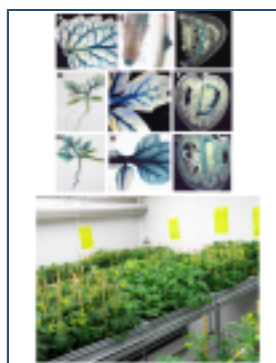


# Facilities in the GBF laboratory

## Reverse genetics and Plant transformation



*Jean-Paul Roustan, Lydie Tessarotto Lemonnier, Olivier Berseille, Dominique Saint-Martin*

As the rapid development in plant genomics research identifies more genes potentially involved in the development and maturation of tomato fruit, their functional analysis relies on strategies such as complementation, overexpression, gene silencing or promoter GUS/GFP fusion. Plant genetic transformation is a critical technology required in the application of these strategies.

Tomato agrobacterium-mediated transformation is routinely used in our laboratory and we have access to controlled environment growth facilities, containment glasshouses suitable for GM trials.

## Bioinformatics



*Mohamed Zouine, Elie Maza, Matthieu Lauvernier*

In collaboration with Genotoul-Bioinfo platform, the activity of the team is organized in three main topics focusing on sequence analysis. The topics are i) Gene annotation to interpret sequence data ii) Omics data analysis iii) Integrative web-portals to integrate bioinformatics resources in order to provide biologists with unified user interfaces.

Our primary goal is to provide our collaborators either in the lab or in other laboratories with bioinformatics tools permitting an efficient and fast exploitation of molecular data.

## Transcriptomics



*Pierre Frasse, Alexandra Legendre*

### **Microarray:**

This tool is implemented in all the projects developed in our laboratory and help to the definition of target genes involved in the regulation of the different pathways with regard to biotic or abiotic stress.

Our laboratory elaborate the tomato microarrays called : EU Tom1 12K oligo-arrays. They contain 12,160 long oligos (70 mers) including 300 controls randomly placed throughout the array.

11,860 genes from the tomato are represented, the majority of the probes being designed from gene sequences gathered from the *Lycopersicon* Combined Build #3 Unigene database at Cornell University. The remaining number of oligos was designed from sequences in GenBank.

For complete documentations on the array see below:

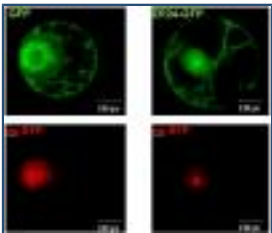
- \* EU\_TOM1\_12K [description](#)

- \* GenePix [.Gal file](#) for EU\_TOM1\_12K microarrays
- \* [Gene ID](#) file for EU\_TOM1\_12K microarrays
- \* Protocol for [target synthesis](#) (labelled aRNA)
- \* Protocol for [manual hybridization](#)

### RNA-Seq & ChIP-Seq:

The availability of the tomato genome sequence lead us to implement this new technic to the new projects started in our lab.

## Single Cell and Microscopy



*Isabelle Mila*

We use tobacco protoplasts transient expression assays to study characteristics and functions of genes, regulatory cis-acting elements, subcellular localization and transactivation/repression activity of transcription factors that are studied in our laboratory.

## Rapid phenotyping of tomato lines

*Lydie Tessarotto Lemonnier and Christian Chervin*



Using a near infra-red portable spectrometer, the lab has expertise in screening hundreds of fruit per day for at least the six following parameters: color Hue, color Chroma, juice soluble

solid content, juice pH, firmness and water content. More developments can be initiated for the prediction of additional quality parameters of the fruit and other plant organs.