

# Analyses of Chloroplast Genomic and Morphological Evolutionomy of Yulania Subsect. Cylindricae (Magnoliaceae)

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**Abstract:** To scientifically settle the puzzle of origin of fruit plants, the chloroplast genomic sequences of three species of Yulania subsect. Cylindricae (Spongb.) D. L. Fu, subsect. comb. nov. (Magnoliaceae) were determined, which were compared with some taxa by means of the typical algorithm, a new method for genomic evolutionomy based on the evolutionary continuity principle. The results indicated that among some representative species of Gymnospermophyta, Yulania puberula D. L. Fu, sp. nov. has the closest relatively evolutionary relationship with Ginkgo biloba, not with the species of Cycas, Welwitschia or Ephedra, which indicated that fruit plants originated from Ginkgoopsida, not from Cycadopsida thought by the euanthium-theory or Chlamydopermopsida thought by the pseudoanthium-theory. Among some representative species of Fructophyta, Ginkgo biloba has the closest relatively evolutionary relationship with Yulania puberula indicating that the new species is the relatively most primitive species of fruit plants, which is consistent with the results of morphological evolutionomy. The evolutionary system of Magnoliaceae includes 4 natural genera: Yulania Spach, Magnolia L., Michelia L. and Liriodendron L., whose boundaries all are PHS(17bp)=0.93. Furthermore Yulania subsect. Cylindricae and its three species were described or emended. The holotype of new species of Yulania puberula was designated, whose main typici-evolutionary characters, including diagnostic differences and particularities, was given and illustrated. The epitype of Y. shizhenii was designated and four synonyms of Y. cylindrica were listed. Typical algorithm is a scientific method of genomic evolutionomy and a scientifically new tool to solve the puzzle of evolutionomy of fruit plants.

**Keywords:** Typical Algorithm, Chloroplast Complete Genome, Evolutionomy, Yulania Puberula, Yulania Subsect. Cylindricae, Magnoliaceae, Fructophyta, New Species

## 1. Introduction

Fructophyta D. L. Fu & H. Fu [1], a new division built in 2018, including all fruit or flowering plants, commonly called angiosperms, occupy the highest evolutionary phylum taxa and an important position in terrestrial ecosystems and human wellbeing. The origin and evolution of fruit plants remain a

mystery, as that the British plant taxonomists P. H. Davis and V. H. Heywood pointed out in their famous book *Principles of Angiosperm Taxonomy*, the origin and phylogeny of angiosperms have puzzled plant systematics for quite some time. The famous botanist, Professor Zhang Hongda [2] also

pointed out that: "because of the long age, it is rare to find the complete fossils of original flowering plants belonging to the Triassic.... at present, that we do not have a rational evolutionary system of flowering plant is understandable."

There are two opposite theories about the origin of fruit plants: euanthium-theory and pseudoanthium-theory. The representative systems of pseudoanthium-theory were Engler system [3] and H. D. Zhang system [2], which thought flowering plants originated from Chlamydropsermopsida of Gymnospermophyta. Casuarinaceae R. Br. are the most primitive taxa in Engler system [3] and Trochodendraceae Prant. are the most primitive taxa in H. D. Zhang system [2]. The representative systems of euanthium-theory were Hutchinson system [4], Takhtajan system [5], Cronquist system [6] and C. Y. Wu System [7], which thought flowering plants originated from Cycadopsida of Gymnospermophyta. Winteraceae Lindley are the most primitive taxa of flowering plants in Takhtajan system [5] and Cronquist system [6], and Magnoliaceae Juss. are the most primitive taxa of flowering plants in Hutchinson system [4] and C. Y. Wu system [7].

The rapid development of molecular biology has promoted the development of plant systematics. The main basis of plant systematics is the "tree of life" of Darwin's theory of evolution [1], based on the theory of "common ancestor" and "germogenesis" [8]. The system can show phylogenetic relationships among different beings, but cannot show evolutionary relationships, which can lead to a subjective system sometimes [1]. For example, the APG system considers the family Amborellaceae Pinch. as the most primitive angiosperm and establish taxonomic taxa such as Eudicots and Core eudicots [8]. These unscientific conclusions and taxa are concrete manifestations of the theoretical limitations. The phylogenetic theory itself offers no scientific ideas and methods for understanding the evolutionary veins of fruit plants, because how to find and process some "noise [5]" occurred in the evolution of fruit plants is still a puzzle (here, "noise" means DNA sequences not having important evolutionary significance).

