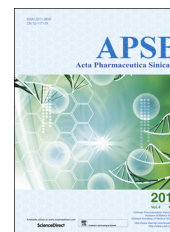




Chinese Pharmaceutical Association  
Institute of Materia Medica, Chinese Academy of Medical Sciences

Acta Pharmaceutica Sinica B

[www.elsevier.com/locate/apsb](http://www.elsevier.com/locate/apsb)  
[www.sciencedirect.com](http://www.sciencedirect.com)



ORIGINAL ARTICLE

## Commercialized non-*Camellia* tea: traditional function and molecular identification



Ping Long<sup>a,b</sup>, Zhanhu Cui<sup>a,b</sup>, Yingli Wang<sup>a,b</sup>, Chunhong Zhang<sup>b</sup>,  
Na Zhang<sup>b</sup>, Minhui Li<sup>a,b,\*</sup>, Peigen Xiao<sup>c,d,\*\*</sup>

<sup>a</sup>National Resource Center for Chinese Materia Medica, China Academy of Chinese Medical Sciences, Beijing 100700, China

<sup>b</sup>Baotou Medical College, Baotou 014060, China

<sup>c</sup>School of Chinese Pharmacy, Beijing University of Chinese Medicine, Beijing 100102, China

<sup>d</sup>Institute of Medicinal Plant Development, Chinese Academy of Medical Science, Peking Union Medical College, Beijing 100193, China

Received 10 November 2013; revised 16 December 2013; accepted 10 February 2014

### KEY WORDS

Non-*Camellia* tea;  
Traditional function;  
Molecular identification;  
BLASTN;  
Phylogenetic tree

**Abstract** Non-*Camellia* tea is a part of the colorful Chinese tea culture, and is also widely used as beverage and medicine in folk for disease prevention and treatment. In this study, 37 samples were collected, including 33 kinds of non-*Camellia* teas and 4 kinds of teas (*Camellia*). Traditional functions of non-*Camellia* teas were investigated. Furthermore, non-*Camellia* teas of original plants were characterized and identified by molecular methods. Four candidate regions (*rbcl*, *matK*, *ITS2*, *psbA-trnH*) were amplified by polymerase chain reaction. In addition, DNA barcodes were used for the first time to discriminate the commercial non-*Camellia* tea and their adulterants, and to evaluate their safety. This study showed that BLASTN and the relevant phylogenetic tree are efficient tools for identification of the commercial non-*Camellia* tea and their adulterants. However, some sequences from original plants have not been found and there is a limitation of sequence number of original plants in GenBank. Submitting more original plant sequences to the GenBank will be helpful for evaluating the safety of non-*Camellia* teas.

© 2014 Chinese Pharmaceutical Association and Institute of Materia Medica, Chinese Academy of Medical Sciences. Production and hosting by Elsevier B.V. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

\*Corresponding author at: Baotou Medical College, Baotou, Inner Mongolia 014060, China. Tel./fax: +86 472 7167 795.

\*\*Corresponding author at: School of Chinese Pharmacy, Beijing University of Chinese Medicine, Beijing 100102, China.

Tel.: +86 10 57833152; fax: +86 10 62899715.

E-mail addresses: [li\\_minhui@aliyun.com](mailto:li_minhui@aliyun.com) (Minhui Li); [xiaopg@public.bta.net.cn](mailto:xiaopg@public.bta.net.cn) (Peigen Xiao).

Peer review under responsibility of Institute of Materia Medica, Chinese Academy of Medical Sciences and Chinese Pharmaceutical Association.



Production and hosting by Elsevier

## 1. Introduction

Tea (the leaves from *Camellia* plants) has been one of the most widely consumed non-alcoholic beverages in the world for thousands of years. It plays important roles in commerce, health, and culture. However, many other kinds of plants have been widely used as tea as well. These are not from *Camellia* (Theaceae), and are called non-*Camellia* tea, such as kuding tea, huangqin tea, laoying tea<sup>1,2</sup>. More than 20 kinds of non-*Camellia* tea are reportedly used within the Chinese culture<sup>3</sup>. Modern pharmacology studies have reported that non-*Camellia* tea may prevent and/or treat chronic metabolic diseases, by producing hypolipidemic, hypoglycemic, or hypotensive actions. Moreover, most kinds of non-*Camellia* tea have also been used as medicine for disease prevention and treatment in folklore<sup>4–6</sup>.

In recent years, with the increasing international demand for herbal medicines, non-*Camellia* tea has attracted increasing attention. However, original plants of non-*Camellia* tea are confused, and some adulterants have begun to appear in the market. Furthermore, fatalities and serious illnesses have occurred after drinking non-*Camellia* teas, caused by overdose, mislabeled products, or allergic reactions<sup>7,8</sup>. For instance, kuding tea is suitable for high blood pressure, body fat or hot body, but not for the person whose body 'slants cold' in traditional Chinese medicine theory. According to this theory, a person whose body 'slants cold' will receive no improvement from ingestion of kuding tea and symptoms may appear or worsen, including abdominal pain, severe diarrhea and other symptoms<sup>9</sup>. The significant differences in chemical components among different kinds of the original plants could account for such variations in responses. Finally, undefined compounds in some of these teas may be dangerous to health.

