

Comparative proteomic analysis of potato (*Solanum tuberosum* L.) cultivars grown in hydroponics and subjected to different doses of nitrate

Yordan Muhovski¹, Didier Vertommen², Sébastien Pyrot Ruys², Sergio Mauro¹

¹Bioengineering unit, Department of Life Sciences, Walloon Agricultural Research Centre, 5030 Gembloux, Belgium

²Université catholique de Louvain/ de Duve Institute, 1200 Brussels, Belgium

E-mail: y.muhovski@cra.wallonie.be

Context: Potato (*Solanum tuberosum* L.) is the third most important food crop after wheat and rice and as each plant, it is not immunized against the negative impact of various abiotic challenges with over fertilization being one of them. Nitrogen (N) is a vital nutrient and the nitrogen use efficiency (NUE) linked to N is a crucial parameter for growth and development often neglected in potato varietal selection. Excessive loss of nitrate from potato root zone is a serious environmental issue worldwide, therefore, lowering fertilizer input and using varieties with better NUE is more practical way regarding ecology and economy in order to control the nitrogen utilization.

Objective: The objective of the present study was a preliminary characterization of two contrasting potato genotypes and their reaction to different nitrate doses using proteomic approach.

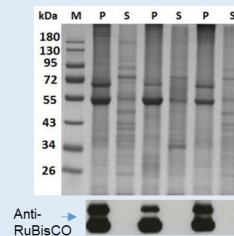
Experimental design set-up, sampling, protein extraction / RuBisCO depletion:



Leaf sampling after 5 weeks



Protein extraction and RuBisCO depletion with 0,1% Protamine sulfate (PS)



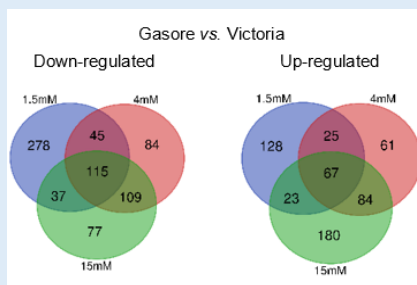
RuBisCO depletion: P- precipitated proteins by PS; S- supernatant enriched with low-abundant proteins; Western blot with Anti-RuBisCO

Mass-spectrometry analysis and label-free quantification

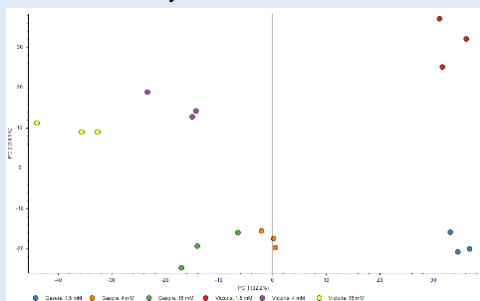
Plant material: potato varieties (Victoria, high NUE; Gasore, low NUE) grown in hydroponics on Hoagland solution with low (1,5mM), medium (4mM) and high (15mM) nitrate content.

Preliminary results:

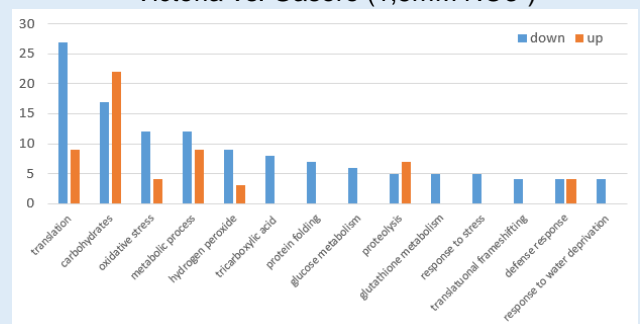
Down- and up-reguated proteins between cultivars and NO₃- treatments



PCA analysis of Victoria/ Gasore



DEPs number of the most enriched pathways: Victoria vs. Gasore (1,5mM NO₃-)



Conclusion: Preliminary proteomic study on potato cultivars with contrasting NUE grown on different doses of NO₃- allowed us to identify cohort of DEPs associated to different metabolic pathways according GO terms. Using protamine sulfate depletion led to identification of low abundant proteins masked by RuBisCO abundance. More in depth characterization of the selected DEPs is on the way.