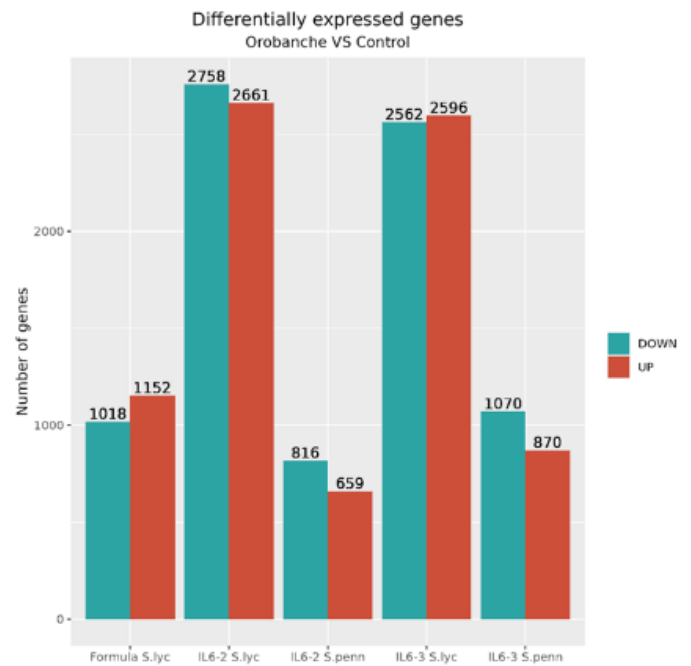


WP4
TASK 4.4
Analysis of the expression of host genes associated to resistance.

Screening and comparative evaluation of tomato commercial hybrids and introgression lines, potentially resistant to broomrape was carried out, by combining high throughput techniques (Next Generation Sequencing-NGS) and gene expression profiles (qPCR) for further validation of the most promising Differentially Expressed Genes-DEGs, aiming to identify genes related to tomato resistance against broomrape.

Whole Genome Sequencing (WGS) followed to find potential genetic markers like Single Nucleotide Polymorphisms (SNPs) in the regions of the DEGs, aiming to develop a quick and trustworthy tool for identification of tomato genetic material with resistance to broomrape.

Did you know?
Next Generation Sequencing (NGS) reveals an impressive number of Differentially Expressed Genes (DEGs) in tomato roots, parasitized by broomrape.



Number of DEGs revealed from NGS analysis for all the tested samples.

