

# Evolution of plant specialized metabolism in Solanaceae from a multi-omics perspective

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UNIVERSIDAD  
NACIONAL  
DE COLOMBIA



Max Planck Institute  
of Molecular Plant Physiology



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# Project background



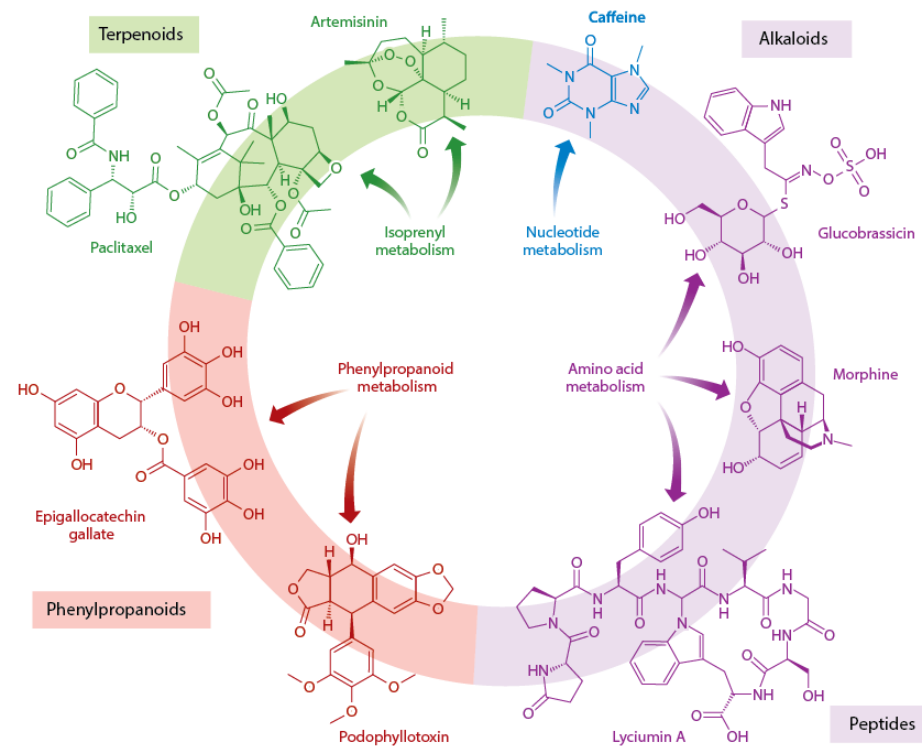
*Solanum lycopersicum*

## Primary metabolism

Compounds that are essential for survival, growth, and development

## Specialized metabolism

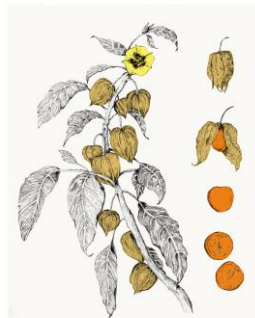
Metabolites associate with biotic and abiotic interactions



