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What about dried blood spot for cannabinoid quantification?

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While there has been a growing interest in understanding the pharmacological and physiological properties of cannabinoids in the last decades, analytical methodologies including sample preparations, remain one of the most challenging topics for their quantification in biological matrices. Moreover, the low sample weight or volume coupled to the complexity of biological samples (i.e. whole blood, plasma, etc.) could overwhelm the analyst expectations.

In this study, we explored different possibilities to quantify a mixture of 8 natural phytocannabinoids present in biological samples (cannabinol, cannabigerolic acid, cannabinochromene, cannabigerol, cannbidiolic acid, tetrahydrocanninol, tetratracannabinolic acid and cannabidiol).

The evaluation was carried-out using plasma and whole blood samples using different usual extraction protocols (solid phase extraction, liquid-liquid extraction, protein precipitation and blood spot sampling). Stability of tested molecules was also evaluated in several matrices (plasma, serum, *ex vivo* and pharmacokinetic profiles).

The results showed a moderate matrix effect resulting by signal suppression (≤30%) and acceptable recoveries (≥60%) for most of the different tested extractions and matrices, except for whole blood when using acetonitrile for protein precipitation, which appears to be the less efficient approach for cannabinoid extraction, with a recovery lower than ≤40%.

The applicability of tested methodologies was also applied for the determination of pharmacokinetic profiles and showed that dried blood spot sampling (DBS) could become an interesting alternative for *in vivo* studies. DBS is a rapid, acute and minimally invasive technic based on a single blood drop (10µL–25µL) that reduces handling and quantity of blood to be sampled, which consequently also reduces the cost of analysis. According to these aspects, DBS could become a reference methodology for *in vivo* pharmacokinetic experiments.

Biography

Lounès Haroune is manager of the bioanalytical platform of the pharmacology institute of Sherbrooke University. After 5 years as analytical development manager in an analytical laboratory and graduated in analytical chemistry, he is working on the development of analytical methodology and sample preparations for the detection and quantification of biomolecules in biological matrices. He also works on the metabolomics and peptidomics methodologies in complex matrices. He also focuses on the development and implementation of new analytical workflow for molecular characterizations (biocatalysis, physico-chemistry reaction, etc).

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