

# Development of effective arbuscular mycorrhizal symbiosis: traits of plant and fungal selection

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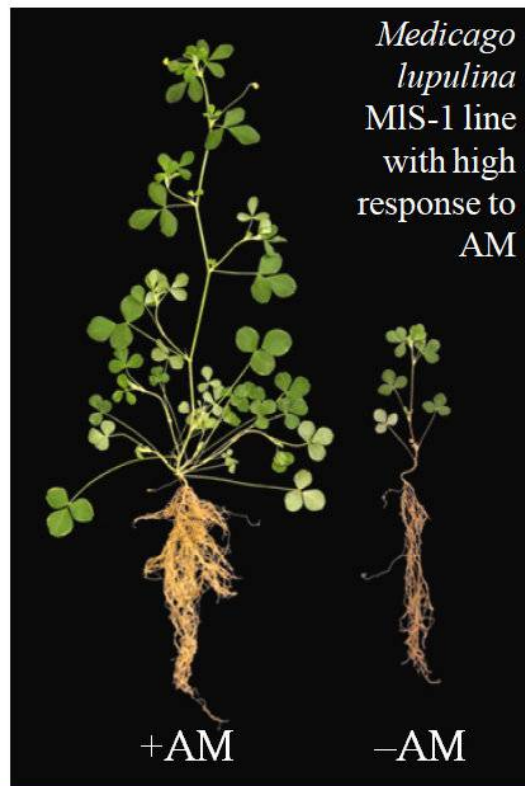
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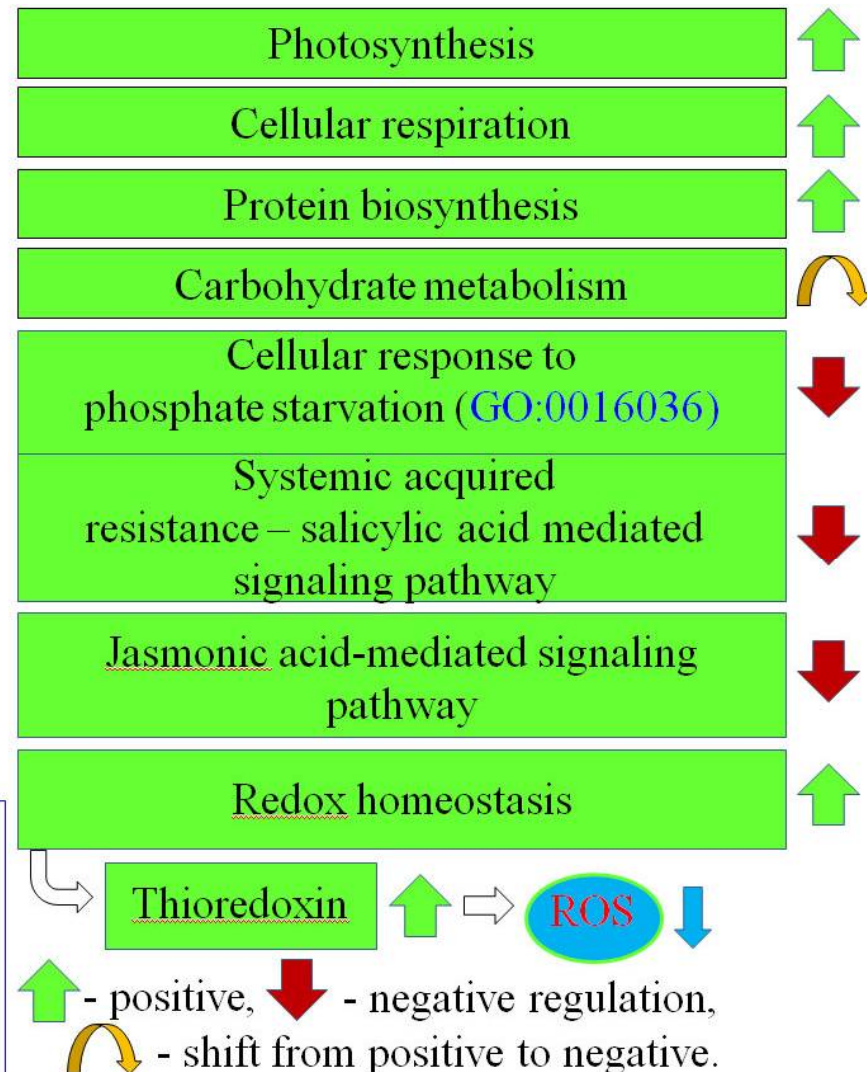
**Objective:** to develop a highly effective plant-microbial system “*Medicago lupulina* + *Rhizophagus irregularis*” based on the inoculation-responsive plant, MIS-1 line, and effective AM fungus, strain RCAM00320.

