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PP2. Cannabis terpene profiling in therapeutic products by means of gas chromatography coupled with mass spectrometry

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It is well-known that cannabinoids provide non-toxic medical benefits and have an effective role in the treatment of chronic pain due to their interaction with the endocannabinoid system. Recently, in addition to the "classical" therapeutic usage, like inhalation or ingestion of cannabis, newer ways of cannabinoid-based products utilization are also being developed. The skin application of topicals including balms, lotions, and oils that are infused with active cannabinoids is a minimally invasive method for the medical cannabis use and allows them to be absorbed directly into the affected area for faster and more focused relief.

According to the terpene profile, the medicinal effect of cannabinoids can change significantly. Terpenes, in fact, have various roles: can make the adsorption of cannabinoids faster, or lessen their effect, interact with cannabinoids, decrease the side-effects of the cannabinoid therapy, and help to relax and calm the patient.

Gas chromatography-mass spectrometric (GC-MS) analysis is a powerful analytical tool for detailed characterization of the volatile fractions of any kind of complex sample. For the identification, mass spectral databases are used, but in many cases, misidentification could occur due to the high spectral similarity of terpenes. The Linear Retention Index (LRI) approach combined with conventional mass spectral search provide a more reliable solution for peak assignment. The FFNSC 4.0 (Flavour and Fragrance Natural and Synthetic Compounds), a dedicated MS Library with embedded LRI information, including almost all of the 140 known cannabis terpenes can be a great support in terpene profiling, thereby also in the optimization of the therapy.

Aroma constituents of cannabinoid-containing medicinal products were analyzed by GC-MS. To obtain the characteristic volatile fraction, sample preparation method was optimized for each sample type. Terpenes were identified using FFNSC 4.0 database.

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