The Sol Genomics Network
Intro and Tools

PAG, San Diego, 2016

https://solgenomics.net
https://github.com/solgenomics
https://citrusgreening.org
https://cassavabase.org
https://yambase.org
https://sweetpotatobase.org
https://musabase.org

New responsive design
**The SGN carousel**

Linked to the genome paper

Direct access to JBrowse, BLAST, and the genome data

More visibility for news, events and biological data

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**Solanum Genomes**

- *Solanum lycopersicum*
- *Solanum tuberosum*
- *Solanum pennellii*
- *Solanum pimpinellifolium*
- *Solanum melongena*

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**Nicotiana Genomes**

- *Nicotiana benthamiana*
- *Nicotiana tabacum* (K326, Flue-cured)
- *Nicotiana tabacum* (TN90, Burley)
- *N. tabacum* Basta Xanthi (BX, Oriental)

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**Other Genomes**

- *Capsicum annuum*
- *Capsicum chinense*
- *Coffea canephora*
- *Petunia spp.*

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**Accounts**

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<thead>
<tr>
<th>Account Type</th>
<th>Privileges</th>
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<tr>
<td>&quot;user&quot;</td>
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<td>&quot;submitter&quot;</td>
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**Create Account**

Create an account to access more features.

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**Sol Genomics Network**

1/19/2016
Data Querying and Curation

- Loci & Locus Annotation
- Curation of Plant Accessions
- Structural Gene Curation
Structural Gene Curation in Tomato using WebApollo

http://tomato-webapollo.sgn.cornell.edu/WebApollo
Tools

- Comparative Map Viewer
- SolCyc (Pathway Tools)
- BLAST
- JBrowse
- SGN VIGS Tool
- Tomato Expression Atlas

Maps

Maps
Extract Sequences from BLAST dataset II

Sol Genomics Network

Gene models, markers, SNPs, RNA-seq alignments, RNA-seq coverage

Click on track: edit style, save data for region or whole track, GFF3, BED, Fasta

Tomato genes linked to SGN on click

Right click view details, highlights, zoom

Navigation, zoom in and out selecting a region

360 Tomato variants

Genomic analyses provide insights into the history of tomato breeding

SB 06, Kango, Dru, Kanto, Chang, Kao, Kanto, Ko, Kanto, Zhen, Zhe, Zheng, Zhao, Zhang, Zhe, Zh, Zhou, Zhe, Zhou, Zhao, Zhe, Zh, Zhu, Zhe, Zh, Zhu

Nicotiana benthamiana

A draft genome sequence of Nicotiana benthamiana to enhance molecular plant-pesticide strategy research
Virus-Induced Gene Silencing (VIGS)

Transformation
mediated by

A. tumefaciens

Figure adapted from Azorsa et al. 2006


21 - 24 nt

VIGS Tool input

VIGS Tool output
The SGN VIGS tool simulates in silico the recognition of the mRNA by RISC and the siRNA, and tries to predict the best construct avoiding off targets.
Summary

- **Genomes & Loci** for community curation
- **GMOD Tools** common bioinformatics tools implemented on SGN
- **SGN VIGS Tool** to design VIGS constructs
- **SGN CRISPR Tool** to design sgRNA to silence multiple paralogous genes
- **Tomato expression Atlas** a high resolution expression atlas for tomato fruit developmental stages