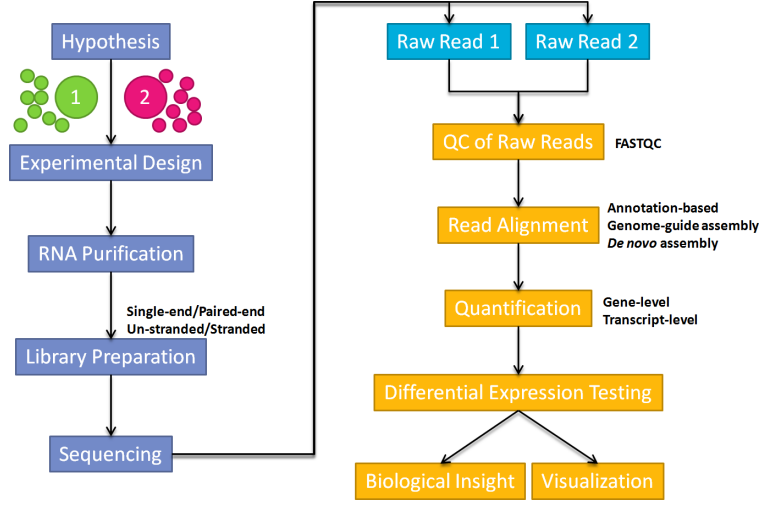
- ✓ All the genomic counterparts which are **expressed as RNA transcripts**, including coding (mRNA) and non-coding (e.g., tRNA, miRNA) RNAs at a given time in a cell or population of cells under a given set of environmental conditions - **TRANSCRIPTOME**
- ✓ Microarray and Next Generation Sequencing – for elucidation



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TRANSCRIPTOMICS

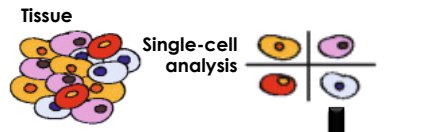
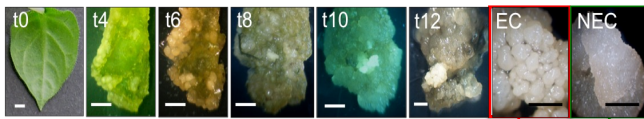
Transcriptome analysis workflow



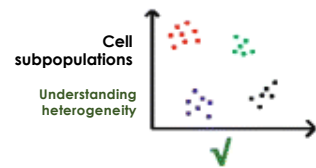
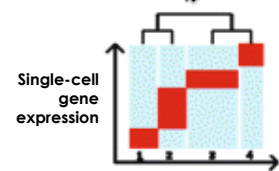
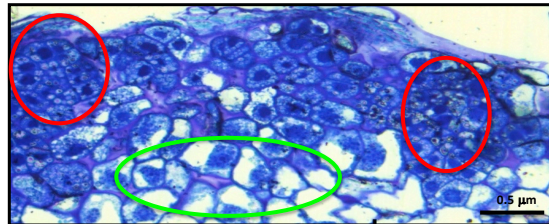
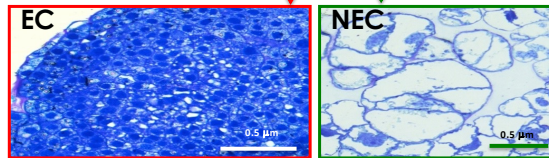
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TRANSCRIPTOMICS

What makes a cell embryogenic competent?



Case study:
Tamarillo (*Solanum betaceum* Cav.) somatic embryogenesis system



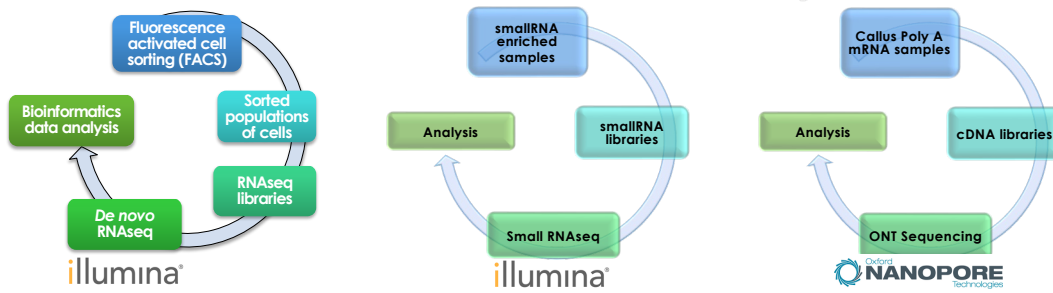
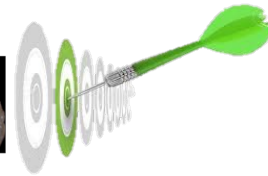
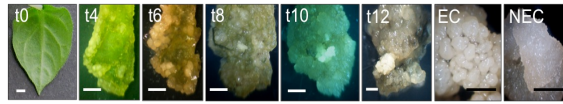
Adapted from Ye et al. (2017) Journal of Hematology & Oncology. 10:27

