P.O. Box 144345 Austin, TX 78714-4345 ▪ 512.926.4900 ▪ Fax: 512.926.2345 ▪ www.herbalgram.org

HerbClip™

File: ■ Maca (*Lepidium meyenii*, Brassicaceae)
■ Flow Injection Mass Spectrometry
■ Metabolite Profiling

HC 082052-650

Date: October 15, 2020

RE: Chemical Composition of Maca Powder Varies when Grown in Different Regions

Geng P, Sun J, Chen P, et al. Characterization of maca (*Lepidium meyenii/Lepidium peruvianum*) using a mass spectral fingerprinting, metabolomic analysis, and genetic sequencing approach. *Planta Med*. July 2020;86(10):674-685. doi: 10.1055/a-1161-0372.

Maca (*Lepidium meyenii* syn. *Lepidium peruvianum*, Brassicaceae) tuber is historically grown in the Andes mountains in Puna, Peru at elevations of 3500 to 4500 meters. The native habitat in Puna has intense sunlight, extremely low temperatures, fierce wind, low humidity, and a large diurnal temperature range. These harsh conditions contribute to Maca's chemical composition; its secondary metabolites are believed to contribute to its health benefits. The root has color variations (black, purple, red, and yellow), which are believed to be genetically and phenotypically distinct; however, the relationship between color and secondary metabolites remains inconclusive. Due to its rise in popularity, maca root is now cultivated outside of Puna. Maca grown in lower altitudes (i.e., Prague, Czech Republic and Western China) contain levels of macamides and alkaloids that are different from maca grown in Puna.

Genomics and metabolomics are useful for the taxonomy, identification, and characterization of plant material. Genomics is the description of plant genome to provide identification when taxonomic identification is not possible (i.e., for powdered materials). Metabolomics is used to authenticate botanicals via a comprehensive description of the molecules. Non-targeted metabolite profiling provides a comprehensive profile rather than just looking for individual compounds (targeted metabolite profiling). According to the authors, only targeted metabolite profiling has been conducted on maca. The purpose of this in vitro study was to conduct a non-targeted metabolite profile of maca obtained from various regions.

Seventy-one maca samples were obtained including processed commercial botanical supplements, unprocessed raw tubers collected from farms and markets in Peru and China, and one historic wild-grown non-tuber sample from Peru. Samples were from yellow, purple, black, and red maca. All tubers were ground into powder. The samples

were analyzed via flow injection mass spectrometry (FIMS) to obtain spectral fingerprints. Ultra-high-performance liquid chromatography-high resolution accurate mass/tandem mass spectrometry (UHPLC-HRAM/MS) was used for metabolic profiling. Genetic sequencing at common plant barcoding regions was conducted. Compounds identified on metabolic profiling were used to identify ions in the spectral fingerprints. Variations between country of origin and color were examined and compared with metabolic composition.

Analysis of technical replication indicated that there was minimal variance between replications (each sample was analyzed multiple times); this demonstrates the stability and reproducibility of the results. Samples fell into three clusters based on country of origin and processing. Country of origin was the largest source of variance, followed by color. Similarly, colored tubers had different compositions based on country of origin. The historic sample was distinguishable from the tubers because it contained leaves, stems, and non-tuber roots. Sixty-seven compounds were identified in the negative ionization mode, and 51 compounds were identified in the positive ionization mode. There were no unique marker compounds identified. The same compounds were observed in all colors/origin combinations but the patterns were unique.

Metabolite profiling revealed that composition of organic acids, saccharides, amino acids, imidazole alkaloids, glucosinolates, and macamides can play a role in distinguishing the samples. The Chinese maca had higher levels of glucosinolates, while the Peruvian maca had higher levels of imidazole alkaloids. According to the authors, this emphasizes the need for FIMS fingerprinting and demonstrates the value of non-targeted analysis. Genetic sequencing revealed that all of the maca samples evaluated were closer to *L. Meyenii* than to other *Lepidium* species. However, the extent of the genetic variation between maca from Peru and China, between tubers of different colors, and between cultivated and historic maca need further examination.

The authors conclude that the commercial maca supplements, unprocessed raw tubers from Peru and China, and the historic wild-grown non-tuber sample have statistically different chemical compositions, with origin exceeding color as the source of variance. Patterns are necessary for differentiation. A limitation of the analysis is that harvest stage, drying process, and storage time were not taken into account. The authors declare no conflicts of interest.

—Heather S. Oliff, PhD

Referenced article reprinted with permission from Georg Thieme Verlag.