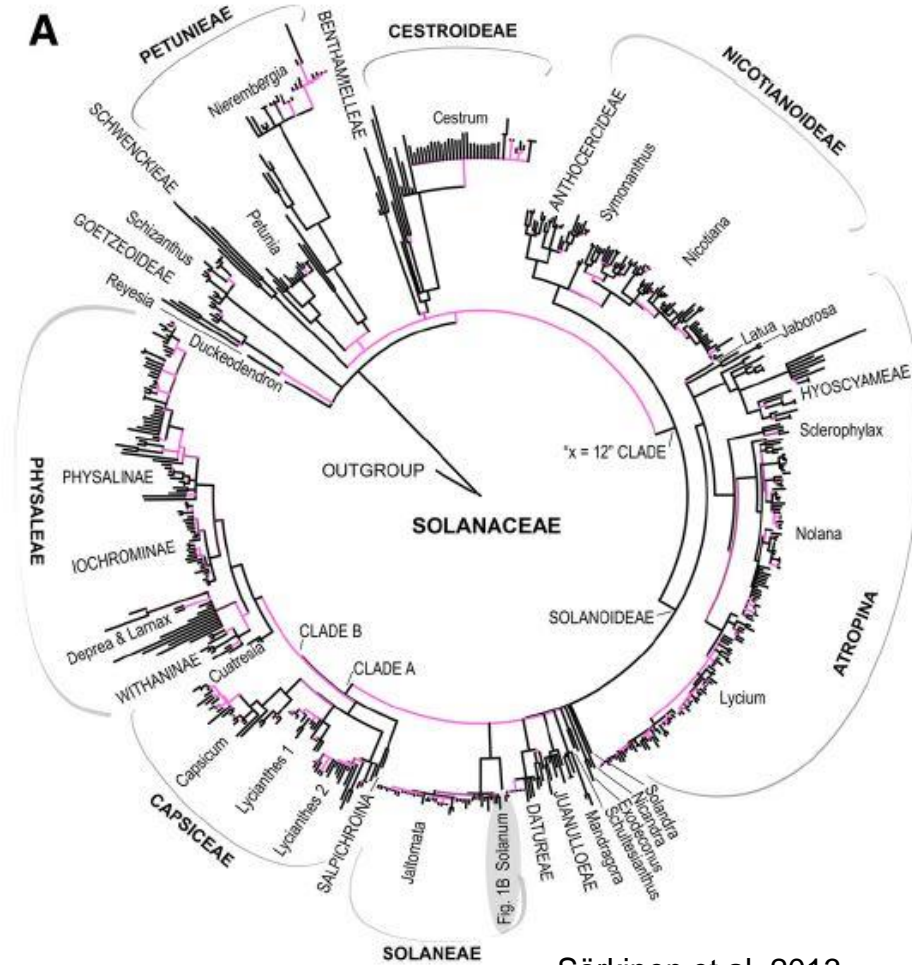
# Project background



*Solanum lycopersicum*



*Physalis peruviana*



Särkinen et al. 2013



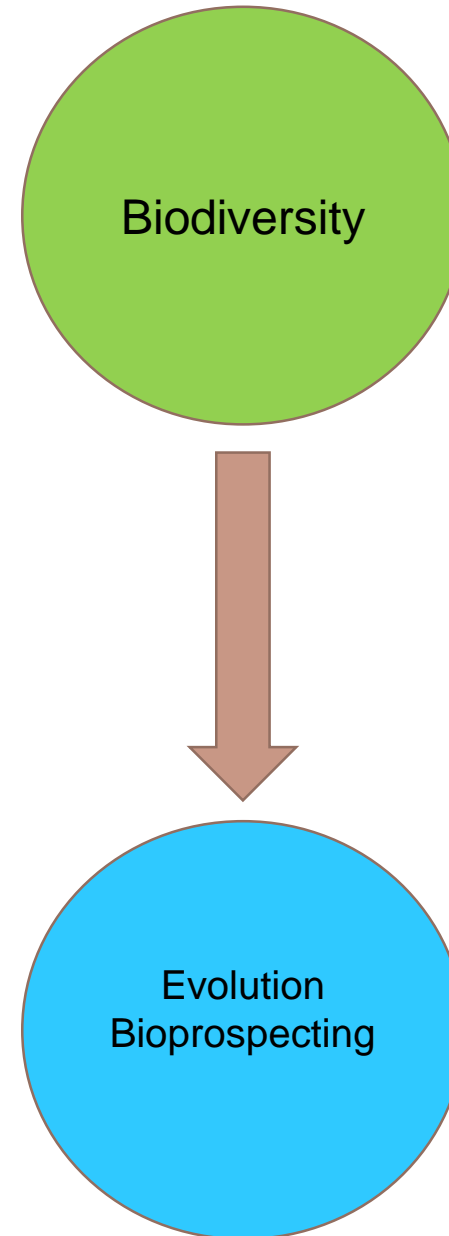
*Brugmansia sp.*



*Capsicum annum*

Specialized metabolites are the result of complex metabolic pathways and usually are not found in high concentrations in plants, making their isolation, purification, and synthesis difficult.

# Plant collections (> 30 filed explorations; > 960 collections; > 250 species; > 37 genera)



- **Transcriptomics**
- **Metabolomics**
- **Genomics**

# Plant Collection

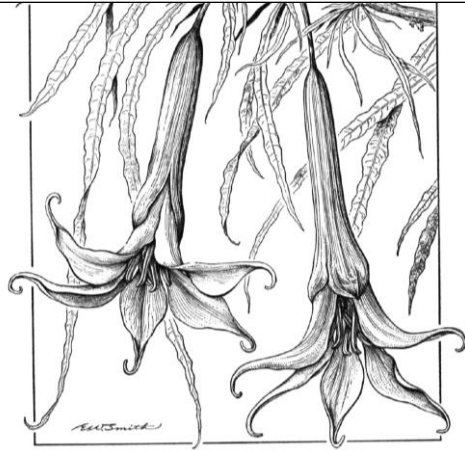
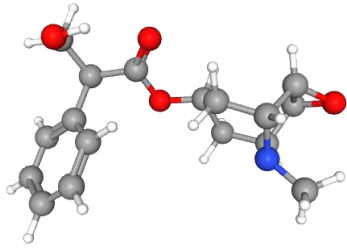