How scientifically settle the puzzle of origin of fruit plants? The chloroplast genomic sequences of three primitive species of *Yulania* subsect. *Cylindricae* (Spongob.) D. L. Fu, subsect. comb. nov. (Magnoliaceae Juss.) were determined and compared with some primitive taxa by means of the typical algorithm based on the evolutionary continuity principle [1]. The results and analyses are as follows.

## 2. Materials and Methods

### 2.1. Chloroplast Genome Sequencing, Assembly and Annotation

Total genomic DNA was isolated from silica-dried leaves of three species of *Yulania* subsect. *Cylindricae*: *Y. cylindrica* (Wils.) D. L. Fu from Xiuning county of Anhui province, *Y. shizhenii* D. L. Fu et F. W. Li from Chengdu City of Sichuan province and new species of *Y. puberula* D. L. Fu from Mountain Wudang in Hubei Province, using a modified CTAB

method [9]. After quantification and qualification, a paired-end library was constructed, and high-throughput sequencing was performed using the Illumina Hiseq 2500 platform (Lemont, IL, USA). After cleaning the raw data, all remaining high quality sequences were assembled into contigs using de novo assembly, and the complete chloroplast genomes were assembled using the software SPAdes v3.9.0. The circular map of fully annotated genomes were drawn in OGDRAWv1.2 [10]. All three chloroplast genomes of *Yulania* subsect. *Cylindricae* were deposited in the GenBank database.

### 2.2. Evolutionary Analyses of Chloroplast Complete Genomes

By analyzing the morphological characters using evolutionary continuity principle of Evolutionomy [1], the chloroplast genomes of three species of *Yulania* subsect. *Cylindricae* (Spongob.) D. L. Fu, subsect. comb. nov. (Magnoliaceae) were compared with other primitive groups such as Amborellaceae Pinch., Winteraceae Lindley, Trochodendraceae Prant., in order to scientifically determine the evolutionary position of *Yulania* subsect. *Cylindricae* (Spongob.) D. L. Fu in the evolution of fruit plants. The evolutionary analyses of chloroplast genomes mainly adopted the typical algorithm, by comparing EVS = the evolutionary similarities between the designated type and species or taxa, and PHS = the phylogenetic similarity between the designated type and species or taxa, to determine the relatively evolutionary relationship among different taxa. The formulas are as follows:

$$EVS=SEVL/AEVL$$

EVS = evolutionary similarity; SEVL = same evolutionary loci between the type and taxon; AEVL = all evolutionary loci between the type and taxa (evolutionary loci statistics just including SNB of transitions and transversions in the middle of barcode; SNB = Single Nucleotide Barcode)

$$PHS=SPHL/APHL$$

PHS = phylogenetic similarity; SPHL = same phylogenetic loci between the type and taxon; APHL = all phylogenetic loci of the type (the loci statistics according NB; NB = Nucleotide Barcode)

## 3. Chloroplast Genomes of Three Species of *Yulania* Subsect. *Cylindricae*

The chloroplast genomes of three species of *Yulania*, similar to the chloroplast genomes of other higher plants, contains two inverted repeats, IRA and IRB, which make the entire genes component into four parts, the remaining LSC large single copy area and SSC small single copy area. For the basic information of genomic length, partition length, GC content, and number of coding genes of chloroplasts of three species, see Table 1 and Figure 1.

**Table 1.** Basic characteristics of chloroplast genomes of three species of *Yulania* subsect. *Cylindrica*.

Chloroplast genome	<i>Yulania cylindrica</i>	<i>Yulania puberula</i>	<i>Yulania shizhenii</i>
Total length	160,079 bp	160,067 bp	160,062 bp
LSC	88,118 bp	88,108 bp	88,103 bp
SSC	18,779 bp	18,779 bp	18,779 bp
IR	26,591 bp	26,590 bp	26,590 bp
GC%	39.3%	39.3%	39.3%

