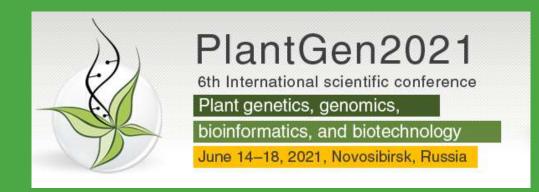
Investigation of SWEET family sugar transporter genes and their role in arbuscular mycorrhiza



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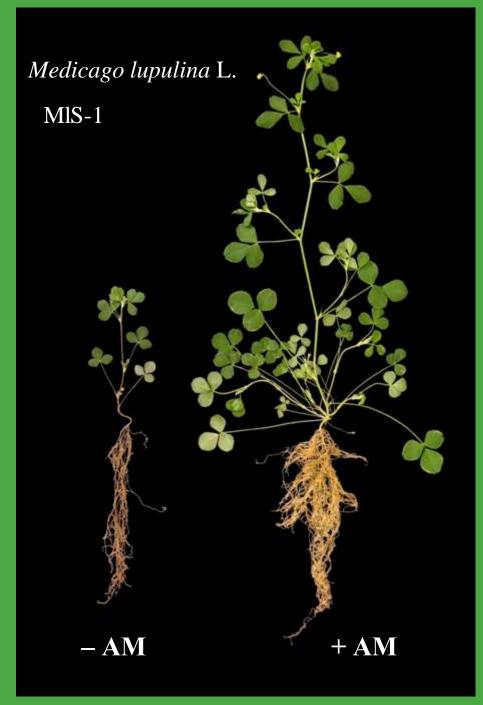


Most of the land plants form symbiosis with arbuscular mycorrhiza (AM) fungi. These fungi help plants to absorb minerals, especially phosphorus, and receive from plants products of photosynthesis, carbohydrates. AM contributes to a significant increase in plant growth and their adaptation to both biotic and abiotic environmental stress factors, such as pathogenic bacteria and fungi, pollutants in soil, air and water.

In this regard, <u>the study of the mechanisms</u> <u>controlling the formation of effective AM is</u> <u>one of the urgent problem in fundamental</u> <u>and applied biology.</u>

We have previously developed a unique model system "plant-host - AMF".

The system includes the highly responsive to inoculation with AMF an obligatory mycotrophic plant Medicago lupulina line MIS-1, and the highly effective AMF strain Rhizophagus irregularis RCAM00320.



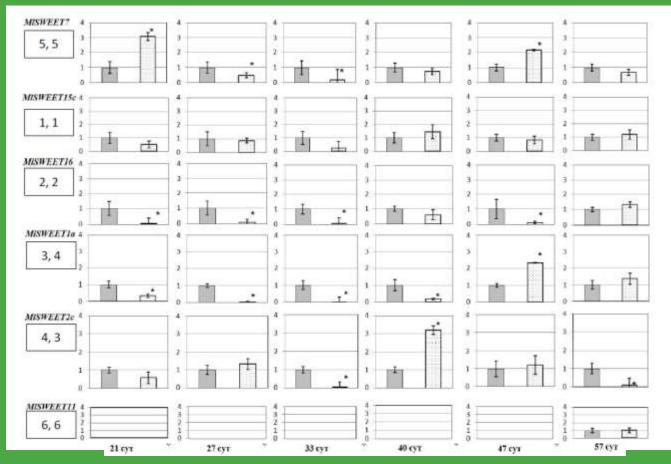
<u>The aim</u> of the study is to assess the expression levels of genes of the SWEET family transporters (possibly a key family among others) in Medicago lupulina, levels symbiotic efficacy and activity in the development of arbuscular mycorrhiza, formed by Medicago lupulina c Rhizophagus irregularis in conditions of different levels phosphorus available for plant nutrition in the substrate.

Methods include:

