



***Universidad Científica del Perú***

***EVENTO NACIONAL: DESARROLLO DE CTI EN FRUTALES NATIVOS AMAZÓNICOS, PATRIMONIO AMBIENTAL Y ALIMENTARIO***

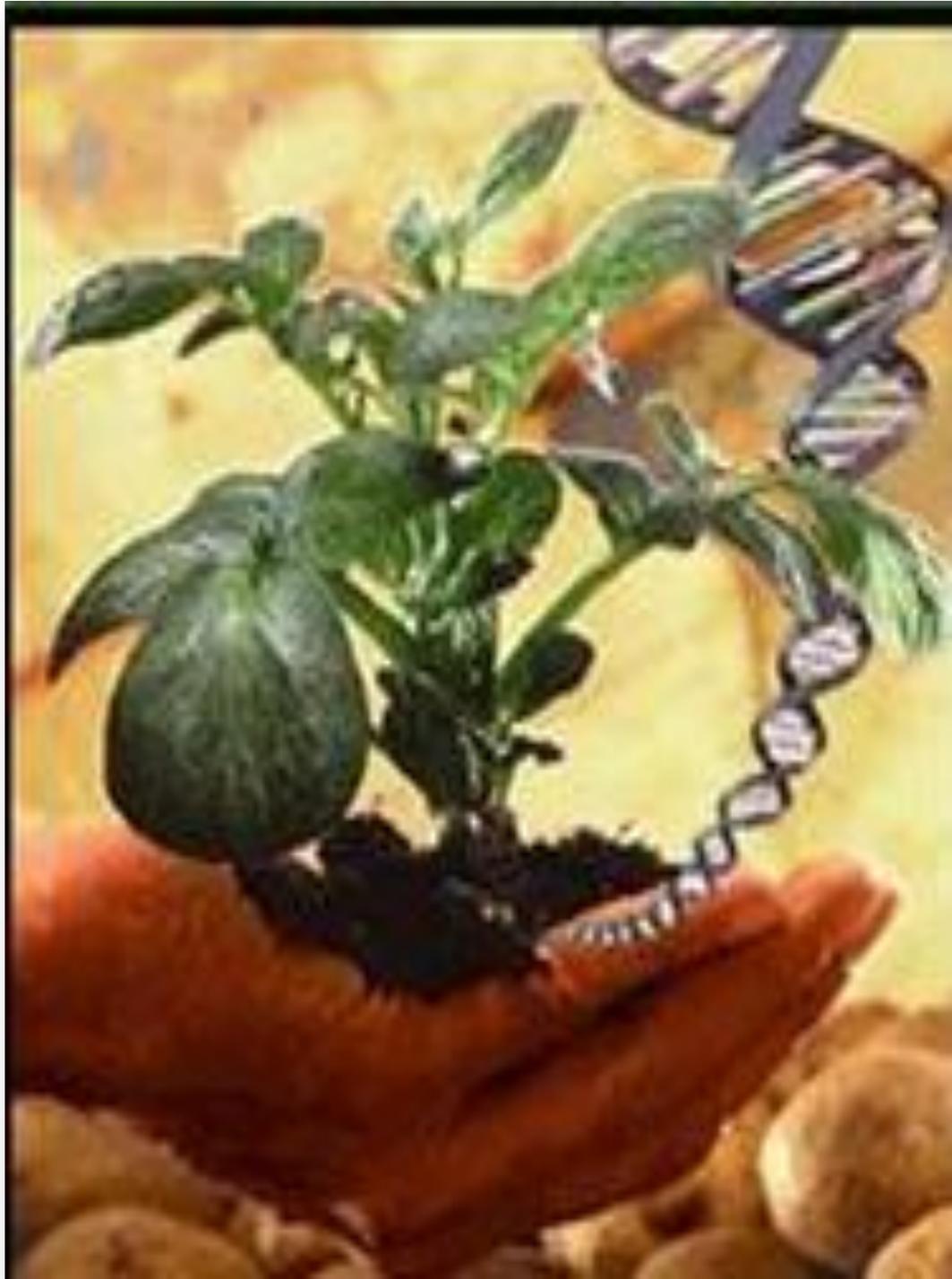
# **PLATAFORMAS PARA MEJORAMIENTO GENÉTICO EN FRUTALES NATIVOS**

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# Amazonía Peruana: Biodiversidad (organismos desconocidos por la ciencia).



