Transcriptomics as a tool for identification of potato genotypes associating pathogen resistance and high efficiency of nitrogen utilization

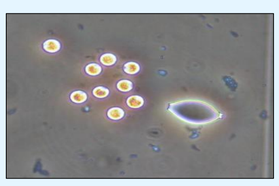
Model: *Solanum tuberosum* x *Phytophthora infestans* x nitrogen

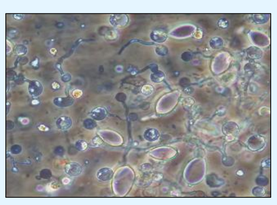
Yordan MUHOVSKI, Aurore ANTOINE, Emmanuelle GONZALEZ & Sergio MAURO

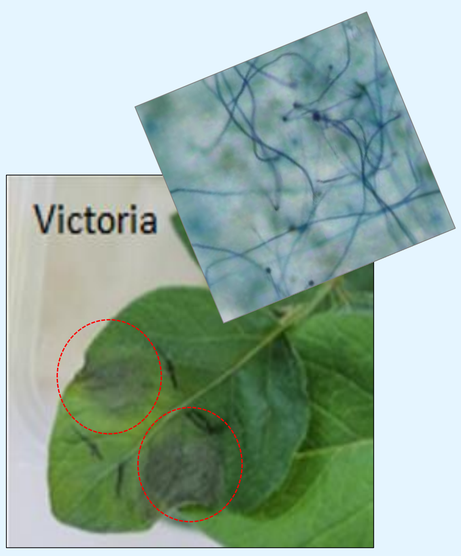
Bioengineering unit, Department of Life Sciences, Walloon Agricultural Research Centre, 5030 Gembloux, Belgium

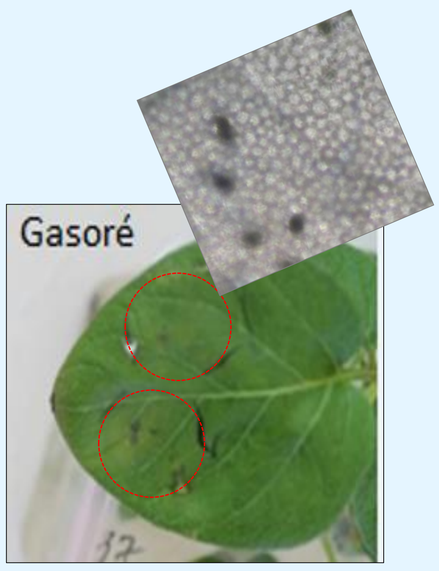
Context: Potato (*Solanum tuberosum* L.) is the third most important food crop and frequently is subjected to the negative impact of various biotic and abiotic challenges (pathogens, inappropriate fertilization...). Late blight caused by the oomycete *Phytophthora infestans* is among the most devastating potato diseases and often 15 to 18 fungicide treatments per growing season are needed. Therefore, using more resistant varieties is more practical way to control the disease. Another point is the loss of nitrate-nitrogen due to leaching from the bottom of the crop root zone which is a serious environmental issue worldwide, so developing of potato cultivars which utilize N more efficiently is a long-term alternative in reducing such a loss. Combining these two major biotic and abiotic issues and a whole transcriptome analysis by *RNA-seq,* we try to depict mechanisms for resistance/sensitivity and better N utilization in potato genotypes. The below present data are part from project "FIRST" developed at CRA-W.

Experimental design set-up and sampling:







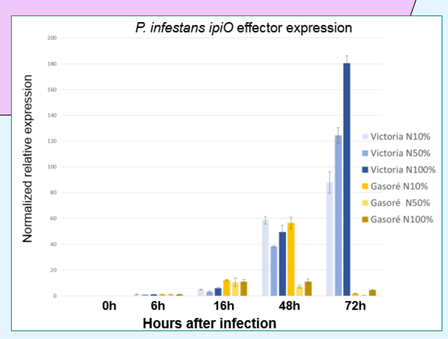


Plant material: Hydroponics potato culture; cultivars Victoria & Gasoré, sensitive and resistant to late blight, respectively, grown on Hoagland solution with low (10 %), medium (50%) & high (100%) nitrate content.

Pathogen and « O-ring plant infection »: *P. infestans 37_A2* zoospores culture; the infectious solution was deposited onto adaxial leaf surface inside a rubber ring in order to depict precisely the infected plant area; the plants were kept at 90% humidity, 18°C, 16/8 light-dark.

***P. infestans* infection monitoring by: i)** trypan blue staining and **ii)** qPT-PCR expression of pathogen growth specific marker genes (ex. biotrophic *ipiO)*.

