Network analysis of the metabolome and transcriptome reveals novel regulation of potato pigmentation.

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Overview

- **Keywords:** Anthocyanin, metabolomics, colored potato, RNA-seq, ultrapressure liquid chromatography quadrupole time-of-flight mass spectrometry (UPLC-Q-TOF-MS)
- **Aim of the study:** Understanding of regulatory networks related to anthocyanin biosynthesis and identification of key regulatory genes
- **Application:** UPLC-Q-TOF-MS, RNA sequencing
- **Sample type:** Three potato cultivars (light-red Hongyoung, dark-purple Jayoung and white Atlantic)
- **Material:** FastPrep-24™ instrument

Protocol and Parameters

1. 200 mg of frozen potato sprouts were ground in the FastPrep-24™ instrument
2. Samples has been processed 3 times at speed of 4.5m/s for 25 sec
3. Mixed sprouts were suspended in 600 µL methanol and a 0.125% formic acid solution
4. The solution was kept at 4 °C for 30 min and then sonicated at 4 °C for 20 sec by using three repetitions at 20kHz and 250W
5. The solution was then centrifuged at 3000 rpm for 15 min at 4 °C
6. The supernatant solution was centrifuged during 10 min at 13 000 rpm and at 4 °C

Conclusion

FastPrep® is the technology of choice for metabolites extraction and characterization. In the present work, metabolites were successfully extracted from potato samples allowing their profiling.

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