□ Explotarlo con **estrategias sostenibles**, ecoamigables que mejoren la situación socioeconómica de la región y el país.



Una de las estrategias más viables es con el **desarrollo de procesos biotecnológicos** basados en el potencial genético de los frutales nativos.

Pues, éstos contienen una **mina de genes** que no han sido explotado hasta el momento.



# Existen muchos vacíos de información genética en frutales nativos

*Bactris gasipaes*  
“pijuayo”



Sotero y García, 2002  
Vitamina A: 867.7 UI

## Genetics

<b>ClinVar</b>	0	Human variations of clinical significance
<b>dbGaP</b>	0	Genotype/phenotype interaction studies
<b>dbVar</b>	0	Genome structural variation studies
<b>GTR</b>	0	Genetic testing registry
<b>MedGen</b>	0	Medical genetics literature and links
<b>OMIM</b>	0	Online mendelian inheritance in man
<b>SNP</b>	0	Short genetic variations

## Proteins

<b>Conserved Domains</b>	0	Conserved protein domains
<b>Identical Protein Groups</b>	17	Protein sequences grouped by identity
<b>Protein</b>	117	Protein sequences
<b>Protein Clusters</b>	0	Sequence similarity-based protein clusters
<b>Sparcle</b>	0	Functional categorization of proteins by domain architecture
<b>Structure</b>	0	Experimentally-determined biomolecular structures

## Genomes

<b>Assembly</b>	0	Genome assembly information
<b>BioCollections</b>	0	Museum, herbaria, and other biorepository collections
<b>BioProject</b>	0	Biological projects providing data to NCBI
<b>BioSample</b>	1	Descriptions of biological source materials
<b>Clone</b>	0	Genomic and cDNA clones
<b>Genome</b>	0	Genome sequencing projects by organism
<b>GSS</b>	0	Genome survey sequences
<b>Nucleotide</b>	496	DNA and RNA sequences
<b>Probe</b>	0	Sequence-based probes and primers
<b>SRA</b>	0	High-throughput sequence reads
<b>Taxonomy</b>	1	Taxonomic classification and nomenclature

## Chemicals

<b>BioSystems</b>	0	Molecular pathways with links to genes, proteins and chemicals
<b>PubChem BioAssay</b>	0	Bioactivity screening studies
<b>PubChem Compound</b>	1	Chemical information with structures, information and links
<b>PubChem Substance</b>	1	Deposited substance and chemical information

# *Mauritia flexuosa* "aguaje"



## Genetics

<b>ClinVar</b>	0	Human variations of clinical significance
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<b>dbVar</b>	0	Genome structural variation studies
<b>GTR</b>	0	Genetic testing registry
<b>MedGen</b>	0	Medical genetics literature and links
<b>OMIM</b>	0	Online mendelian inheritance in man
<b>SNP</b>	0	Short genetic variations

## Genomes

<b>Assembly</b>	0	Genome assembly information
<b>BioCollections</b>	0	Museum, herbaria, and other biorepository collections
<b>BioProject</b>	2	Biological projects providing data to NCBI
<b>BioSample</b>	1	Descriptions of biological source materials
<b>Clone</b>	0	Genomic and cDNA clones
<b>Genome</b>	0	Genome sequencing projects by organism
<b>GSS</b>	0	Genome survey sequences
<b>Nucleotide</b>	843	DNA and RNA sequences
<b>Probe</b>	0	Sequence-based probes and primers
<b>SRA</b>	1	High-throughput sequence reads
<b>Taxonomy</b>	1	Taxonomic classification and nomenclature