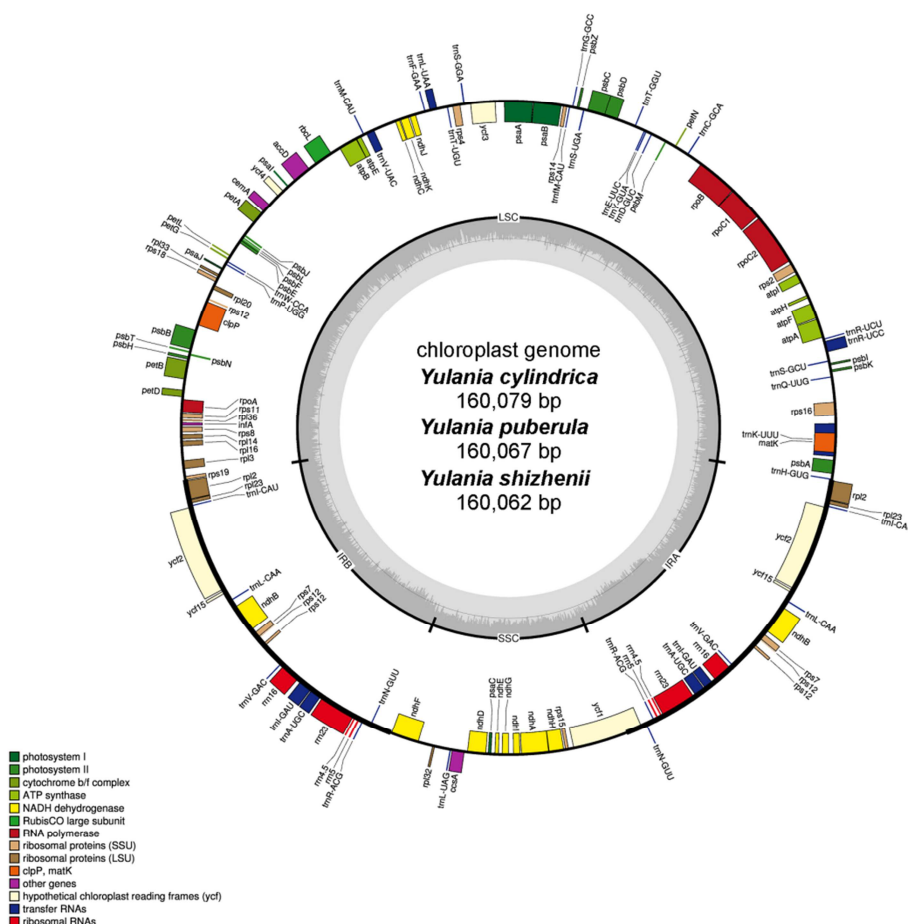
**Table 2.** List of genes present in the chloroplast genomes of three species of *Yulania* subsect. *Cylindrica*.

Function	Group of genes Gene names
ATP synthase	<i>atpA, atpB, atpE, atpF*, atpH, atpI</i>
Cytochrome b/f complex	<i>petA, petB, petD, petG, petL, petN</i>
NADH dehydrogenase	<i>ndhA*, ndhB*, ndhC, ndhD, ndhE, ndhF, ndhG, ndhH, ndhI, ndhJ, ndhK</i>
Photosystem I	<i>psaA, psaB, psaC, psal, psaJ</i>
Photosystem II	<i>psbA, psbB, psbC, psbD, psbE, psbF, psbH, psbI, psbJ, psbK, psbL, psbM, psbN, psbT, psbZ</i>
Proteins of unknown function	<i>ycf1<sup>1</sup>, ycf2, ycf3**, ycf4</i>
Ribosomal proteins (SSU)	<i>rps2, rps3, rps4, rps7, rps8, rps11, rps12<sup>#</sup>, rps14, rps15, rps16, rps18, rps19</i>
Ribosomal proteins (LSU)	<i>rpl2*, rpl14, rpl16, rpl20, rpl22, rpl23, rpl32, rpl33, rpl36</i>
Ribosomal RNAs	<i>rrn4.5<sup>1</sup>, rrn5<sup>1</sup>, rrn16<sup>1</sup>, rrn23<sup>1</sup></i>
RNA polymerase	<i>rpoA, rpoB, rpoC1*, rpoC2</i>

Function	Group of genes Gene names
Other genes	<i>accD, ccsA, cemA, clpP**, matK, rbcL, infA</i> tRNA-Lys*, tRNA-Gln, tRNA-Ser, tRNA-Gly*, tRNA-Arg, tRNA-Cys, tRNA-Asp, tRNA-Tyr, tRNA-Glu, tRNA-Thr, tRNA-Ser, tRNA-Gly, tRNA-Met, tRNA-Ser, tRNA-Thr, tRNA-Leu, tRNA-Phe, tRNA-Val, tRNA-Met, tRNA-Trp, tRNA-Pro, tRNA-Ile, tRNA-Leu*, tRNA-Val*, tRNA-His, tRNA-Ile* <sup>1</sup> , tRNA-Ala* <sup>1</sup> , tRNA-Arg <sup>1</sup> , tRNA-Asn <sup>1</sup> , tRNA-Leu, tRNA-Asn, tRNA-Arg, tRNA-Ala, tRNA-Ile, tRNA-His
Transfer RNAs	
Other	ORF302 <sup>1</sup>