Pictures by F. Roda, D. Granados, and P Pérez

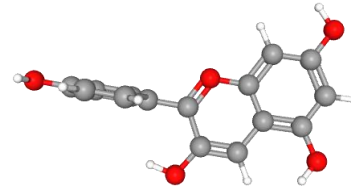


Pictures by F. Roda, Unimedios, and P Pérez

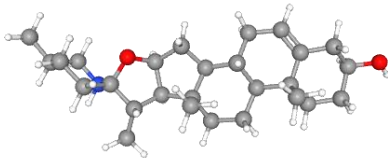
### Tropane alkaloids in *Brugmansia*



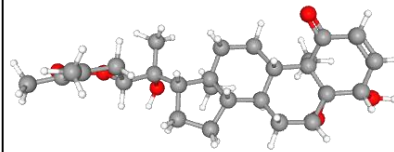
### Anthocyanins in Potato



### Acyl-sugars and SGAs in *Solanum*



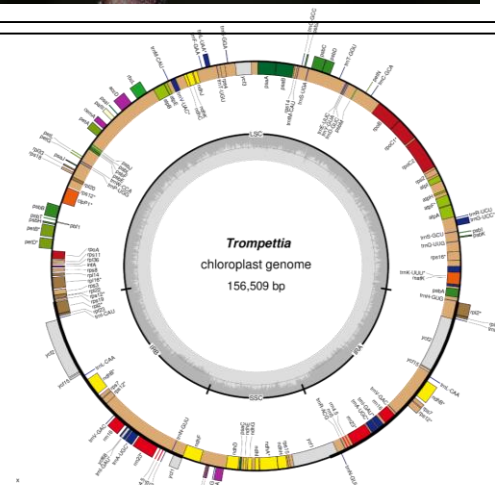
### Withanolides in Physalideae



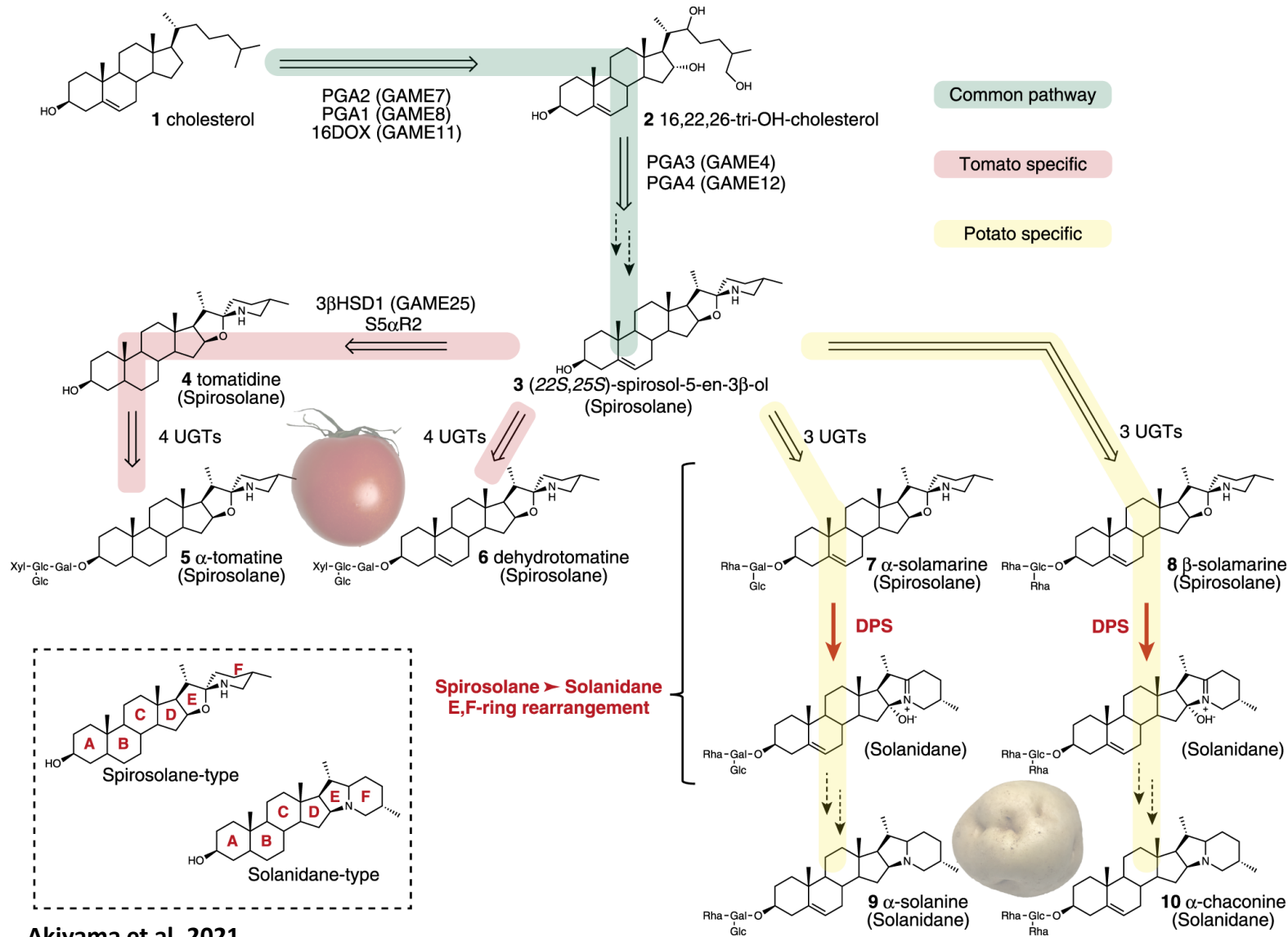
### Metabolomics of Solandreae



### Phylogenomics of Solanaceae



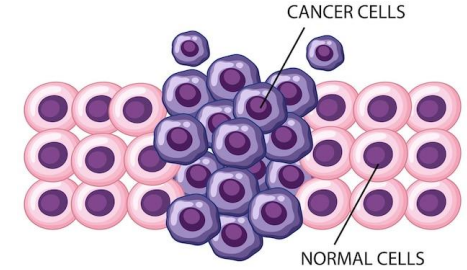
# Steroidal glycoalkaloid metabolism (SGA) in Solanaceae



Akiyama et al. 2021.