## Proteins

<b>Conserved Domains</b>	0	Conserved protein domains
<b>Identical Protein Groups</b>	92	Protein sequences grouped by identity
<b>Protein</b>	441	Protein sequences
<b>Protein Clusters</b>	0	Sequence similarity-based protein clusters
<b>Sparcle</b>	0	Functional categorization of proteins by domain architecture
<b>Structure</b>	0	Experimentally-determined biomolecular structures

## Chemicals

<b>BioSystems</b>	0	Molecular pathways with links to genes, proteins and chemicals
<b>PubChem BioAssay</b>	0	Bioactivity screening studies
<b>PubChem Compound</b>	0	Chemical information with structures, information and links
<b>PubChem Substance</b>	0	Deposited substance and chemical information

***Plukenetia volubilis***  
**“sacha-inchi”**



## Genetics

<b>ClinVar</b>	0	Human variations of clinical significance
<b>dbGaP</b>	0	Genotype/phenotype interaction studies
<b>dbVar</b>	0	Genome structural variation studies
<b>GTR</b>	0	Genetic testing registry
<b>MedGen</b>	0	Medical genetics literature and links
<b>OMIM</b>	0	Online mendelian inheritance in man
<b>SNP</b>	0	Short genetic variations

## Genomes

<b>Assembly</b>	0	Genome assembly information
<b>BioCollections</b>	0	Museum, herbaria, and other biorepository collections
<b>BioProject</b>	3	Biological projects providing data to NCBI
<b>BioSample</b>	4	Descriptions of biological source materials
<b>Clone</b>	0	Genomic and cDNA clones
<b>Genome</b>	0	Genome sequencing projects by organism
<b>GSS</b>	0	Genome survey sequences
<b>Nucleotide</b>	66,363	DNA and RNA sequences
<b>Probe</b>	0	Sequence-based probes and primers
<b>SRA</b>	4	High-throughput sequence reads
<b>Taxonomy</b>	1	Taxonomic classification and nomenclature

## Proteins

<b>Conserved Domains</b>	0	Conserved protein domains
<b>Identical Protein Groups</b>	89	Protein sequences grouped by identity
<b>Protein</b>	104	Protein sequences
<b>Protein Clusters</b>	0	Sequence similarity-based protein clusters
<b>Sparcle</b>	0	Functional categorization of proteins by domain architecture
<b>Structure</b>	0	Experimentally-determined biomolecular structures

## Chemicals

<b>BioSystems</b>	0	Molecular pathways with links to genes, proteins and chemicals
<b>PubChem BioAssay</b>	0	Bioactivity screening studies
<b>PubChem Compound</b>	0	Chemical information with structures, information and links
<b>PubChem Substance</b>	0	Deposited substance and chemical information

*Myrciaria dubia*  
"camu-camu"



## Genetics

<b>ClinVar</b>	0	Human variations of clinical significance
<b>dbGaP</b>	0	Genotype/phenotype interaction studies
<b>dbVar</b>	0	Genome structural variation studies
<b>GTR</b>	0	Genetic testing registry
<b>MedGen</b>	0	Medical genetics literature and links
<b>OMIM</b>	0	Online mendelian inheritance in man
<b>SNP</b>	0	Short genetic variations

## Genomes

<b>Assembly</b>	0	Genome assembly information
<b>BioCollections</b>	0	Museum, herbaria, and other biorepository collections
<b>BioProject</b>	3	Biological projects providing data to NCBI
<b>BioSample</b>	36	Descriptions of biological source materials
<b>Clone</b>	0	Genomic and cDNA clones
<b>Genome</b>	0	Genome sequencing projects by organism
<b>GSS</b>	0	Genome survey sequences
<b>Nucleotide</b>	24	DNA and RNA sequences
<b>Probe</b>	0	Sequence-based probes and primers
<b>SRA</b>	66	High-throughput sequence reads
<b>Taxonomy</b>	1	Taxonomic classification and nomenclature