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TRANSCRIPTOMICS

What makes a cell embryogenic competent?

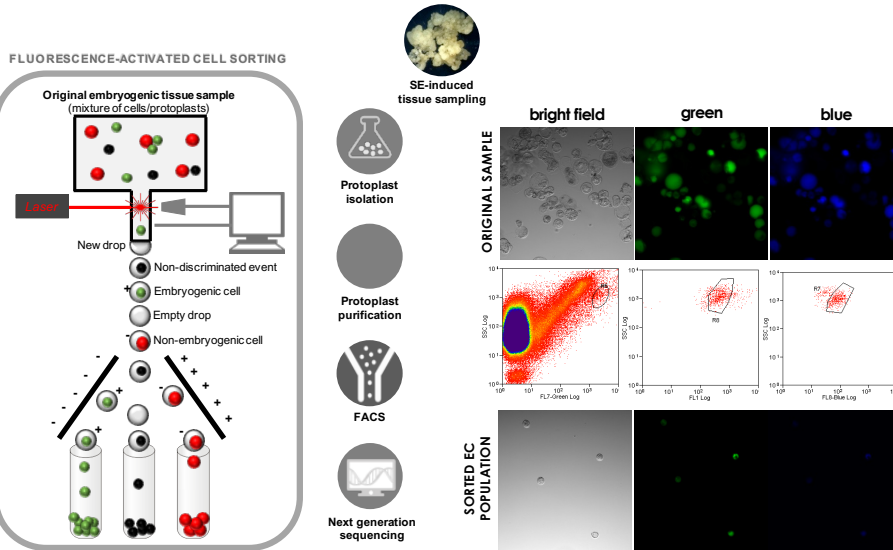
Transcriptional profiling of *in vitro* embryogenic competence acquisition



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RNAseq analysis of FACS cells

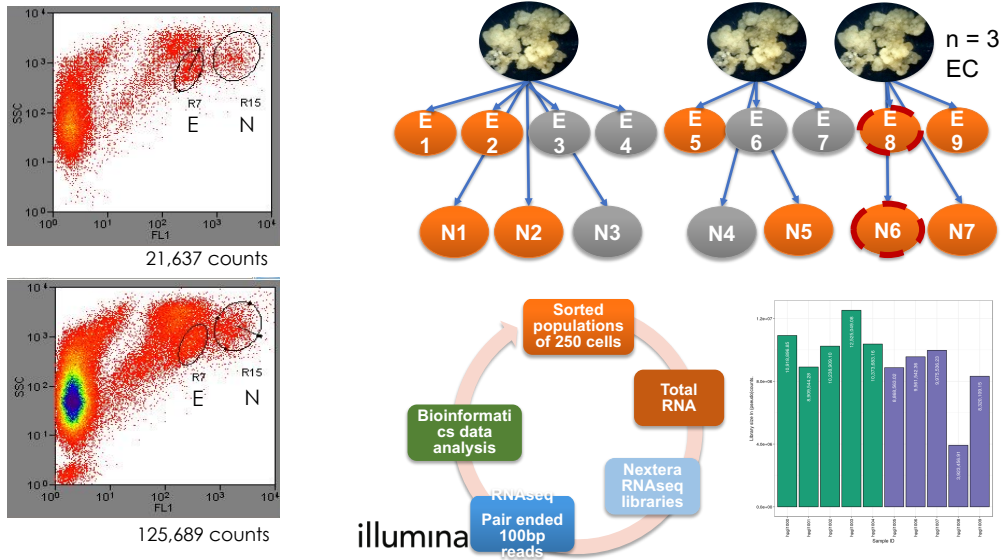
1 – EXPERIMENTAL DESIGN / CELL SORTING



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RNAseq analysis of FACS cells