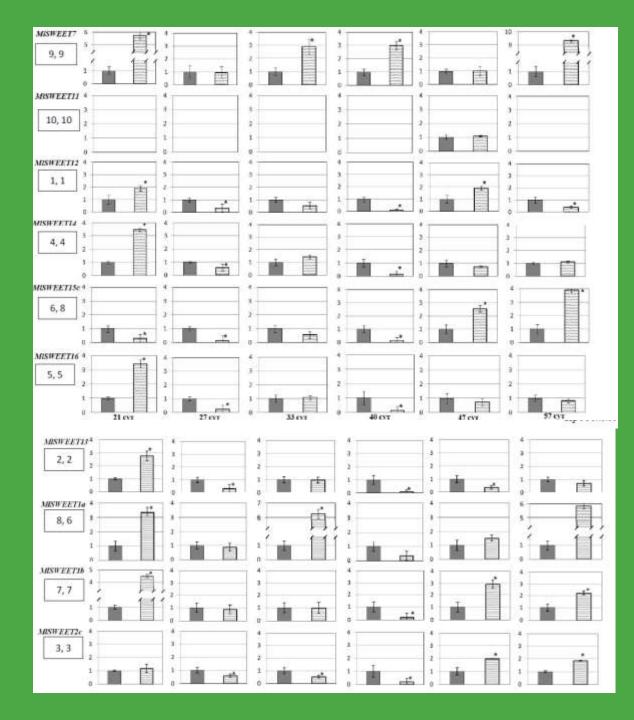
- Growing AM and non AM plants at varying soil phosphorus levels
 (low level in 2020, medium level in 2021 and high level in 2022)
- 2. Isolation of RNA from plant material
- 3. Assessment of the expression of SWEET genes in different phases of the plant life cycle

SWEET1a-2F	TGAAAAATTCTCTGGTGTTCC
SWEET1a-2R	CACTTATTTTCAGCTTCTCC
SWEET1b-3F	TGCTTTGTTTCTCTTCTTAG
SWEET1b-1R	CCTGCTCCGGTGCCAT
SWEET2c-3F	GGAGTTCTTGGCATTTTTG
SWEET2c-3R	TTAGGAAGGTGGAAAGTGAG
SWEET7-1F	GGAGAAGAGCTTGGAGATA
SWEET7-1R	CTGGTGAGAATTGCTCCAC
SWEET11-3F	CAACATTTTACCGAATCTACAAG
SWEET11-3R	TGAGGAGAAGGAGTGTAGC
SWEET12-1F	ACTCGTGAATCTTGGGCTTTT
SWEET12-1R	TTAATGGTGATGAGAAGAAGAAGAG
SWEET13-3F	GTGGGATTTGGCACGATTG
SWEET13-3R	CACAACGTTCGGGAGAGTA
SWEET14-1F	TAGTTGGTATTCTAGGTAACATT
SWEET14-1R	TAGGTAAATTGTTTCTATCACAC
SWEET15c-1F	GCATGCTTGGTAACGTCATT
SWEET15c-1R	TCTCTACCACACATCCAAATG
SWEET16-1F	TCATGTTTCTTTCTCCTGTAC
SWEET16-1R	GGTGCATATATGAGAAATAGAAG
actin7-f	ACGTTTAGCAAAAGATGGCAG
actin7-r	TATGACGAGGTCGGCCAA

The relative level of transcripts of the genes MISWEET7, MISWEET15c, MISWEET16, MISWEET16, MISWEET1a, MISWEET2c, MISWEET2c, MISWEET11 in the **roots of plants** with AM versus plants without AM (gray bar)



The relative level of transcripts of the genes MISWEET7, MISWEET11, MISWEET12, MISWEET14, MISWEET15c, MISWEET16, MISWEET13, MISWEET1a, MISWEET1b, MISWEET2c in plant leaves with AM versus plants without AM (gray bar)



We studied the expression of 10 genes from the SWEET family during the formation of symbiosis between *M. lupulina* and *R. irregularis,* as well as mycorrhization, symbiotic efficiency and plant productivity. We accessed gene expression at different developmental phases of host plant under low phosphorus level in a substrate

The occurrence of mycorrhizal infection, intensity of mycorrhization, and the abundance of arbuscules in roots increased during plant development up to the inflorescence phase. A slight decrease in the abundance of arbuscules was observed on days 27 and 33 after planting, followed by an increase starting from a day 47. The roots/shoots ratio of *M. lupulina* was lower in mycorrhized plants than in plants without mycorrhiza. An inoculation of *M. lupulina* with the AMF increased the productivity of aboveground biomass and accelerated plant development under low phosphorus level.

Gene expression analysis suggests that genes MISWEET1a and MISWEET1b are candidates for specific expression in the leaves of the mycorrhized host plant, MISWEET1a and MISWEET2c are candidate genes for specific expression in the roots.

Further experiments under medium and high phosphorus levels can confirm or reject this hypothesis (with an increase in minerals available for nutrition in the soil, in particular phosphorus, the expression of specific genes may decrease). The study of plant-microbial systems will contribute to their practical implementation in the agriculture of the Russian Federation.

This work was supported by the RFBR 20-016-00245 and partially 19-29-05275.