\*gene containing a single intron, \*\*gene containing two introns, #trans-splicing gene, <sup>1</sup>Two gene copies in Irs

The complete chloroplast genomes of *Yulania cylindrica*, *Y. puberula* and *Y. shizhenii* are 160,079bp, 160,067bp and 160,062 bp in length, respectively. They are all encoded 128 genes. Among them, there are 83 protein coding genes, 8 rRNA genes and 37 tRNAs. *trnK-UUU*, *rps16*, *trnG-UCC*, *atpF*, *rpoC1*, *trnL-UAA*, *trnV-UAC*, *petB*, *petD*, *rpl16*, *rpl2*, *ndhB*, *trnI-GAU*, *trnA-UGC*, *ndhA* genes with an intron for each gene, *clpP*, *ycf3* gene with two introns and the *rps12* is trans-splicing gene, see Table 2 and Figure 1.

**Figure 1.** Chloroplast genome map of 3 species of *Yulania* subsect. *Cylindrica* (Magnoliaceae). The genes inside and outside the circle are transcribed in the clockwise and counterclockwise directions, respectively. Genes belonging to different functional groups are shown in different colors. The thick lines indicate the extent of the inverted repeats (IRA and IRB) that separate the genomes into small single-copy (SSC) and large single-copy (LSC) regions.

## 4. Origin of Fruit Plants

According to the evolutionary continuity principle, it is known that Fructophyta D. L. Fu & H. Fu originated from Gymnospermophyta D. L. Fu & H. Fu [1], but we don't know which taxa of Gymnospermophyta have the closest evolutionary relationships with fruit plants especially about the main evolutionary vein of origin and evolution of fruits. Because the new species *Yulania puberula* D. L. Fu of subsect. *Cylindricae* (Spongb.) D. L. Fu has the most primitive peruloid bracts (see Figure 3(7)), so it is selected as the type of fruit plants and calculated the evolutionary similarity and the phylogenetic similarity among the samples of Gymnospermophyta from NCBI, the results are shown in Table 3.

**Table 3.** EVS and PHS of chloroplast genomes between *Yulania puberula* and different species of Gymnospermophyta from NCBI.

Phylum	Class	Species name and Genomic number of NCBI	EVL /19bp	EVS	PHL /19bp	PHS	EVL /21bp	EVS	PHL /21bp	PHS
Fructophyta	Magnoliopsida	<i>Yulania puberula</i>	2022	1	133320	1	1691	1	133377	1
Gymnospermophyta	Ginkgoopsida	<i>Ginkgo biloba</i> _JN867578.1	542	0.2681	8456	0.0634	453	0.2679	7310	0.0548
Gymnospermophyta	Cycadopsida	<i>Cycas panzhihuaensis</i> _NC031413.1	528	0.2611	8506	0.0638	451	0.2667	7280	0.0546
Gymnospermophyta	Cycadopsida	<i>Cycas revoluta</i> _NC020319.1	524	0.2591	8484	0.0636	446	0.2637	7264	0.0545
Gymnospermophyta	Cycadopsida	<i>Cycas taitungensis</i> _AP009339.1	521	0.2577	8457	0.0634	443	0.262	7250	0.0544
Gymnospermophyta	Coniferopsida	<i>Pinus tabuliformis</i> _NC028531.1	410	0.2028	6409	0.0481	356	0.2105	5565	0.0417
Gymnospermophyta	Coniferopsida	<i>Cunninghamia lanceolata</i> _NC021437.1	326	0.1612	5078	0.0381	269	0.1591	4214	0.0316
Gymnospermophyta	Taxopsida	<i>Cephalotaxus oliveri</i> _NC021110.1	289	0.1429	4586	0.0344	242	0.1431	3723	0.0279
Gymnospermophyta	Taxopsida	<i>Taxus mairei</i> _NC020321.1	263	0.1301	4433	0.0333	217	0.1283	3628	0.0272
Gymnospermophyta	Coniferopsida	<i>Cupressus gigantea</i> _NC028155.1	251	0.1241	4443	0.0333	206	0.1218	3661	0.0274
Gymnospermophyta	Chlamydropsermopsida	<i>Welwitschia mirabilis</i> _NC010654.1	230	0.1137	3819	0.0286	184	0.1088	3245	0.0243
Gymnospermophyta	Chlamydropsermopsida	<i>Gnetum montanum</i> _NC021438.1	173	0.0856	3361	0.0252	140	0.0828	2870	0.0215
Gymnospermophyta	Chlamydropsermopsida	<i>Gnetum ula</i> _AP014923.1	173	0.0856	3363	0.0252	141	0.0834	2875	0.0216
Gymnospermophyta	Chlamydropsermopsida	<i>Ephedra foeminea</i> _NC029347.1	163	0.0806	3220	0.0242	132	0.0781	2716	0.0204

