

Metabolic alterations in pea leaves and roots during arbuscular mycorrhiza development

P-07.4-21

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For the proper use of arbuscular mycorrhizal (AM) symbiosis in agriculture, a detailed understanding of the molecular basis of the plant developmental response to mycorrhization is needed. Information for pea (*Pisum sativum* L.) is scarce and its biochemical aspects need further study. Using GC-MS, we analyzed metabolic alterations in pea leaves (previously published in: Shtark OY et al. (2019) PeerJ 7, e7495) and roots (unpublished) associated with root colonization by *Rhizophagus irregularis*. Plants were analyzed at three time points, which corresponded to key developmental stages of the pea – I: first leaf with two pairs of leaflets and a complex tendril; II: the first open flower; and III: when the pod is filled with green seeds. Both the leaf and root metabolic profiles showed a strong correlation with plant age, and, to a lesser extent, was influenced by mycorrhization. Metabolic shifts influenced the levels of sugars, amino acids and other intermediates of nitrogen and phosphorus metabolism, and lipophilic compounds. Significant differences were revealed between the metabolic profiles of roots and leaves, as well as between those of individual organs at distinct time points. Particularly, in the roots of AM plants at stage II (characterized by the most intensive AM development) higher levels of fatty acids in comparison to roots of both the control plants and the AM plants at other stages were observed. At stages II and III, both the leaf and root metabolic profiles of AM plants shifted towards the profiles of the control plants at earlier developmental stages. Thus, mycorrhization led to the retardation of plant development, which was also associated with an extended vegetation period. This effect promises to be beneficial for agriculture, especially for the green pea cultivars which are harvested before seed maturation. This work is supported by the grants of RSF (20-16-00107) and RFBR (20-04-01136).

* The authors marked with an asterisk equally contributed to the work.