Supplementary materials

**Material and methods**

2.3 HPLC assay of CGA in EFEE

EFEE (0.1975 g) was dissolved in 25 mL of 50 % (v/v) methanol solution and mixed by ultrasonic. The sample was refluxed for 30 min, at 60 ℃. After the sample was cooling to room temperature, the loss of sample weight was supplemented with 50% (v/v) methanol solution. The sample filtered through 0.45 µm syringe filters for HPLC assay. The standard curve exhibited a good linear relationship between absorbance and CGA concentration from 20.4 to 408 μg/L (R2 = 0.9993). The chromatographic conditions of HPLC are listed in Table S1 (Hou et al.,2016).

2.10 Network pharmacology

The main components and their related genes in EF were collected by summarizing the research work on chemical components of EF (He et al., 2014; Wang et al., 2019) and searching TCMSP (Ru et al., 2014) (http://tcmspnw.com), Pharm Mapper (Wang et al., 2017) (http://www.lilab-ecust.cn/pharmmapper/) and other traditional Chinese medicine components databases.

In this study, the compounds are selected out with favorable pharmacokinetics properties according to the ADME system (absorption, distribution, metabolism and excretion), whose parameters includes oral bioavailability (OB), and drug-likeness (DL). The threshold values for ADME evaluation system are OB ≥ 20%; DL ≥ 0.2 (Xu et al., 2012;Tao et al*.*, 2013). In addition, some compounds with high content and high bioavailability were supplemented by literature search.

In order to identify the targets of chemical compounds of EF, the reverse pharmacophore matching database: PharmMapper was used to hunt for targets. First, all the “.Sdf” format of the chemical structure of EF are downloaded from the PubChem database (Kim et al., 2016) (https://pubchem.ncbi.nlm.nih.gov/), and upload. Then, users select “Druggable Pharmacophore Models”, set the number of matching targets to 300, click submit to get the targets of each chemical compounds. The UniProt database (Bairoch et al., 2005) (http://www.uniprot.org/uniprot/) was used to correct official symbols of all the targets by inputting the target names and limiting the species to “Mus musculus”. Finally, the targets that do not meet the setting parameters and duplicated will be eliminated.

The selected genes were analysed by literature search, Kegg (Kanehisa et al., 2017) (https://www.kegg.jp/kegg/) and KOBAS (http://kobas.cbi.pku.edu.cn/) enrichment to investigate the possible biological functions of the potential targets and the biological pathways involved. Finally Cytoscape version 3.5.1 was used to draw the network diagram of "component-target-pathway-function" (Shannon et al., 2003; Killcoyne et al., 2009).

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**Figure and table caption**

FIGURE S1. HPLC assay of CGA in EFEE. (A) The chromatogram of EFEE. (B-F) The chromatogram of CGA concentration from 2.04 to 408 μg/L. (G) The standard curve of CGA, and the content of CGA in EFEE.

TABLE S1. qRT-PCR Primers

TABLE S2. HPLC conditions