## 5. Relatively Original Species of Fruit Plants

### 5.1. Relatively Evolutionary Relationships Among Different Classes or Subclasses of Fructophyta

For only one species survived in Ginkgoopsida, so *Ginkgo biloba* is consequentially selected as the type of Gymnospermophyta. To represent 5 classes and 20 subclasses, 22 species were selected and calculated the evolutionary similarity and the phylogenetic similarity with the type, the results are shown in Table 4.

It can be seen from Table 4 that EVS and PHS between *Ginkgo biloba* and *Yulania puberula* is 0.2776 and 0.0608 respectively, obvious higher than other species such as *Trochodendron aralioides* and *Amborella trichopoda*. So Magnoliidae is primitive subclass of fruit plants. it is not

It can be seen from Table 3 that there are 1,691 evolutionary loci (SNB = 21bp) between the species of *Yulania puberula* and gymnosperms, of which 453 are the same with the species of *Ginkgo biloba* and the EVS is 0.2679, which is higher than other gymnosperm samples. Therefore *Yulania puberula* and *Ginkgo biloba* has the closest relatively evolutionary relationship. PHS between *Yulania puberula* and *Ginkgo biloba* (PHS=0.0548) is also obviously higher than other samples of gymnosperms. According to the evolutionary continuity principle, it can be determined that fruit plants originated from Ginkgoopsida, not from Cycadopsida thought by the euanthium-theory or Chlamydropsermopsida by the pseudoanthium- theory.

supported that *Trochodendron Siebold & Zucc.* are original family in H. D. Zhang system and *Amborella Baill.* Are original family in APG system by chloroplast genomic evolutionomy.

### 5.2. Relatively Evolutionary Relationships Among Different Families of Magnoliidae

For only 10 families having chloroplast complete genomes in NCBI, 10 species were selected and calculated the EVS and PHS with *Ginkgo biloba*, the results are shown in Table 5.

It can be seen from Table5 that EVS and PHS between *Ginkgo biloba* and *Yulania puberula* is 0.2475 and 0.0608 respectively, obvious higher than other species such as *Drimys granadensis*. So Magnoliaceae is the most primitive family of fruit plants. It is not supported that Winteraceae R. Br. ex Lindl. were the most primitive family in Takhtajan system and Cronquist system by chloroplast genomic evolutionomy.

**Table 4.** EVS and PHS of chloroplast genomes between *Ginkgo biloba* and different species of *Fructophyta* from NCBI.

