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New method for effective identification of adulterated Camellia oil basing on *Camellia oleifera*-specific DNA

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Abstract: Camellia oil obtained from Camellia oleifera seeds is rich in unsaturated fatty acids and unique flavors, and has become a rising high-quality edible vegetable oil in the world. However, honored as the "Oriental olive oil", Camellia oil was widely adulterated for the situation of high price and short supply. At present, the identification of adulterated plant edible oil is mainly based on the composition and content of fatty acids. Here, the fatty acid composition and content of the main vegetable edible oils were determined. It is found that the fatty acid composition and content are susceptible to the change of the origin, variety and climate of the raw materials, and adulterated oils could even be made extremely similar to Camellia oil by the target combination of fatty acid content, therefore it is difficult to accurately identify the adulteration of Camellia oil through the composition and content determination of fatty acids. Camellia oleifera DNA was used as the breakthrough point for adulteration identification. Basing on the EST library and transcriptome data of Camellia oleifera, 116 candidate specific DNAs were screened out by bioinformatics, then the optimized methods of trace DNA extraction in Camellia oil were established. Further, three specific Camellia oleifera DNAs that could only be PCR amplified using Camellia oil- extracted DNA as template were finally screened out, which were confirmed by exclusive PCR amplifications using DNAs of other edible oils as templates. One of the specific DNAs was used to make the concentration regression curves of trace DNA by qPCR (Quantitative real-time PCR). The computational model was successively established between the adulteration ratio and the Ct value of the qPCR by adulteration imitation of different proportions of Camellia oil. Finally, a complete identification system of Camellia oil adulteration was firstly established basing on the specific DNA of Camellia oleifera, and it may provide a new idea and method for identification of adulterated Camellia oil.

KEYWORDS: Camellia oil, Specific DNA; Adulteration identification; Camellia oleifera; Fatty acids

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1. Introduction

Camellia oil is the vegetable oil obtained from Camellia oleifera seeds, and is a kind of edible tree-bearing oil with high quality originated from China. C. oleifera has been widely cultivated in more than 10 provinces in South China. Some Asian countries such as Vietnam have also started cultivating C. oleifera widely in recent years. The content of unsaturated fatty acids in Camellia oil is over 85% fromdata prepared by Yang et al. (2016) and Ma et al (2011), Shamsudin et al. (2017), Rahman et al. (2017), Khan et al. (2017). Camellia oil is one of edible high-quality oils recommended by FAO. It's known as oriental olive oil because its fatty acid composition is extremely similar to olive oil. Camellia oil also contains polyphenols, sasanquasaponin and other bioactive substances from data prepared by Ye et al. (2014), Sukor et al. (2017), Basheer et al. (2017), Razali and Said, (2017). Long-term intake of Camellia oil can help to cure cardiovascular and cerebrovascular diseases from data prepared by Bumrungpert et al. (2016), reduce the level of cholesterol, and protect the liver from data prepared by Cheng et al. (2015), Ghafar et al. (2017), etc. In addition, through deep processing technology, Camellia oil can also be used as a base oil for advanced natural skin care cosmetics from data prepared by Liu et al. (2012), Hassan et al. (2017), Ismail and Hanafiah, (2017).

In recent years, with the improvement of people's living standard, more and more people pursue healthy diet. The increasing demand of Camellia oil results in rising price. At the same time, the adulteration of Camellia oil becomes more and more serious in China. Over the years, scholarsalways pursued the methods of detecting and identifying edible oil adulteration, such as chromatography was used by Ma et al. (2016), Zhang et al. (2014), Christopoulou et al. (2004), Zhang et al. (2016); Xu et al. (2014) used nuclear magnetic resonance spectroscopy ; spectroscopy was used by Farley et al. (2017), Tan et al. (2017), Biswas et al. (2016), Souza et al. (2015), Yuan et al. (2013); Wu et al. (2004) used atomic mass spectrometry and Vietina et al. (2013) used dissolved conversion curve . All the above methods are based on the chemical constituents of edible vegetable oils, such as fatty acids and flavor compounds. However, the content and composition of these chemical constituents will change accompanied with the origin, variety and growth condition of the raw materials. Therefore, it's very difficult to form the unique fatty acid characteristics of Camellia oil, resulting in inability to accurately identify whether it is adulterated and what percentage it is.

With the development of gene and genomics technology, the method basing on specific DNA is adopted to detect and identify the adulteration of edible vegetable oil according to Scollo, et al. (2016), Halim and Phang, (2017), Halim et

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