Identification of non-*Camellia* tea is difficult, partly due to a lack of unified standards. Traditionally, morphological features remain as the main basis of taxonomy<sup>10</sup>. However, many of these commercial products are dried and processed, rendering the authentication by morphological methods very difficult. When morphological characteristics are absent, a DNA barcoding technique can identify and detect species utilizing one or a few DNA fragments<sup>11</sup>. DNA barcoding technique is a supplement to traditional authentication method which has been able to solve some identification problems<sup>11–13</sup>. In this study, we randomly collected non-*Camellia* tea from the medicinal material market in China. Using DNA barcoding technique, the original plants from which the teas were derived were identified to (1) explore which DNA regions are better for the authentication of non-*Camellia* tea traditionally used by Chinese people and (2) evaluate their safety.

## 2. Materials and methods

### 2.1. Plant materials

We collected 37 commercialized tea samples, including 33 kinds of non-*Camellia* tea and 4 kinds of *Camellia* tea from 16 provinces (Yunnan, Sichuan, Guangxi, etc.) in China during 2012, and recorded the detailed information of these medicinal non-*Camellia* tea samples, including the local tea name, collecting location and time, and therapeutic effects (Table 1). All the samples were pressed and deposited at the Herbarium of the Institute of Medicinal Plant Development (IMPLAD).

### 2.2. DNA barcoding

Four candidate barcodes (*rbcL*, *matK*, *psbA-trnH* and ITS2) were selected based on previous barcoding studies<sup>71–73</sup>. We isolated the total genomic DNA from approximately 100 mg of dried powder from each sample using the cetyl trimethylammonium bromide method.<sup>74</sup> Extracted DNA was stored in sterile microcentrifuge tubes at  $-20^{\circ}\text{C}$ .

The selected regions were amplified by polymerase chain reaction (PCR) on a PCR system 9700 thermocycler (Gene Co., USA). DNA was amplified in 20  $\mu\text{L}$  of reaction mixtures containing 1 U ExTaq polymerase with 10  $\times$  ExTaq buffer (100 mmol/L pH 8.3 Tris-HCl, 500 mmol/L of KCl) (Takara, China), 1.25 mmol/L of deoxyribonucleotide triphosphate, 0.05 mmol/L of each primer, and 20 ng of template DNA. Primers and reaction conditions used in the present study were listed in Table 2. The amplified products were sequenced in forward directions with the primers used for amplification in the Beijing Genomics Institute (China). Sequences were assembled and aligned using Bioedit Sequence Alignment editor version 7.0.9.

### 2.3. BLASTN and phylogenetic analysis

BLASTN and the nearest distance method were used to identify obtained relative accurate identification of species. First, the measured DNA sequences from non-*Camellia* tea were determined using BLASTN<sup>75</sup> against the NCBI databases to identify the original plants of non-*Camellia* tea with similarity over 95%. To optimize correct identifications, DNA sequences of four candidate regions (*rbcL*, *matK*, ITS2, *psbA-trnH*) from non-*Camellia* tea were determined from the best reciprocal hits. In most cases this corresponded to the sequence with the highest BLAST score. Second, in order to find a suitable reference sequence, all of *rbcL*, *matK*, *psbA-trnH*, and ITS2 were extracted from the National Center for Biotechnology Information (NCBI) database according to the names of origin plant of the non-*Camellia* tea. After cluster and phylogenetic analysis, individual sequences were eliminated because of their ambiguous nucleotides shorter than 100 bp. Finally, the download sequences including 29 *rbcL*, 26 *matK*, 22 *psbA-trnH*, and 29 ITS2 (Table 3) combining with the sequences of commercial non-*Camellia* tea were used to construct phylogenetic trees by Mega 5.0<sup>76</sup> and Clustal X<sup>77</sup> with a bootstrap value of 1000 replicates, respectively. Preliminary trees were reconciled by setting the bootstrap value greater than 50%, yielding a more credible consensus tree.

## 3. Results

### 3.1. Traditional uses

According to the literature (Table 1), original plants of 33 kinds of non-*Camellia* tea are distributed across 29 genera in 22 families. The most widely used plant portions are leaves (26), followed by flowers (7), herbs (3), stems (3), and the least used plant portions are seeds (1) and branches (1). The investigated non-*Camellia* teas have a variety of therapeutic applications (Table 1). The non-*Camellia* teas have been mainly used for three therapeutic effects: (I) heat-clearing tea (20), such as vine tea, qingqiangliu tea, yeju tea; (II) digestant tea (8), such as laoying tea, zhegu tea, liangwang tea; (III) health tea (9), such as jiaogulan tea, kuqiao tea, lvluohua tea.

Download English Version:

<https://daneshyari.com/en/article/2474798>

Download Persian Version:

<https://daneshyari.com/article/2474798>

[Daneshyari.com](https://daneshyari.com)