Anti-Inflammatory



Anti-cancer

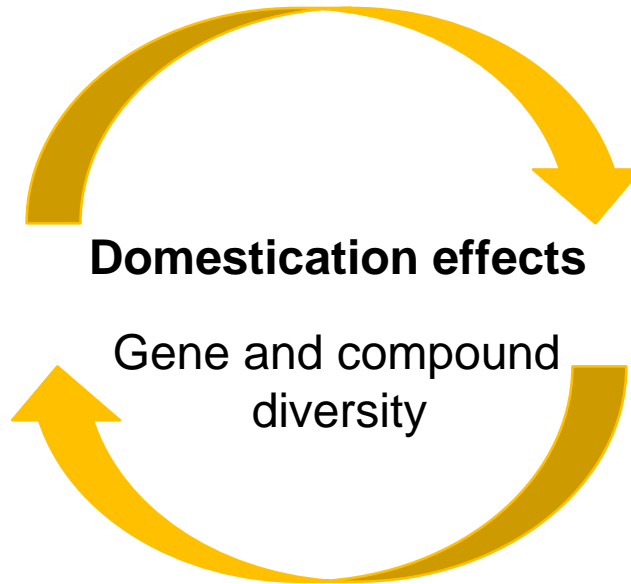


Biotic protection

# Goal of the project



Wild plants



Crop plants

- Synteny analysis between wild and domesticated species to look for gene biosynthetic cluster structure variation
- Gene expression and co-expression analyses
- Metabolite characterization of plants using LC-MS and correlation analysis using transcriptomes and metabolomes



# PhD project

1

To study from the evolution, and the structural, and functional genomics the diversity of the metabolic pathway of the steroidal glycoalkaloids (SGAs) in wild species of the *Solanum* genus with potential medicinal uses.

2 Genomes

More than 130  
Transcriptomes

More than 130  
Metabolomes  
(in process)



*S. stellatiglandulosum*



*S. ovalifolium*

PacBio



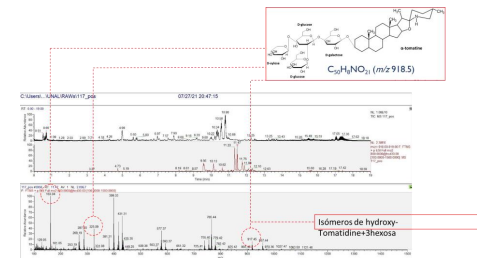
illumina

Illumina NovaSeq™ 6000 S4 Sequencing



Novogene  
Advancing Genomics, Improving Life

Max Planck Institute  
of Molecular Plant Physiology



Transcriptomes for leafs, roots, stems, and flowers

132 species already assembled

# PhD project

1

To study from the evolution, and the structural, and functional genomics the diversity of the metabolic pathway of the steroidal glycoalkaloids (SGAs) in wild species of the *Solanum* genus with potential medicinal uses.

2 Genomes

132  
Transcriptomes

6 candidate  
genes

Synteny analysis

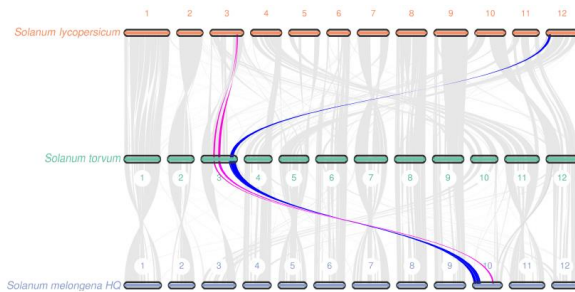
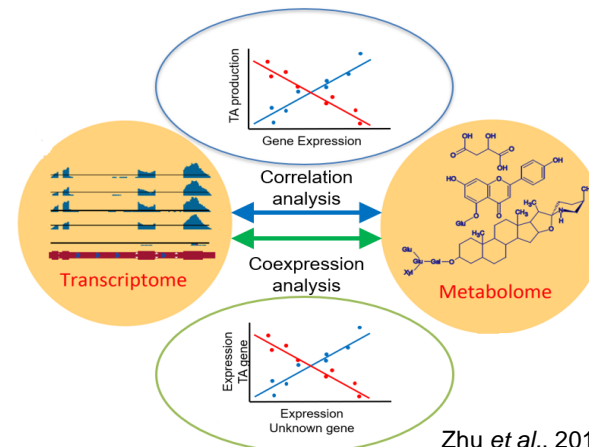


FIGURE 5  
Collinear relationship at the chromosome level among *S. torvum*, *S. lycopersicum* and *S. melongena*. The red and blue lines showed the collinearity of genomic sequences on the chromosome 3 with *S. lycopersicum* and *S. melongena*.