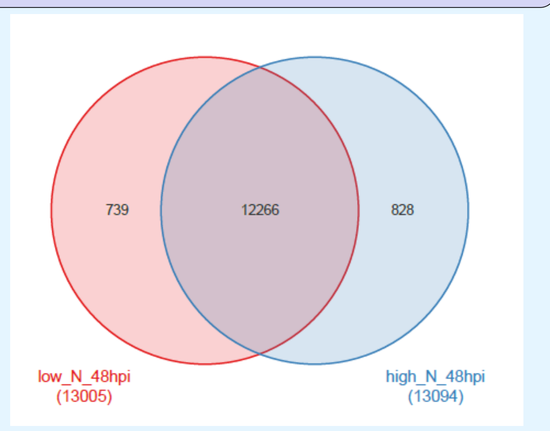
- **Sampling**: 0, 6, 16, 48 & 72 hours after infection (hpi).



RNA-seq analysis:

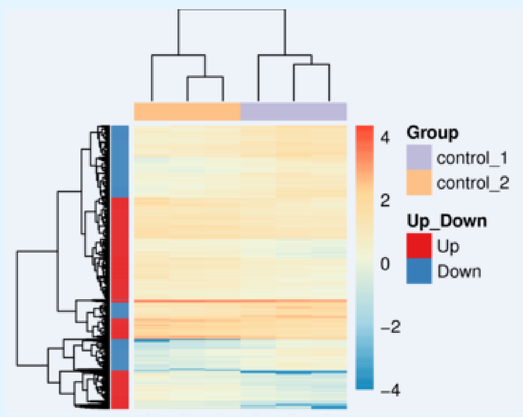
- Total RNA was extracted from cv. Victoria (control and infected, 48hpi) plants grown on high and low N.
- 60M reads per sample were achieved (2x100 PE, HiSeq4000, Illumina platform).
- Bioinformatics and DEG identification.

***P. infestans* expressed genes in *cv*. Victoria grown at low / high NO_3^- after 48hpi**

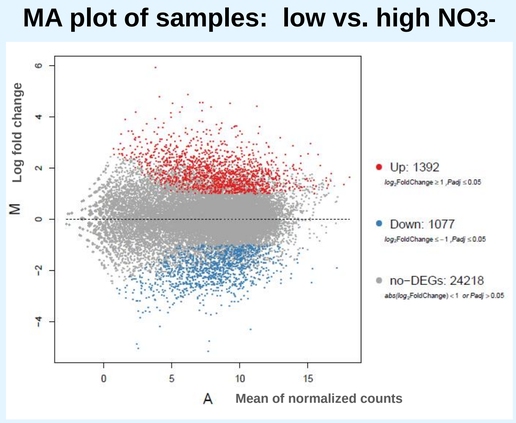


Example for differences in gene expression between samples:
- Low N/48hpi - 26 RxLR /10 Crinkler (CRN) effectors
- High N/48hpi - 18 RxLR/ 7 CRN
- High/Low N - share 204 RxLR/ 152 CRN common transcripts

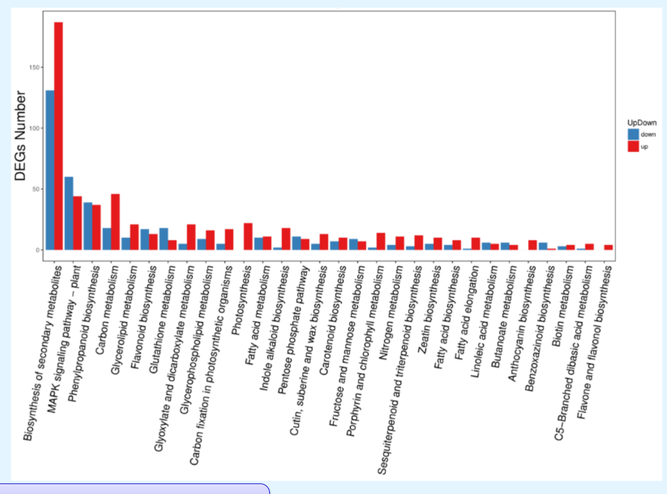
Heatmap for DEG in *cv*. Victoria grown at low (control_1) / high (control_2) NO_3^-



MA plot of samples: low vs. high NO_3^-



DEGs number of the most enriched pathways: low vs. high NO_3^-



Conclusions & Perspectives

RNA-seq transcriptomic study on potato x *P. infestans* x nitrogen interactions allowed us to identify DEG in samples grown on contrasted NO_3^- supply and collected after 48 hpi followed by their association to different metabolic pathways according GO.
More complex time-resolved *RNA-seq* profiling of the infection process on 2 potato genotypes and 3 doses of nitrate is ongoing.