

Case study - Potato

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

Kyoungwon Cho, Kwang-Soo Cho, Hwang-Bae Sohn, In Jin Ha, Su-Young Hong, Hyerim Lee, Young-Mi Kim and Myung Hee

Journal of Experimental Botany. 2016. Vol. 67.

Overview

- **Keywords:** Anthocyanin, metabolomics, colored potato, RNA-seq, ultrahigh pressure 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.

Successful sample preparation using the MP Biomedicals FastPrep® product line has been highlighted in thousands of scientific articles. To access articles and other materials, visit www.mpbio.com/FastPrepLibrary.

www.mpbio.com