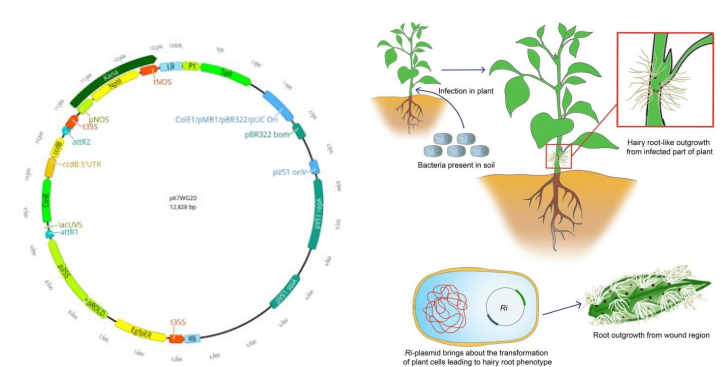
Zhang *et al.*, 2023

Co-expression and co-rrrelation analysis



Zhu *et al.*, 2018

Gene validation Overexpression – Hairy roots



Plantcelltechnology.com

## Pipeline PacBio genome assembly of *S. stellatiglandulosum*

**PacBio HiFi Sequencing DNA** - HiFi reads for highly accurate long-read sequencing (circular consensus sequencing (CCS) mode)

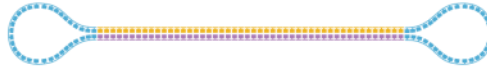


*S. stellatiglandulosum*

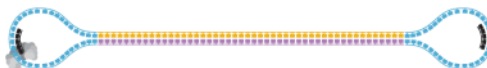
Start with high-quality double stranded DNA