## Proteins

<b>Conserved Domains</b>	0	Conserved protein domains
<b>Identical Protein Groups</b>	9	Protein sequences grouped by identity
<b>Protein</b>	9	Protein sequences
<b>Protein Clusters</b>	0	Sequence similarity-based protein clusters
<b>Sparcle</b>	0	Functional categorization of proteins by domain architecture
<b>Structure</b>	0	Experimentally-determined biomolecular structures

## Chemicals

<b>BioSystems</b>	0	Molecular pathways with links to genes, proteins and chemicals
<b>PubChem BioAssay</b>	0	Bioactivity screening studies
<b>PubChem Compound</b>	0	Chemical information with structures, information and links
<b>PubChem Substance</b>	1	Deposited substance and chemical information

# Theobroma cacao "cacao"



## Genetics

ClinVar	0	Human variations of clinical significance
dbGaP	0	Genotype/phenotype interaction studies
dbVar	0	Genome structural variation studies
GTR	0	Genetic testing registry
MedGen	2	Medical genetics literature and links
OMIM	0	Online mendelian inheritance in man
SNP	0	Short genetic variations

## Proteins

Conserved Domains	0	Conserved protein domains
Identical Protein Groups	63,569	Protein sequences grouped by identity
Protein	163,403	Protein sequences
Protein Clusters	0	Sequence similarity-based protein clusters
Sparcle	10	Functional categorization of proteins by domain architecture
Structure	1	Experimentally-determined biomolecular structures

## Genomes

Assembly	2	Genome assembly information
BioCollections	0	Museum, herbaria, and other biorepository collections
BioProject	43	Biological projects providing data to NCBI
BioSample	976	Descriptions of biological source materials
Clone	0	Genomic and cDNA clones
Genome	1	Genome sequencing projects by organism
GSS	3,024	Genome survey sequences
Nucleotide	80,497	DNA and RNA sequences
Probe	1,491	Sequence-based probes and primers
SRA	630	High-throughput sequence reads
Taxonomy	1	Taxonomic classification and nomenclature

## Chemicals

BioSystems	497	Molecular pathways with links to genes, proteins and chemicals
PubChem BioAssay	0	Bioactivity screening studies
PubChem Compound	0	Chemical information with structures, information and links
PubChem Substance	0	Deposited substance and chemical information

Hay diferencias marcadas en los genomas de los cultivares "Criollo" (2011) y Matina 1-6 (2013)

# **Necesitamos generar más información científica de los frutales nativos**

## **Desarrollando los estudios “ómicos”:**

- Genómicos
- Transcriptómicos
- Proteómicos
- Metabolómicos
- Fenómicos (la suma total de sus rasgos fenotípicos)

**como base para la mejora genética moderna de**

Actualmente contamos con tecnología de punta para algunos estudios “ómicos”