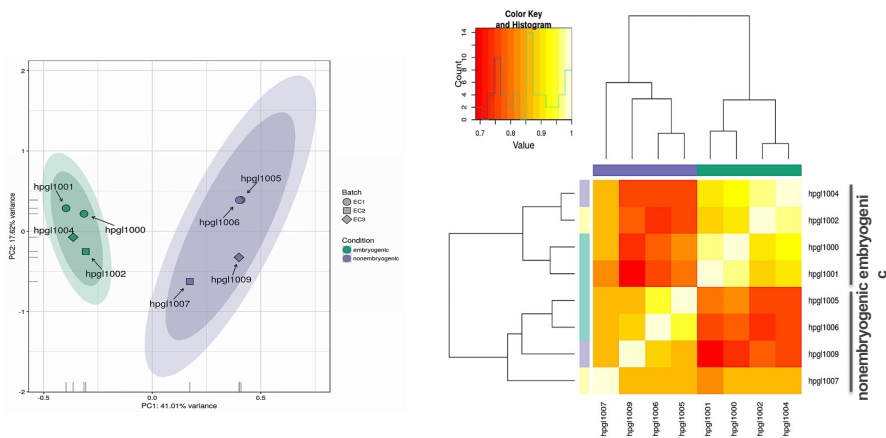
2 – RNAseq LIBRARIES PREPARATION



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RNAseq analysis of FACS cells

3 – De novo transcriptome data analysis

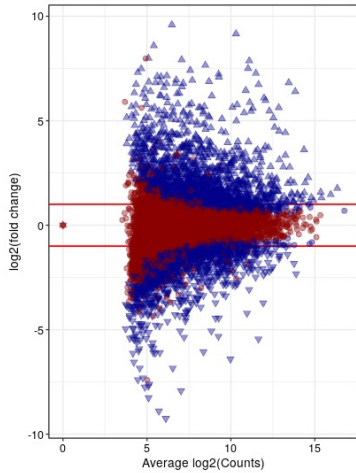


Global statistical assessment of biological replicates. Principal Component Analysis (PCA) plots and Heat-map of RNA-Seq data generated from the libraries sequenced.

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RNAseq analysis of FACS cells

4 – Differential gene expression analysis



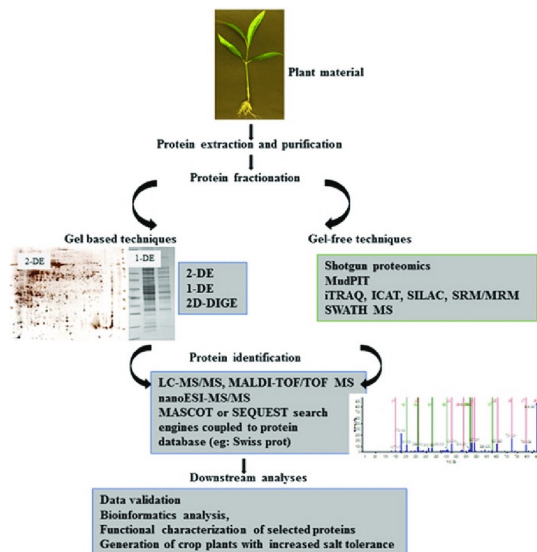
	BlastX Name	logfc
Embryogenic	LOB domain-containing protein 22 TF	5.37
	Ninja-family protein AFP3 TF	5.13
	Protein FEZ TF	4.32
	Transcription factor bHLH30 TF	3.91
	Late embryogenesis abundant protein EM	3.45
	Transcription factor bHLH14 TF	2.81
	Transcription factor bHLH112 TF	2.68
	Protein flowering locus (Histone deacetylase) EP	2.50
	Lisine-specific demethylase (Histone demethylase) EP	2.27
	DNA (cytosine-5)-methyltransferase 1 EP	2.26
Non-embryogenic	Auxin-responsive protein IAA17 TF	-1.17
	Transcription factor bHLH68 TF	-5.46
	Auxin-responsive protein IAA14 TF	-5.74
	LOB domain-containing protein 18 TF	-6.07
	Ethylene-responsive transcription factor 13 TF	-7.49

Comparative global transcriptional expression patterns of tamarillo genes. MA plot depicting the log2 fold change of genes against the average expression level in embryogenic and non-embryogenic samples.

