

## PRIMARY AND SECONDARY METABOLITES PROFILING IN AN INTERSPECIFIC APPLE GERMPLASM COLLECTION

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Food security and climate change are leading topics in genetic analysis and breeding

programs, and require continuous innovation and research. In particular, the re-introduction of

resistant, resilient and health-promoting traits, especially in apples, is highly desirable, as

domesticated varieties are often susceptible to diseases and poorly adapted to climate

variations. To this end, wild accessions offer a valuable alternative for the introgression of

potential traits absent in domesticated varieties. However, these wild accessions are not yet

comprehensively characterized both phenotypically and genetically. The present study aims to

investigate the concentration of specific classes of primary and secondary

metabolites in

different apple species, comparing the phytochemical profile of domesticated and wild apples.

These metabolites, potentially characterized by health promoting properties and associated

with pathogen resistance and resilience to adverse weather conditions, could be further

considered for the future improvement of susceptible varieties.

In this study, a pool of 208 apple accessions was selected, to equally represent

different *malus spp.* In total, 60 species were considered, with *M. domestica* being the most

representative (23.1% of the total), followed by *M. sieversii* (14.9%), *M. sylvestris* and

*orientalis* (both at 3.9%). Pulp and skin were analyzed as separate tissues for the

determination of secondary metabolites. Volatile organic compounds (VOCs) were

investigated using PTR-ToF-MS, while polyphenolic compounds were analyzed using UPLC-

MS/MS. Primary metabolites, such as sugars, organic acids and amino acids, were instead

assessed only on the pulp tissue with NMR spectroscopy.

The data obtained from the various metabolite analysis will be analysed using several

multivariate statistical approaches, to exploit the metabolic variability existing in this

interspecific germplasm collection focusing, moreover, on the two distinct types of tissues.

The present work could help to investigate the variability of important traits of interest

in apples, assessed in a large germplasm collection. This characterization will enable the

identification of the most favorable candidates to be employed in genetic programs oriented

to ameliorate apple performance, addressing the growing challenges of food security and

climate change.