Ligate SMRTbell adapters and size select



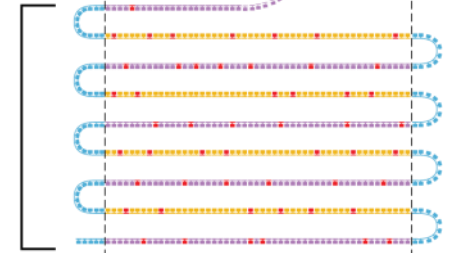
Anneal primers and bind DNA polymerase



Circularized DNA is sequenced in repeated passes



The polymerase reads are trimmed of adapters to yield subreads



Consensus is called from subreads



**HiFi READ**  
(>99% accuracy)

*de novo assembly*

Flye



Annotation

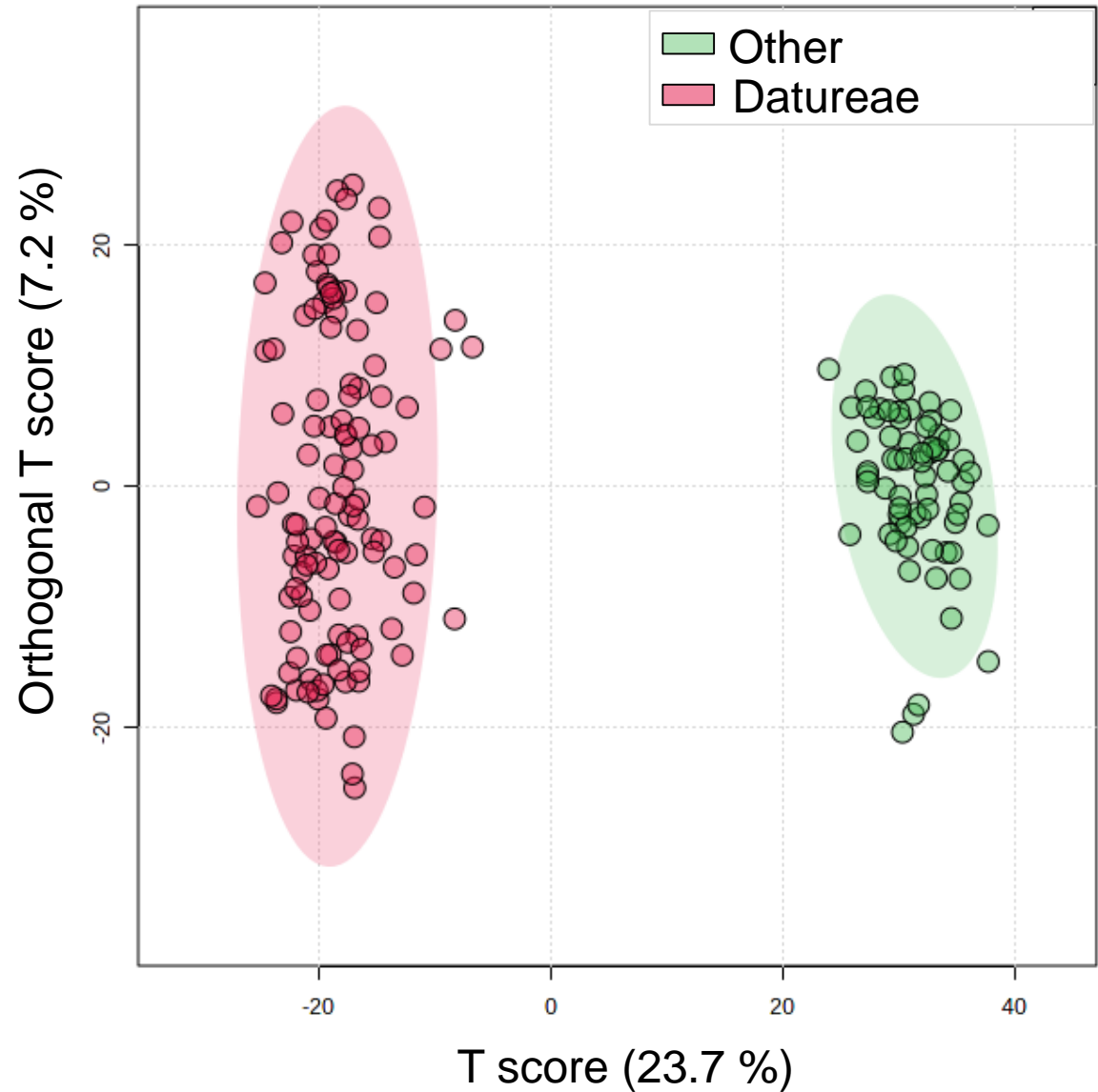
Ryuto/Braker3

- Preliminary results and current progress: Genome assembly

<b>Assembly &amp; annotation</b>	<b><i>S. Stellatiglandulosum</i></b>	<b><i>S. torvum</i></b>	<b><i>S. Melongena HQ</i></b>
Total length of assemblies (Gb)	1.3	1.25	1.07
No. of scaffolds	–	12	12
N50 of scaffolds (Mb)	262	103.02	89.64
No. of contigs	262	309	2263
Total length of contigs (Mb)	1,324.61	1,245.54	–
N50 of contigs (Mb)	28.98	38.65	5.26
Longest contig (Mb)	92.01	99.09	–
Complete BUSCOs (%)	98	98	94.2
Gene number	¿?	31,496	36,582
Transposable element (TE) (%)	¿?	76.73	69.08
Long terminal repeat (LTR) (%)	¿?	68.35	65.8
GC content (%)	¿?	36.6	35.94

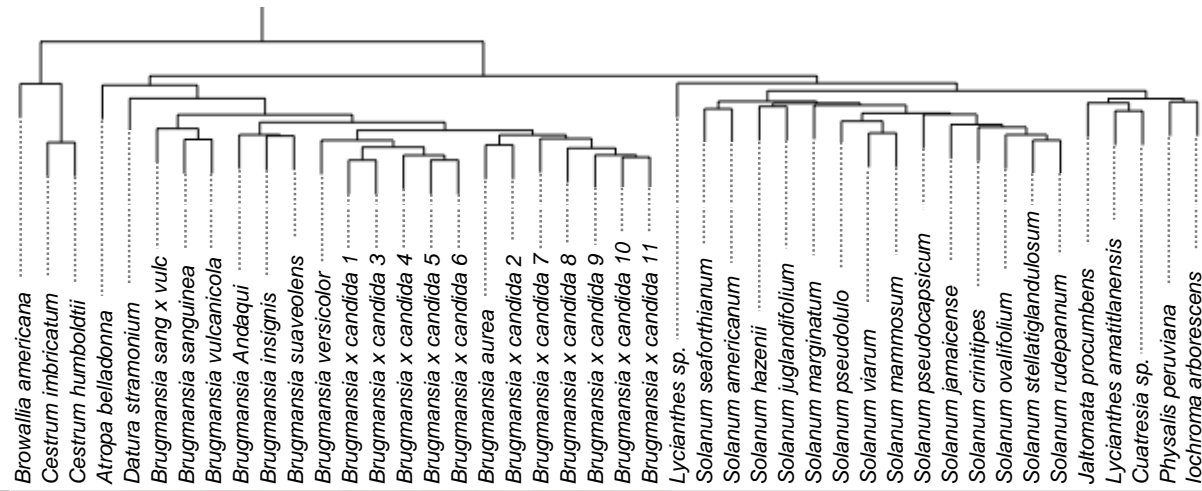
- Preliminary results and current progress: Metabolic content