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PROTEOMICS

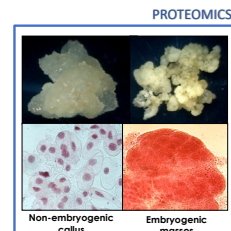
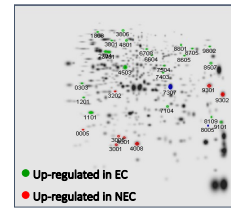
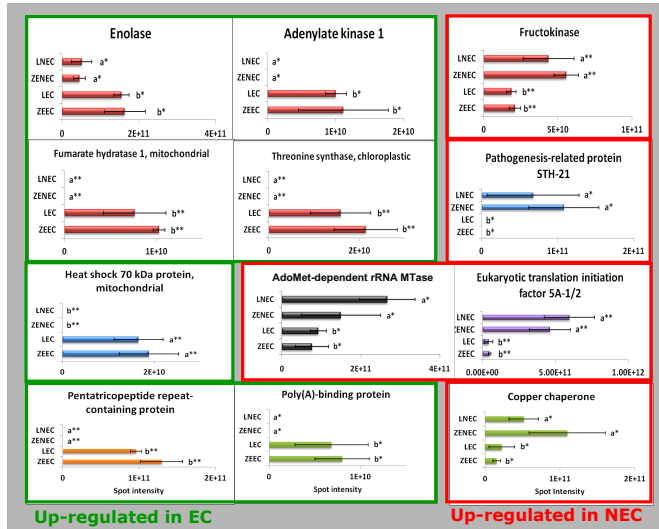
- ✓ Study of **entire protein** complement of the system expressed at a given time and at particular environmental conditions – **PROTEOME**
- ✓ Systematic analysis of proteome - **PROTEOMICS**
- ✓ Analysing **changes in protein expression**, study of **protein structure, function** and **post-translational modifications** (phosphorylation and ubiquitination)



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PROTEOMICS

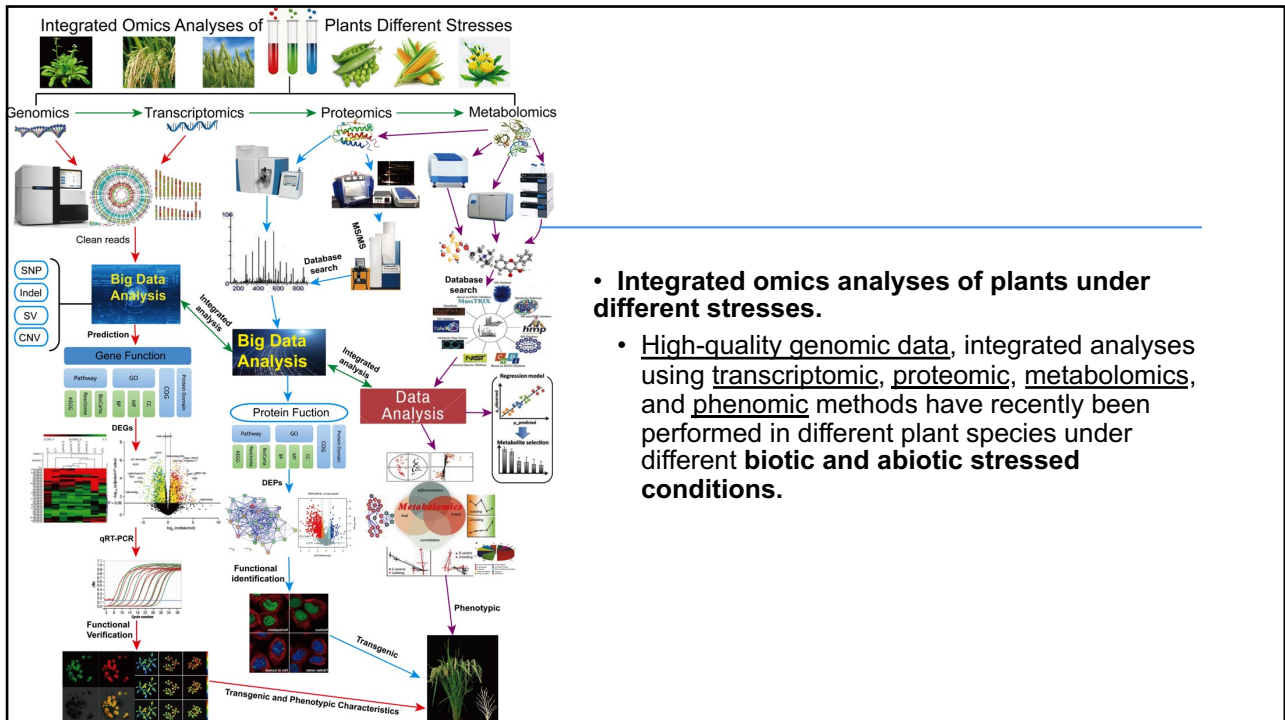
What makes a cell embryogenic competent?



