

Genome-wide approaches in the study of common figs in the Nikita Botanical Gardens

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Fig is one of the most ancient subtropical fruit crops using in food, cosmetic, and soap industries as well as in medicine, which industrial production is hindered by the lack of intensive cultivation technologies.

Genome-wide approaches provide an effective tool for the development and implementation of the modern molecular breeding strategies in the fig cultivation.





NBG-NSC

The Nikita Botanical Gardens (NBG-NSC)

a unique common fig collection represented by 267 cultivars and hybrid forms including of local breeding.

A comprehensive genomic studies of the common fig collection started in the NBG-NSC a few years ago and **four main researcher projects** are ongoing.

- ▶ Reference genome of the **local cultivar Ficus carica 'Sabrutsiya Rozovaya'** was obtained by **hybrid assembly** using combined **long** and **short read** genome wide sequencing datasets.



Illumina NextSeq550
27 Gb, GC 34,34%

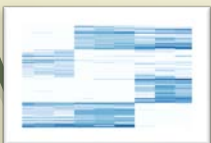


Oxford Nanopore MinION
23,7 Gb GC 34,40%

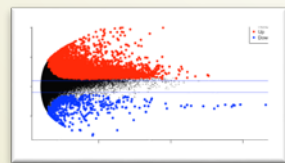


Alignment to the reference genome *F. carica* cv. Dottato UNIPi_FiCari_1.0

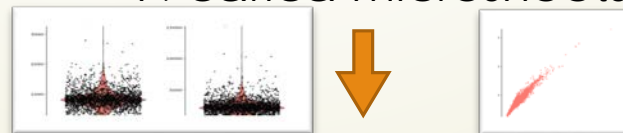
- ▶ **Transcriptomes analysis** of the three *F. carica* cultivars grown *in vitro*, *in vivo*, *ex situ* conditions



Functional genomics



- ▶ **Single-cell RNA-seq** analysis using *in vitro* *F. carica* microshoots



Molecular mechanisms of cell differentiation in plants



- ▶ **WGS genotyping** of the NBG-NSC fig collection

Advanced genomic fig breeding technologies



PlantGen2021
6th International scientific conference

Transcriptome analysis of *Ficus carica* cultivars with alternative phenotypes

F. carica cultivars

- ▶ 'Sabrutsiya Rozovaya',
- ▶ 'Aromatnyy Nikitskiy',
- ▶ 'Nairanneyshiy Fioletovyy'

Growth conditions

- ▶ *in vitro*
- ▶ *in vivo*
- ▶ *ex situ*

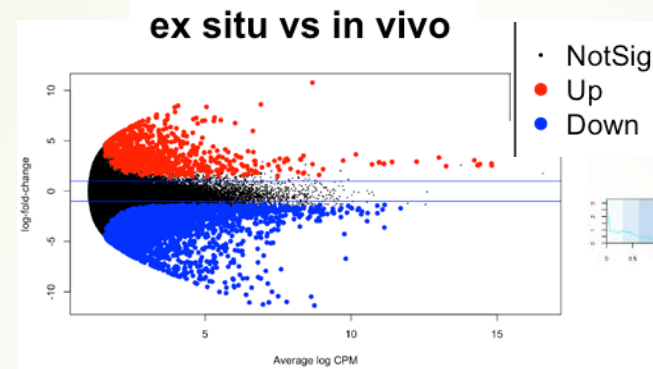
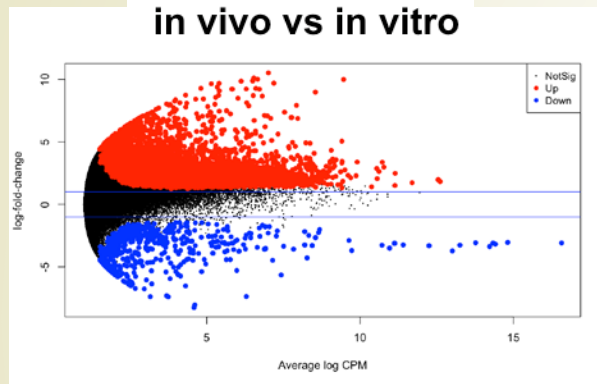
X *in 3 repeats*