**Tasks:** 1) assessment of the mycorrhization effect on the metabolome and transcriptome of the host plant, identification of the main ways of developing effective AM; 2) creation of a collection of AM fungal strains to form effective PMS.

**Materials and methods:** A pot experiment was conducted in conditions of a low and optimal level of phosphorus available for plant nutrition. The effect of mycorrhization on the metabolome (GC-MS data analysis ) and transcriptome (Massive Analysis of cDNA Ends) of the host plant at the key stages of development was evaluated.

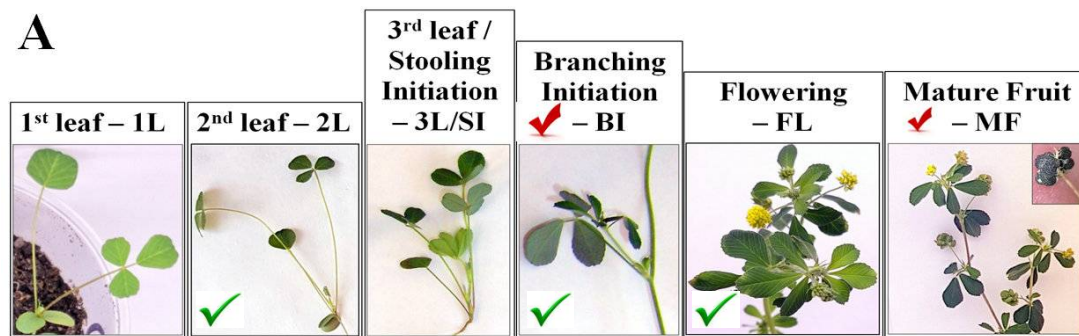


Self-pollinator, diploid ( $2n=16$ ),  
genome size ~1 Gb,  
high seed productivity  
up to 2500 seeds per plant,  
short life cycle (annual)





A



B + - positive and - negative regulation

		AM+P+ vs AM-P+						AM+P- vs AM-P+						AM-P- vs AM-P+					
		1L	2L	SI	BI	FL	MF	1L	2L	SI	BI	FL	MF	1L	2L	SI	BI	FL	MF
<b>Metabolic processes</b>																			
Aminoacyl-tRNA biosynthesis	Protein biosynthesis	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Biosynthesis of cofactors	Protein biosynthesis	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Valine, leucine and isoleucine biosynthesis	Protein biosynthesis	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Arginine biosynthesis	Protein biosynthesis	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Biosynthesis of amino acids	Protein biosynthesis	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Phenylalanine, tyrosine and tryptophan biosynthesis	Protein biosynthesis	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
beta-Alanine metabolism	Protein biosynthesis	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Alanine, aspartate and glutamate metabolism	Protein biosynthesis	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Cyanoamino acid metabolism	Protein biosynthesis	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Starch and sucrose metabolism	Carbohydrate metabolism	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Galactose metabolism	Carbohydrate metabolism	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Fructose and mannose metabolism	Carbohydrate metabolism	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Glycerolipid metabolism	Lipid metabolism	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Glycerophospholipid metabolism	Lipid metabolism	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Fatty acid metabolism	Lipid metabolism	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Biosynthesis of terpenoids and steroids	Lipid metabolism	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Glycolysis / Gluconeogenesis	Energy exchange	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Pyruvate metabolism	Energy exchange	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Pantothenate and CoA biosynthesis	Energy exchange	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Citrate cycle (TCA cycle)	Energy exchange	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Glucosinolate biosynthesis	Protective reactions	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Glutathione metabolism	Protective reactions	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Glyoxylate and dicarboxylate metabolism	Protective reactions	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
<b>Metabolites</b>																			
hexose_RI=1881	Carbohydrate metabolism	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
compstug_RI=3273	Carbohydrate metabolism	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Trehalose	Carbohydrate metabolism	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Glycerol	Lipid metabolism	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Glycerol-3P	Lipid metabolism	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Ethanolaminephosphate	Lipid metabolism	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Campesterol	Lipid metabolism	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
sterol_RI=3260	Lipid metabolism	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
sterol_RI=3362	Lipid metabolism	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
myo-Inositol-2P	Lipid metabolism	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Methyl phosphate	Energy exchange	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Phosphoric acid	Energy exchange	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Citric acid (citrate) content in TCA cycle	Energy exchange	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+
Succinic acid (succinate) content in TCA cycle	Energy exchange	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+