PROTEOMICS
 Comparative Proteomic Analysis of Auxin-Induced Embryogenic and Nonembryogenic Tissues of the Solanaceous Tree *Cupressus betulus* (Tamarillo)
 Susana Gomez¹, Angel Salas¹, Irene Morales¹, Ana del Valle¹, Paula Velasco¹ and Jorge M. Carbon¹

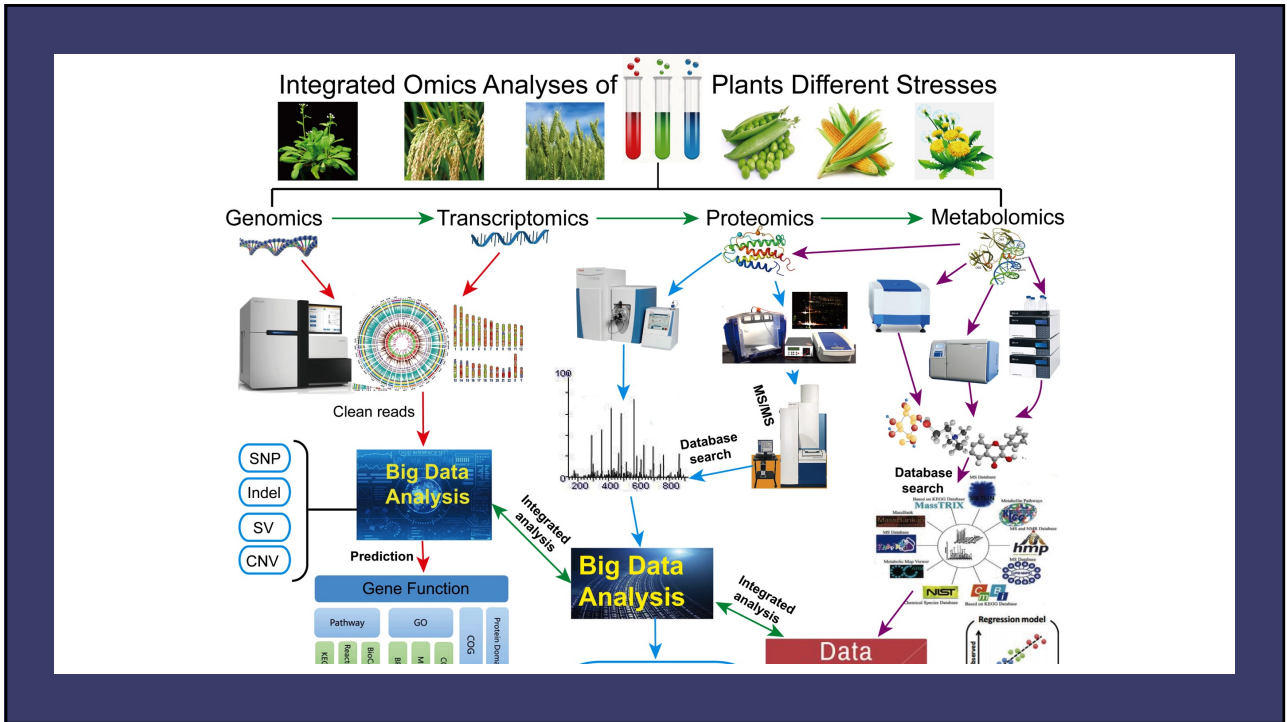


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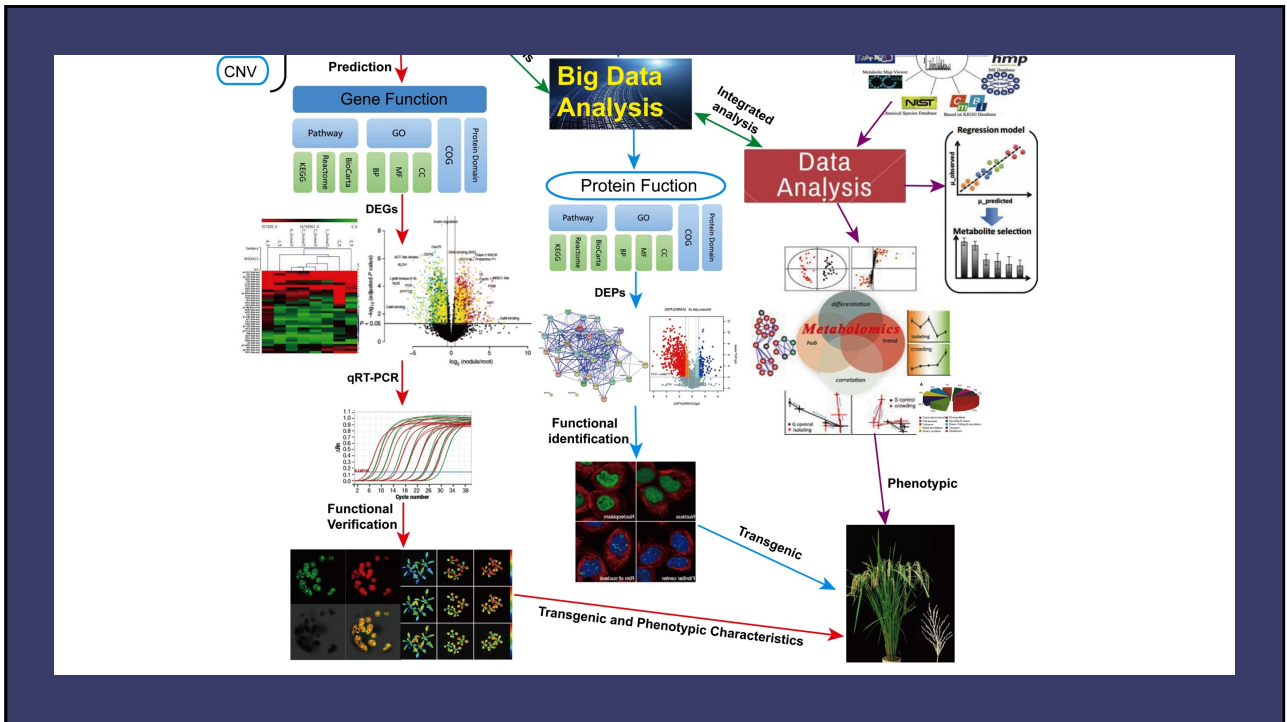


- **Integrated omics analyses of plants under different stresses.**
- **High-quality genomic data, integrated analyses using transcriptomic, proteomic, metabolomics, and phenomic methods have recently been performed in different plant species under different biotic and abiotic stressed conditions.**