**Características:**

Produce de 16 a 120 Giga bases de información genética

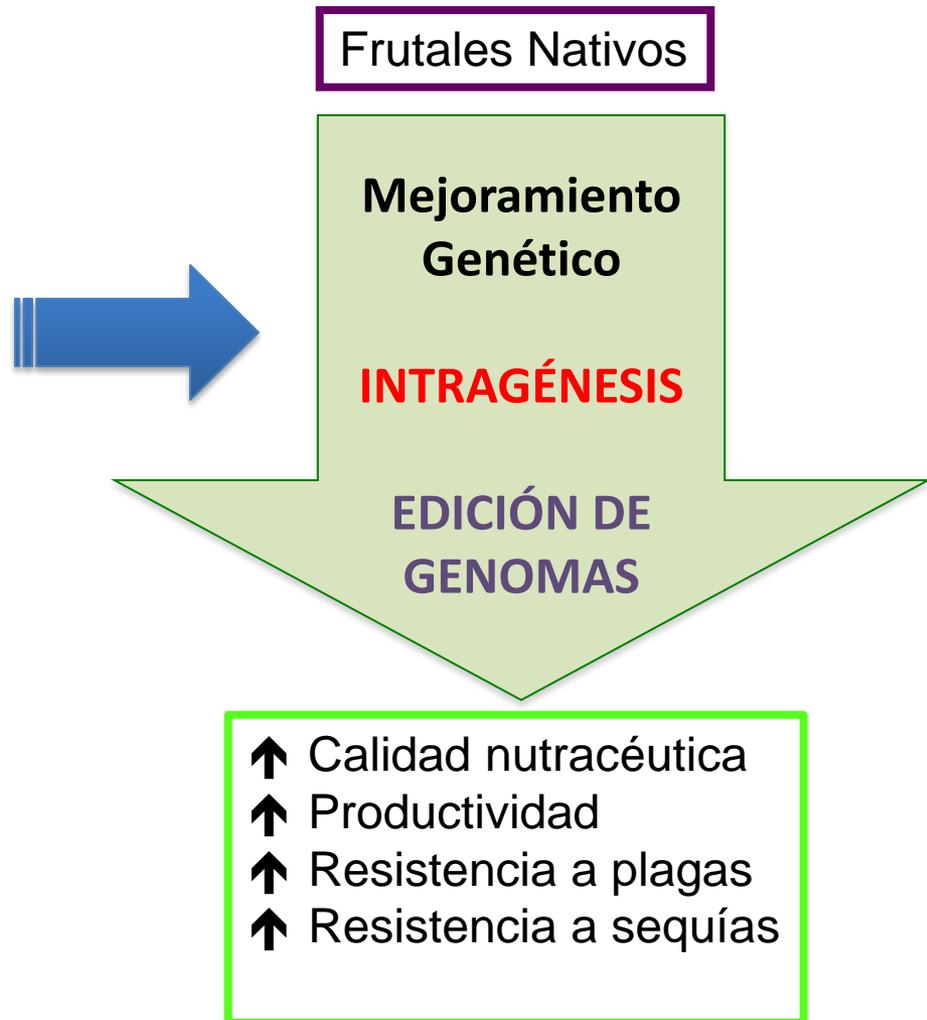
Para analizar GENOMAS y TRANSCRIPTOMAS de microorganismos, plantas, animales, etc

Secuenciador de última generación  
**NextSeq 550 - Illumina**

# También contamos con tecnología para el mejoramiento genético moderno de frutales nativos



**Sistema de Biobalística**  
**PDS-1000/He**



## Resistencia a enfermedades y plagas

- ❑ En cualquier método de mejoramiento, el **factor más importante** para incrementar la producción es la resistencia a las enfermedades y plagas, ya que la mayoría de las plantas son atacadas por patógenos e insectos que reducen o eliminan totalmente las cosechas.
- ❑ En muchos casos resulta incosteable o contraproducente combatirlas por métodos químicos o biológicos.
- ❑ Por lo tanto, el mejor método de control de enfermedades y plagas es el genético, es decir, desarrollar variedades resistentes o tolerantes a patógenos e insectos.