## Conclusions:

The effective plant-microbial model system “*Medicago lupulina* + *Rhizaphagus irregularis*” has been developed.

The main groups of genes and metabolites involved in the development of effective AM symbiosis have been identified.

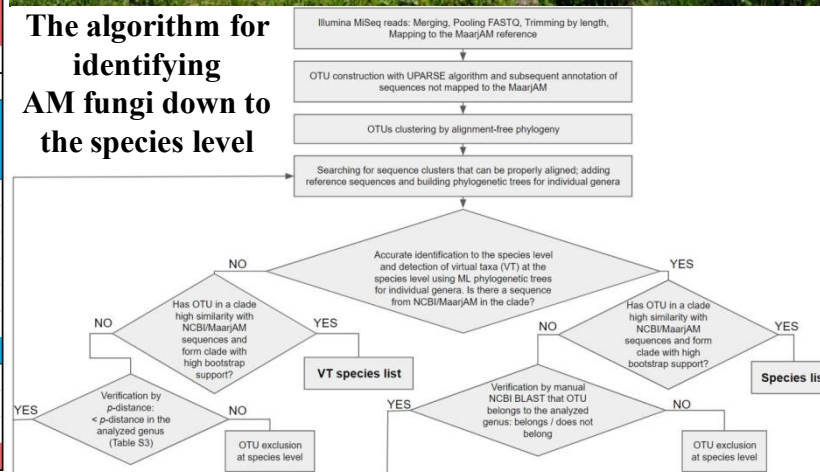
**The first identified Russian center of diversity of arbuscular mycorrhiza fungi (hotspot of AM fungi), the valley of the Teberda River**



43°25'12.0" N  
41°43'45.0" E  
1342 M H.Y.M.

Yurkov et al., J. Fungi, 2024  
DOI: 10.3390/jof10010011

## The algorithm for identifying AM fungi down to the species level





# Thank you for your attention!

## Acknowledgements and funding:

We thank R.K. Puzanskiy, candidate of biology, researcher of the Laboratory of Phytochemistry (BIN RAS), A.L. Shavarda, candidate of biology, head of the Laboratory of Phytochemistry (BIN RAS), E.M. Bogdanova, PhD student (BIN RAS) for invaluable assistance in metabolic research. We thank M.F. Shishova, doctor of biology, professor of the Department of Plant Physiology and Biochemistry (St. Petersburg State University), A.V. Rodionov, doctor of biology, professor, chief researcher, head of the Laboratory of Biosystematics and Cytology (BIN RAS) for a fruitful discussion of the results. The work was carried out using the equipment of the Central Collective Use Center “Genomic Technologies, Proteomics and Cell Biology” (ARRIAM) with the support of the grant of the Russian Science Foundation 22-16-00064-π.



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**2025**