The complete chloroplast genome sequence of three medicinal species; *Curcuma longa*, *Curcuma wenyujin*, and *Curcuma phaeocaulis* (Zingiberaceae)

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**ABSTRACT**

*Curcuma longa*, *C. wenyujin* and *C. phaeocaulis* are important herbal medicine which of rhizomatous herbaceous perennial plant of the family Zingiberaceae. This study generated a complete chloroplast genome sequence of three medicinal species were characterized by de novo assembly with whole genome sequencing data. The length of complete chloroplast genome were 162,180 bp (*C. longa*), 162,266 bp (*C. wenyujin*), and 162,133 bp (*C. phaeocaulis*), respectively, with four structures that were included in large single copy region (87,001 bp, 87,042 bp, and 87,013 bp), small single copy region (15,681 bp, 15,710 bp, and 15,622 bp), and duplicated inverted regions (29,749 bp, 29,757 bp and 29,749 bp of each). Based on phylogenetic trees, *C. longa*, *C. wenyujin*, and *C. phaeocaulis* were grouped by high bootstrap value with *Curcuma* species. This result approved that *C. longa*, *C. wenyujin* and *C. phaeocaulis* were comprised in *Alpinia* and *Wurfbainia*. Therefore, this chloroplast genome data firstly generated valuable genetic resource in discrimination of herbal materials, phylogeny and development DNA marker.

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of ten taxa, consisting of genus *Curcuma*, *Alpinia*, and *Wurfbainia*. These sequences were aligned using MAFFT (http://mafft.cbrc.jp/alignment/software/, Katoh and Standley 2013). The Phylogenetic relationship was constructed by eight species, and 1000 bootstrap replications in MEGA6 (Tamura et al. 2013). Phylogenetic analysis was conducted with chloroplast genome sequences of *Curcuma longa*, *C. wenyujin*, and *C. phaeocaulis* with eight species belonging to the family Zingeraceae (Figure 1). This chloroplast genome data could be supported to discriminate between three similar medicinal species for herbal medicine and adulterations, analyze the relation of closely related taxa, and study phylogeny and identification marker.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

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**Data availability statement**

The data that support the findings of this study are openly available in NCBI, National Center for Biotechnology Information at https://www.ncbi.nlm.nih.gov/nuccore/MK109020.1/, and https://www.ncbi.nlm.nih.gov/nuccore/MK109018.1/, reference number [accession No. MK109018, MK109019, and MK109020].

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**Figure 1.** Maximum-likelihood analysis of *C. longa*, *C. wenyujin*, and *C. phaeocaulis* with related species in Zingiberaceae based on complete chloroplast genome sequences. Numbers on branch indicated bootstrap values.