Proceedings of the LXV SIGA Annual Congress
Piacenza, 6/9 September, 2022
ISBN: **978-88-944843-3-5**

Oral Communication Abstract – 2.03

ARBUSCULAR SYMBIOSIS IN SOILLESS CULTURE: TRANSCRIPTOMIC AND BIOCHEMICAL ANALYSES IN LACTUCA SATIVA PLANTS.

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lettuce, symbiosis, transcriptomic, biofertilisier, soilless culture

Lettuce (*Lactuca sativa* L.) is an annual autogamous diploid plant belonging to Asteraceae and amongst the top ten most profitable crop worldwide due to its nutritional value. Nevertheless, extensive cultivation of lettuce has led to major problematics, especially in fertiliser exploitation both in soil and extra soil system, which represents a damage to the ecosystem and has an increasing cost for the farmer and the final consumer. In this context, arbuscular mycorrhizal (AM) fungi could help to reduce the impact of fertilisers improving plant nutrition, in particular for phosphorus (P) and nitrogen, contributing to grow healthier plants for human consumption. In our work, we compared lettuce plants (cv. Salinas) grown in soilless culture (peat-filled pots with subirrigation) with optimal P (phosphate) concentration (1 Mm) in the nutrient solution (+P/-AM), with under optimal phosphate nutrition (-P/-AM) and, finally, with plants grown with lower P concentration (0.5 Mm) and inoculated with the AM fungus *Funneliformis mossae* before transplanting (-P/+AM). Gene expression profile was analysed in both roots and leaves, and transcriptomic values were associated with physiological and biochemical parameters determined at the end of the experiments. Overall, in comparison with -P/-AM plants, 3,057 genes were differentially regulated by mycorrhizal symbiosis (1,505 in roots and 1,552 in leaves) and 2,606 genes were induced by optimal phosphate nutrition (926 in roots and 1,680 in leaves). Interestingly, the pattern of differentially expressed genes showed major differences for -P/+AM plants, and suggested an extensive regulation of genes related to photosynthesis, solute transport (phosphate, nitrogen and sugar), metabolism of phytohormones (gibberellin, auxin), redox homeostasis, and transcriptional regulation (MYB, GRAS, WRKY, DELLA). Concerning metabolic pathways, -P/+AM plants

exhibited the activation of genes involved into production of phenylpropanoids, carotenoids, and vitamins, whereas starch and sucrose metabolism was similar in these plants and in the +P/-AM plants. These data are coherent with the results of physiological and biochemical analyses (i.e. leaf area, dry biomass accumulation, leaf content of chlorophylls, total phenols and carotenoids). Finally, co-expression analysis allowed to find a possible network, formed by 19 genes, which could explain the greater growth rate observed in -P/+AM plants as compared with +P/-AM plants. In conclusion, transcriptomic, physiological and biochemical data suggest a possible exploitation of AM symbionts as biofertilisers for lettuce soilless cultivation with beneficial effects on both plant growth and leaf content of health promoting phytochemicals.