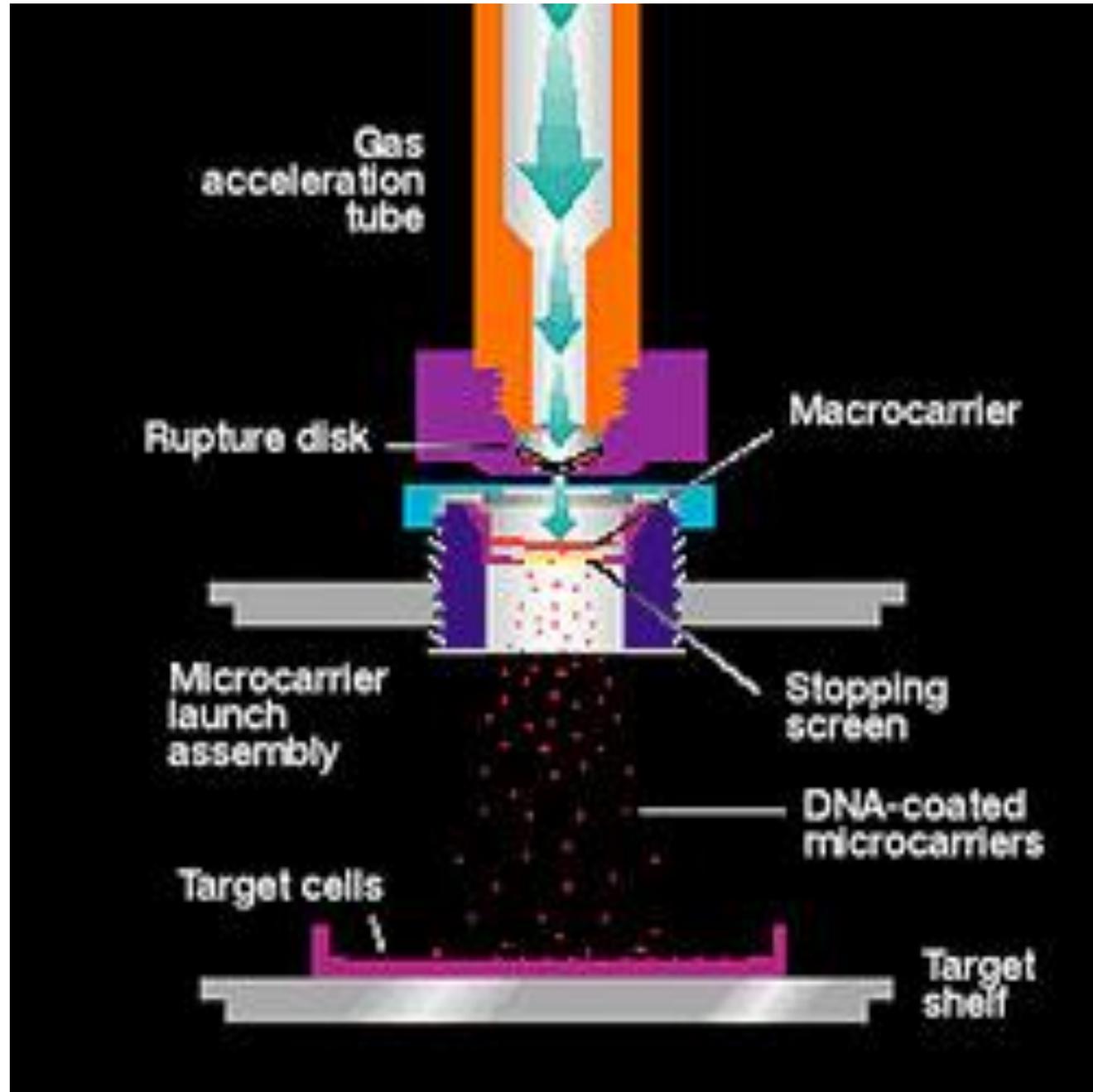
## Pistola de Helio



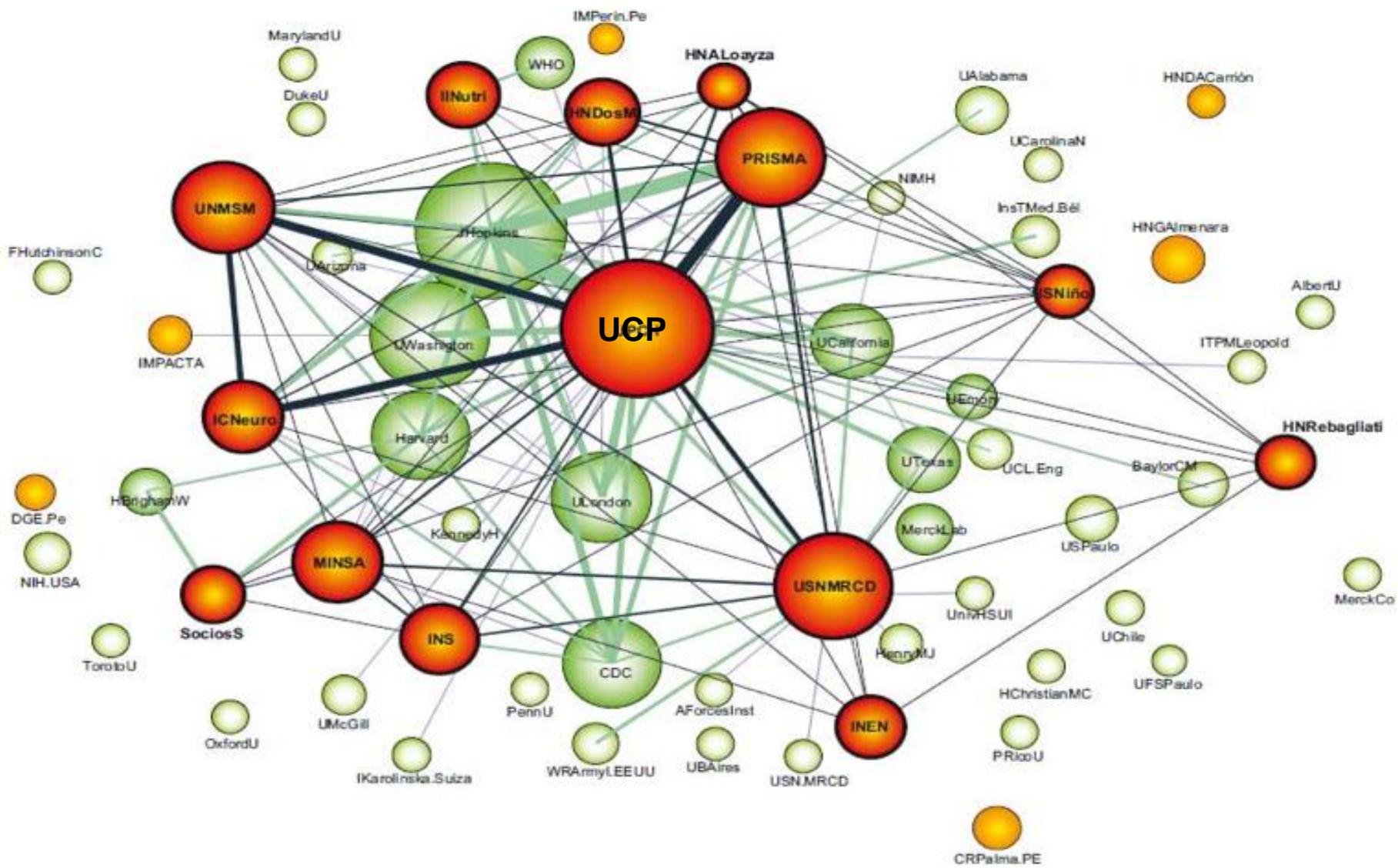
- Con el uso de **plataformas biotecnológicas moleculares** que ofrecen la ventaja de disminuir el tiempo para el mejoramiento genético, permitiendo la producción de materiales sanos, sobresalientes en una o varias características, y al mismo tiempo conservando las bondades de la variedad.

❑ **biobalística** es uno de los métodos directos de transformación.

❑ Se basa en disparar hacia el núcleo de las células a transformar, con alta aceleración, pequeños proyectiles con ADN adherido en su superficie, permitiendo así la incorporación de ADN foráneo al ADN de la célula.



□ Fortalecer la **red de colaboración** entre instituciones públicas y privadas.





*Instituto Nacional de Innovación Agraria*



PONTIFICIA UNIVERSIDAD  
CATOLICA  
DE VALPARAISO



The **Field**  
Museum

Pritzker Laboratory for Molecular Systematics and Evolution

# AGRADECIMIENTO

**Innóvate**<sup>Perú</sup>

Convenio 295-ECL-INNOVATEPERU-2017



Convenio 018-2018-FONDECYT/BM



Área de  
transferencia



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