Transcriptome assembly statistics	Total trinity 'genes'	Total trinity transcripts	% GC	ALL transcript contigs				ONLY LONGEST ISOFORM per 'GENE'			
				Contig N50	Median contig length	Average contig	Total assembled bases	Contig N50	Median contig length	Average contig	Total assembled bases
'Sabrutsiya Rozovaya'	111143	174613	40.45	2092	478	1063.09	185 629 376	1366	336	676.47	75 184 415
Aromatnyy Nikitskiy	53445	93975	41.53	2280	860	1344.10	126 311 477	1926	416	932.11	49 816 477
'Nairanneyshiy Fioletovyy'	49198	87162	42.07	2106	856	1281.37	111 686 833	1856	431	933.82	45 942 105

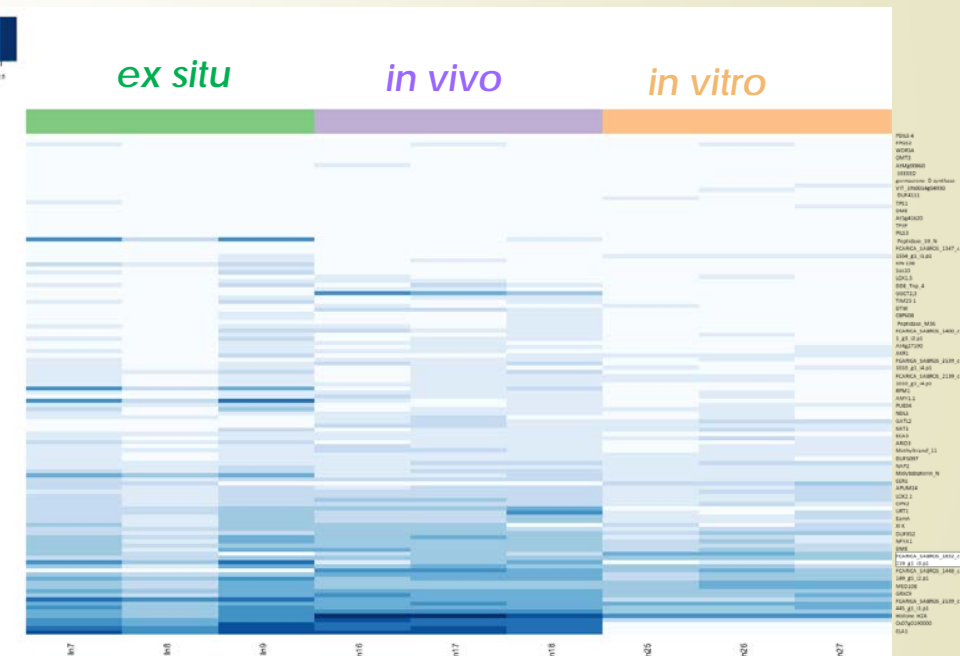
To identify the molecular determinants of fig resistance to complex abiotic stress, changes in a differential gene expression during adaptation of *in vitro* cultivate plants to *in vivo* and *ex situ* conditions was studied.

Transcriptome analysis of *Ficus carica*: differential gene expression during adaptation

'Sabrutsiya Rozovaya'




TOP 30 UP&DOWN regulated genes



in vitro → *in vivo* → *ex situ*

- Total number of significant genes: **8992** **5002**
- Up-regulation: **8286** **1071**
- Down-regulation: **706** **3931**





Researchers teams involved in the common fig genomic projects

- ▶ Biotechnology work was done at Plant Biotechnology and Virology Laboratory, genomic investigations were carried out at Plant Genomic and Bioinformatic Laboratory of Plant Developmental Biology, Biotechnology and Boisafety Department on the base of Unique Scientific Installation "FITOBIOGEN" at the FSFIS "NBG-NSC", and at Kurchatov Genomic Center – NBG-NSC.
- ▶ Sequencing on Illumina NextSeq 550 was done at the Center of Genomic Research ICG SB RAS.
- ▶ Bioinformatic analysis was done in collaboration with the ICG SB RAS (a team led by Ph.D. Afonnikova D.A.) based on Collective Use Center "Bioinformatics" ICG SB RAS.
- ▶ The projects are supported by the grant No. 075-15-2019-1670 of the Ministry of Science and Higher Education of Russian Federation (branch - Kurchatov Genomic Center – NBG-NSC) and by the State Task No. 0829-2019-0038 of FSFIS "NBG-NSC".