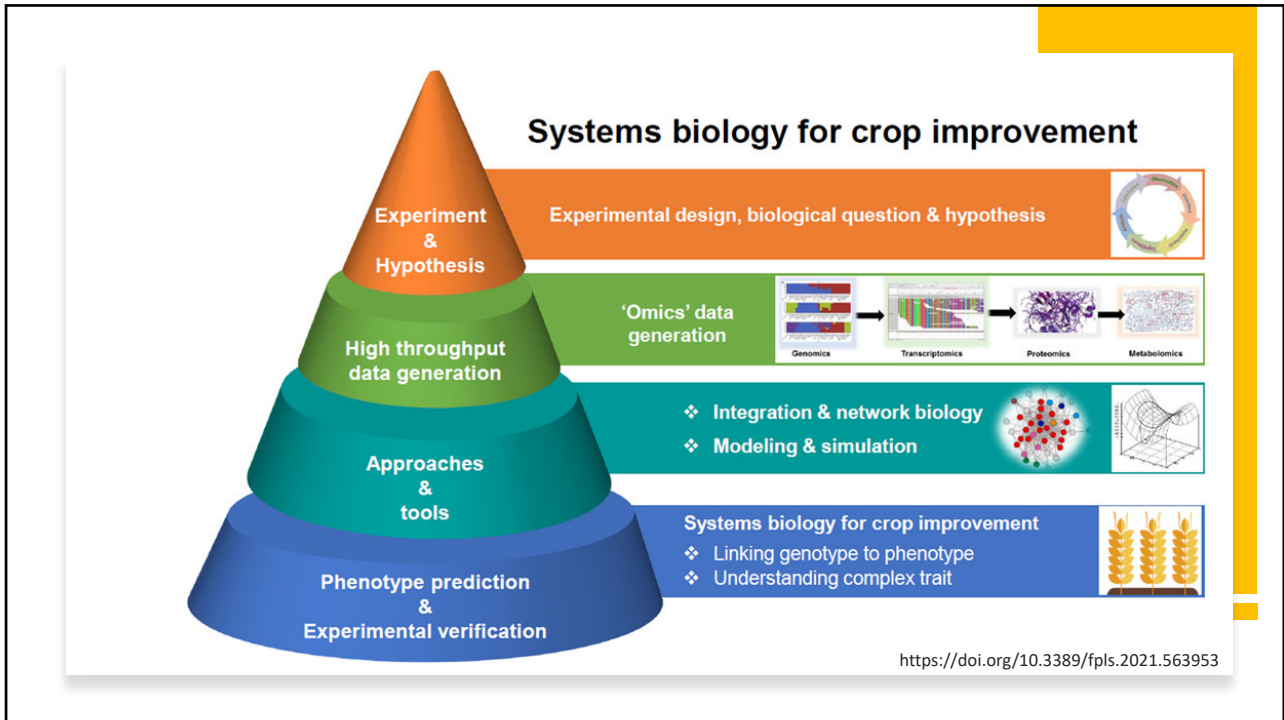
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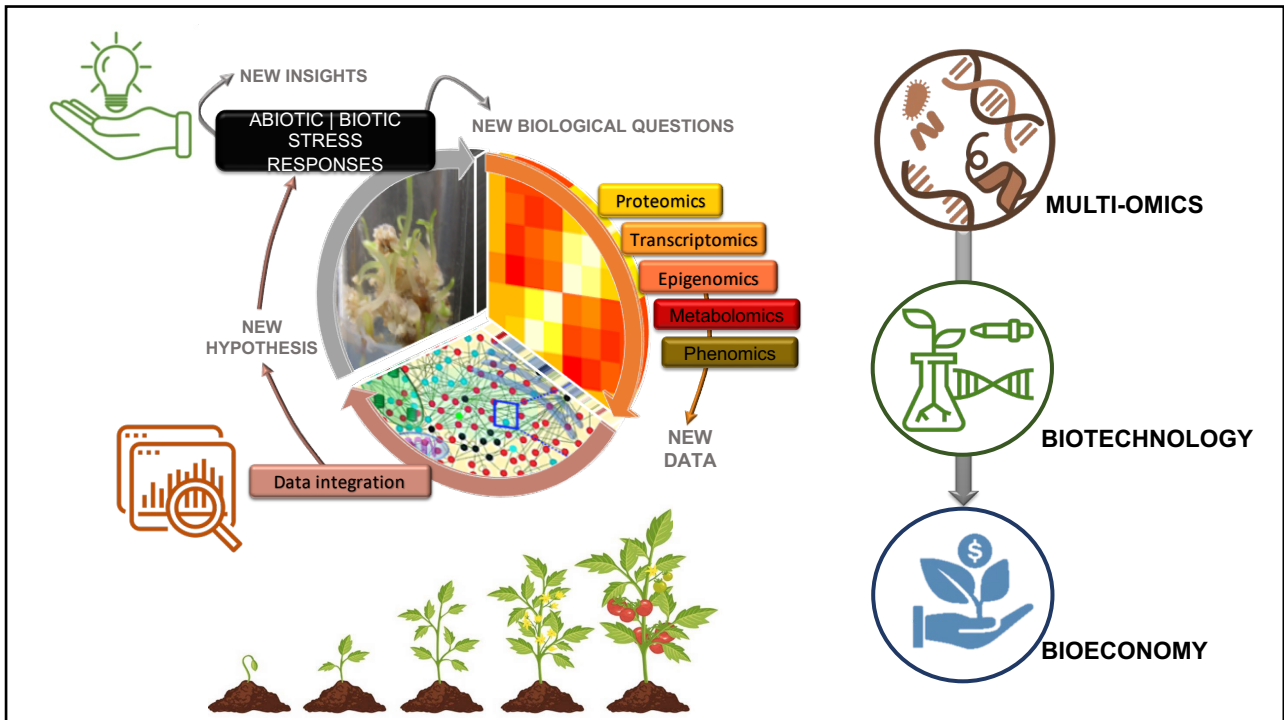
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