### OPLS-DA of leaf metabolomes



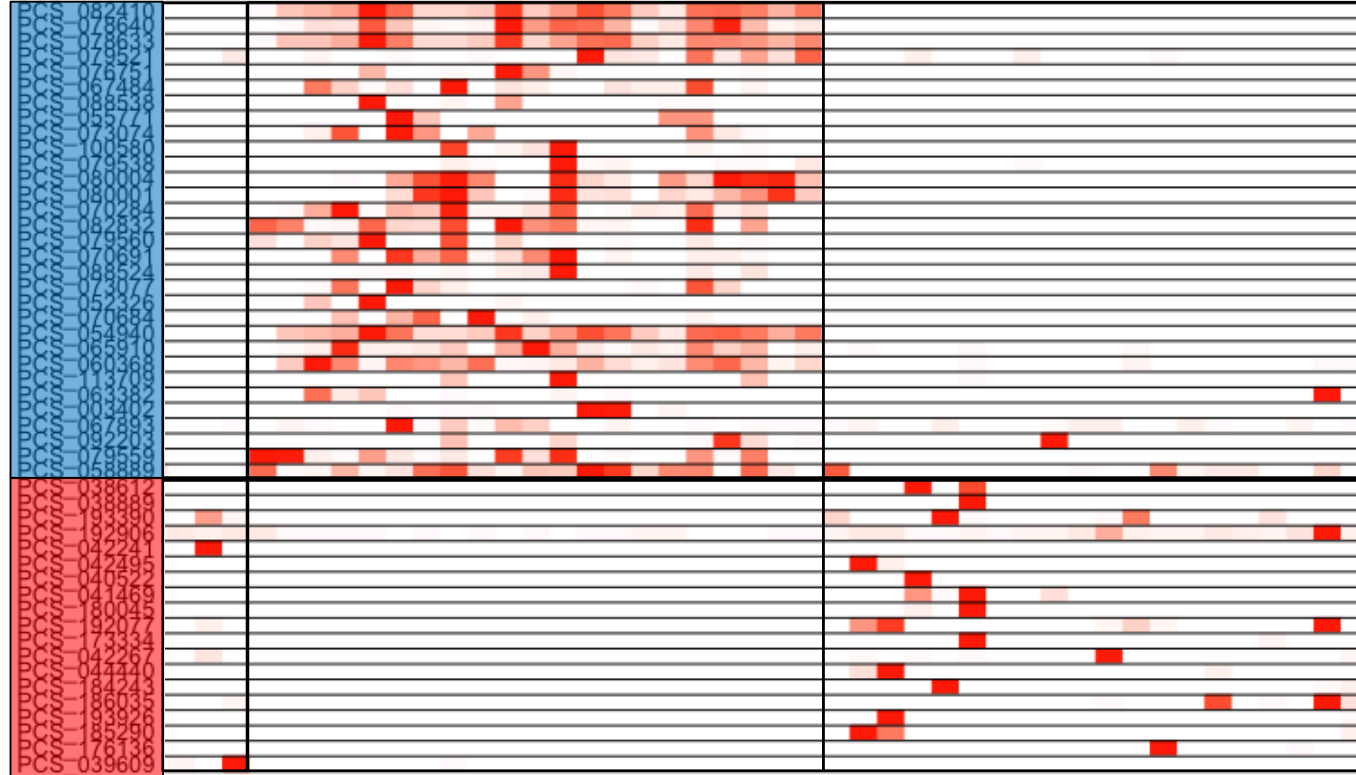
2.500 metabolites used

# Tropane alkaloids vs Steroidal Glycoalkaloids variation



Tas (Tropane alkaloids)

SGAs (Steroidal glycoalkaloids)



SPCs

TPCs

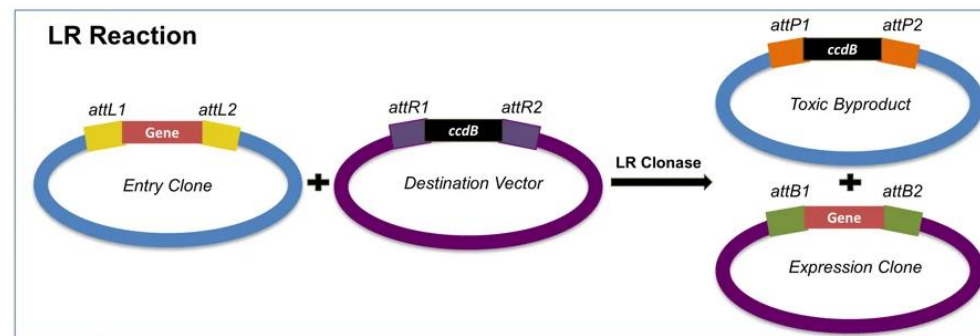
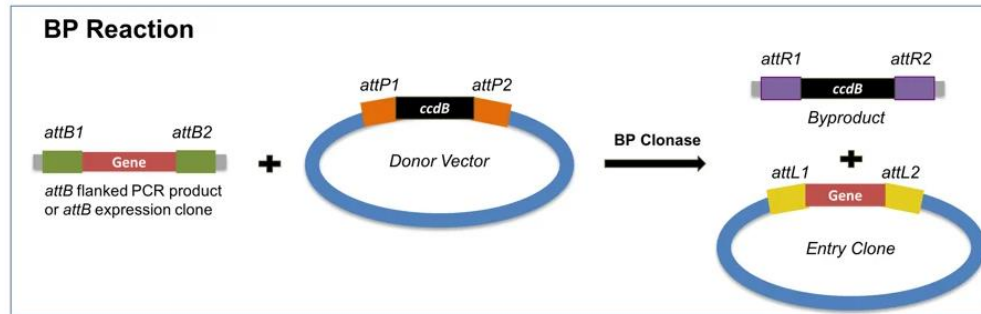
SPCs

