

Metabolite profiling and quantitative genetics of natural variation for flavonoids in Arabidopsis.

Seeds

CASE STUDY

Routaboul, J.-M.; Dubos, C.; Beck, G.; Marquis, C.; Bidzinski, P.; Loudet, O.; Lepiniec, L. *Journal of Experimental Botany*. 2012, 63.

Overview

- **Keywords:** Arabidopsis, flavonoids, metabolite profiling, natural variation, quantitative trait loci
- **Aim of the study:** Identification of genes controlling flavonoid metabolism
- **Application:** Flavonoid extraction and analysis by LC-MS
- **Sample:** Arabidopsis
- **Sample type:** Seeds
- **Material:** FastPrep-24™ instrument
- **Buffer:** Acetonitrile/Water (3/1; v/v) or Methanol/Acetone/Water/Trifluoroacetic acid (30/42/28/0.05; v/v/v/v)

Protocol and Parameters

1. Three representative seed aliquots from three biological replicates were pooled before flavonoid extraction.
2. All seed samples were ground for 90 seconds at maximum speed with a FastPrep-24™ instrument in 1 mL of solvent mixes.
3. A 4 µg aliquot of apigenin was added as an internal standard.
4. Following centrifugation, the pellet was extracted further with 1 mL of the same solvent mixes overnight at 4°C.

Conclusion

The use of FastPrep-24™ system achieved full homogenization of seeds, allowing flavonoid extraction, quantification and complete analysis of their metabolism by LC-MS method.

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