Autentication of *Matricaria recutita* and *Camellia sinensis* herbal products using DNA-Barcoding and UHPLC-MS

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INTRODUCTION

Tea (*Camellia sinensis* (L.) Kuntze) and chamomile (*Matricaria recutita* L.) are medicinal plants with numerous therapeutic properties. They are also two of the most popular herbal teas worldwide. As the market for medicinal plants has grown, the occurrence of contamination, adulteration or counterfeiting has also increased, causing increased concern about safety, efficacy and quality of herbal products.

MATERIAL AND METHODS

Plant Material.- A total of 17 plant samples (9 flowers of *Matricaria recutita* and 8 leaves of *Camellia sinensis*) obtained from pharmacies, herbalists and supermarkets were analysed. **The DNA extraction** kit Speed Tools Biotools Biotechnological & Medical Laboratories was used. The matK gene was chosen in this study. The primers used were MatK-1RKIM-f and MatK-3FKIM-r. For **HPLC analysis** a phenomenex Gemini 5u C18 110A, 150x2mm column (Phenomenex, Alcobendas, Spain) was used. The gradient mode was 7 min 5%-95% Phase B; 8 min 95% Phase B; 8.5 min 5% Phase B using acetonitrile and in phase A 0.1% formic acid in water. The flow rate was 0.5 mL/min and the infection volume was 10 µL.

RESULTS AND DISCUSION

DNA barcoding analysis

DNA sequences were manually assembled and adjusted using the sequence alignment editor software BioEdit (v 7.2). A second editing and assembly of the sequence fragments was done with the SeqMan v.7 program (Lasergene R, DNASTAR, Madison, Wisconsin, USA). Sequence identity was assessed using the mega-BLAST search function in GenBank Each dataset was aligned using MAFFT v.7 implementing the G-INS-I alignment algorithm, scoring matrix '1PAM/K = 2' with an offset value of 0.0, and all other parameters set to default values. The identification of the samples was evaluated using the Barcode of Life Data System (BOLD Systems v3).

The results of the molecular phylogenetic and DNA barcoding analyses were largely congruent (Figure 1).

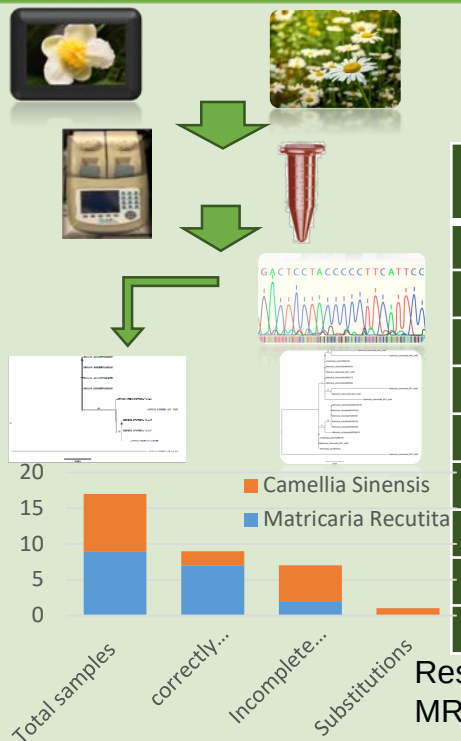

Figure 1

HPLC Analysis

The presence of the compounds apigenin-7-glucoside and epigallocatechin was identified in all study samples (Tables 1 and 2).

Sample	Apigenin-7-glucoside (%)
MH1	0.035
MH2	0.002
MH3	0.005
MS1	0.007
MS2	0.006
MS3	0.016
MF1	0.003
MF2	0.001
MF3	0.003

Table 1.

Sample	Epigallocatechin (%)
CH1	2.12
CH2	4.72
CH3	2.32
CS1	3.29
CS2	3.71
CF1	1.51
CF2	2.59
CF3	2.55

Table 2.

Results and UHPLC-SI-QqQ-MS/MS Chromatograms of qualitative and quantitative MRM-transitions of apigenin-7-glucoside and epigallocatechin present in the samples.