- Preliminary results and current progress: Gene validation

## 6 candidate genes associated to the synthesis of SGAs

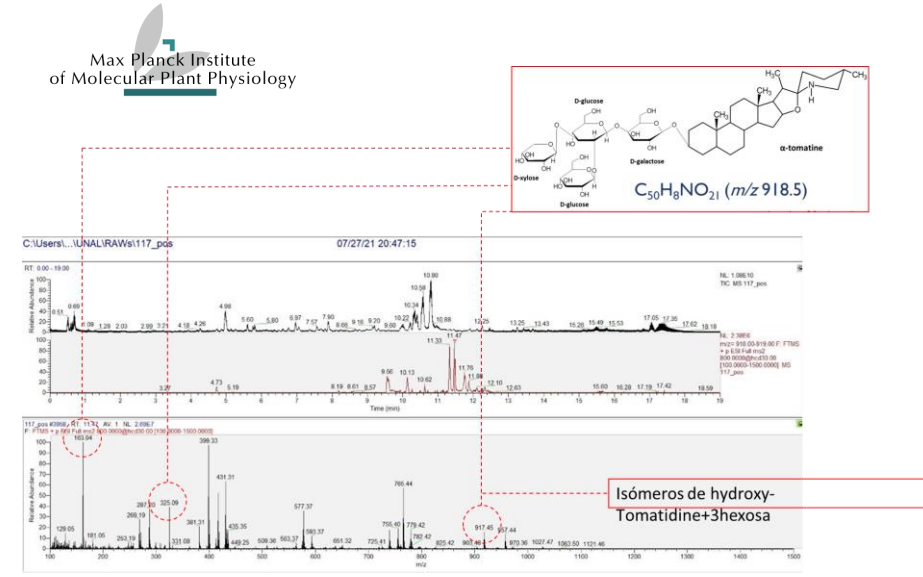
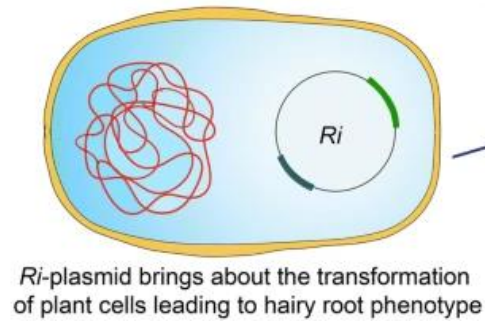
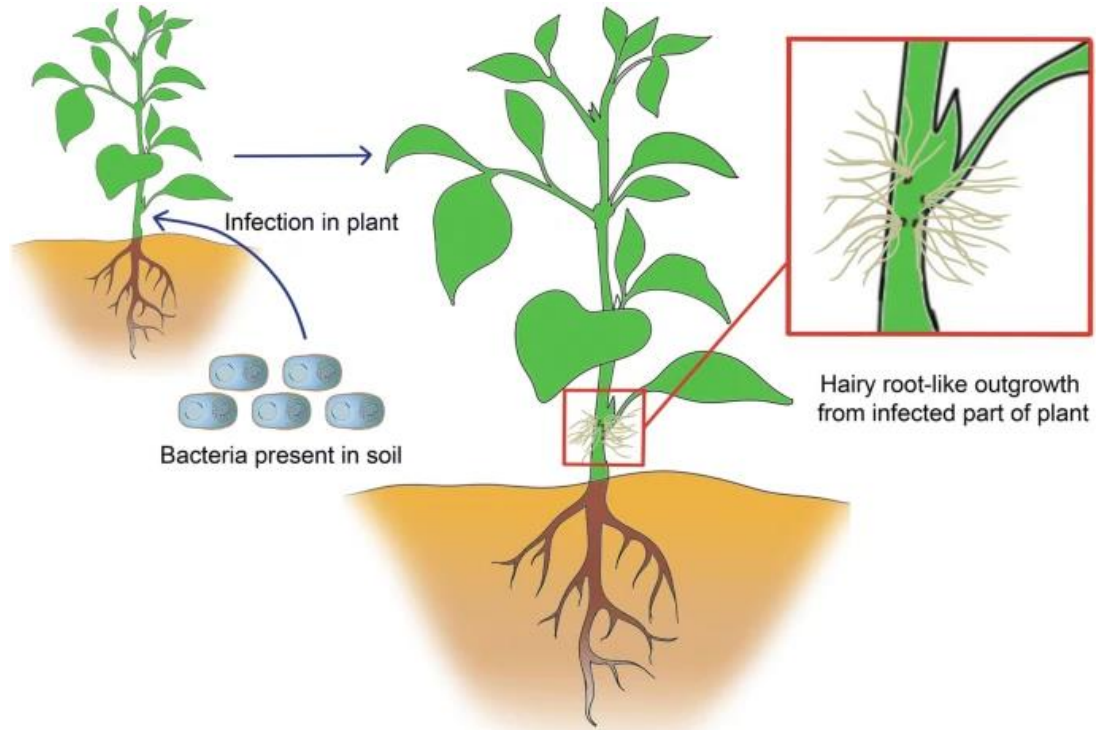
MYB	Solyc07g045000
UGT_8	Solyc07g043100
SRC2	Solyc09g082950
Sec9	Solyc07g025170
Acyltransferase_4	Solyc07g043710
TIC32	Solyc08g081200

### Overexpression in Tomato



- Preliminary results and current progress: Gene validation

# Hairy roots transformation to measure metabolic production





# Outlook

1. Validation of candidate SGA genes using homologous and heterologous expression techniques in tomato plants, to find new metabolic compounds under a domestication framework.
2. The synteny analyses will allow us to understand the evolutionary dynamics of SGA biosynthetic clusters between wild and domesticated species.
3. Co-expression and correlation analyses could let us know more about the diversification and regulatory mechanisms of the SGA metabolism.

# Scholarship project

1

Facilitate international scientific cooperation to understand the genomic basis of SGA diversity in wild and medicinal species of the Solanaceae family.



Max-Planck Tandem Group Universidad Nacional de Colombia



Federico R.



Clara B.



Peter S.



Alisdair F.



Bioinformatik Universität Leipzig

# DAAD

Deutscher Akademischer Austauschdienst  
German Academic Exchange Service



Max-Planck-Institut für molekulare Pflanzenphysiologie



# Aknowledgments



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