Phylum	Class and Subclass	Species name and Genomic number of NCBI	EVL /19bp	EVS	PHL /19bp	PHS
Gymnospermophyta	Ginkgoopsida	<i>Ginkgo biloba</i> _JN867578.1	2554	1	139127	1
Fructophyta	Magnoliopsida Magnoliidae	<i>Yulania puberula</i>	709	0.2776	8457	0.0608
Fructophyta	Magnoliopsida Trochodendridae	<i>Trochodendron aralioides</i> _KC608753.1	659	0.258	8004	0.0575
Fructophyta	Rasopsida Hamamelididae	<i>Hamamelis mollis</i> _NC037881.1	653	0.2557	7760	0.0558
Fructophyta	Magnoliopsida Piperidae	<i>Saruma henryi</i> _NC039933.1	636	0.249	7953	0.0572
Fructophyta	Monocotyledonopsida Arecidae	<i>Phytelephas aequatorialis</i> _NC029957.1	620	0.2428	7927	0.057
Fructophyta	Magnoliopsida Ranunculidae	<i>Nandina domestica</i> _NC008336.1	597	0.2338	7820	0.0562
Fructophyta	Magnoliopsida Nymphaeidae	<i>Amborella trichopoda</i> _NC005086.1	589	0.2306	8442	0.0607
Fructophyta	Monocotyledonopsida Bromeliidae	<i>Ananas comosus</i> _NC026220.1	570	0.2232	7550	0.0543
Fructophyta	Monocotyledonopsida Commelinidae	<i>Heliconia collinsiana</i> _NC020362.1	568	0.2224	7685	0.0552
Fructophyta	Rasopsida Cornidae	<i>Swida controversa</i> _KU852492.1	565	0.2212	7554	0.0543
Fructophyta	Rasopsida Asteridae	<i>Menyanthes trifoliata</i> _NC041436.1	555	0.2173	7295	0.0524
Fructophyta	Rasopsida Lamiidae	<i>Olea exasperata</i> _NC036985.1	538	0.2106	7212	0.0518
Fructophyta	Rasopsida Rosidae	<i>Malus prunifolia</i> _NC031163.1	525	0.2056	7028	0.0505
Fructophyta	Rasopsida Caryophyllidae	<i>Nepenthes mirabilis</i> _MH346374.1	521	0.204	7170	0.0515
Fructophyta	Leguminopsida	<i>Ceratonia siliqua</i> _KJ468096.1	512	0.2005	7052	0.0507
Fructophyta	Monocotyledonopsida Acoridae	<i>Acorus calamus</i> _NC007407.1	510	0.1997	7306	0.0525
Fructophyta	Rasopsida Euphorbiidae	<i>Hevea brasiliensis</i> _NC015308.1	508	0.1989	7022	0.0505
Fructophyta	Monocotyledonopsida Alismatidae	<i>Zantedeschia aethiopica</i> _NC035499.1	507	0.1985	7184	0.0516
Fructophyta	Monocotyledonopsida Orchididae	<i>Elleanthus sodiroi</i> _KR260986.1	494	0.1934	7166	0.0515
Fructophyta	Rasopsida Malvaceae	<i>Tilia paucicostata</i> _KT894775.1	486	0.1903	6894	0.0496
Fructophyta	Rasopsida Geraniidae	<i>Hypseocharis bilobata</i> _NC023260.1	365	0.1429	5802	0.0417
Fructophyta	Scutellopsida	<i>Bambusa multiplex</i> _NC024668.1	318	0.1245	5355	0.0385

**Table 5.** EVS and PHS of chloroplast genomes between *Ginkgo biloba* and different families of *Magnoliidae*.

Phylum	Class or subclass	Family	Species name and Genomic number of NCBI	EVL /19bp	EVS	PHL /19bp	PHS
Gymnospermophyta	Ginkgoopsida	Ginkgoaceae	<i>Ginkgo biloba</i> _JN867578.1	1471	1	139127	1
Fructophyta	Magnoliidae	Magnoliaceae	<i>Yulania puberula</i>	364	0.2475	8457	0.0608
Fructophyta	Magnoliidae	Winteraceae	<i>Drimys granadensis</i> _DQ887676.1	325	0.2209	8093	0.0582
Fructophyta	Magnoliidae	Calycanthaceae	<i>Calycanthus chinensis</i> _NC037504.1	319	0.2169	7963	0.0572
Fructophyta	Magnoliidae	Chloranthaceae	<i>Chloranthus japonicus</i> _NC026565.1	318	0.2162	8185	0.0588
Fructophyta	Magnoliidae	Myristicaceae	<i>Horsfieldia pandurifolia</i> _MH445411.1	311	0.2114	8005	0.0575
Fructophyta	Magnoliidae	Cryptocaryaceae	<i>Cryptocarya chinensis</i> _NC036002.1	301	0.2046	7651	0.055
Fructophyta	Magnoliidae	Lauraceae	<i>Cinnamomum camphora</i> _NC035882.1	286	0.1944	7663	0.0551
Fructophyta	Magnoliidae	Hernandiaceae	<i>Hernandia nymphaeifolia</i> _MG838431.1	277	0.1883	7407	0.0532
Fructophyta	Magnoliidae	Neocinnamomaceae	<i>Neocinnamomum mekongense</i> _MF686120.1	263	0.1788	7362	0.0529
Fructophyta	Magnoliidae	Annonaceae	<i>Annona cherimola</i> _NC030166.1	224	0.1523	6570	0.0472

### 5.3. Relatively Evolutionary Relationships Among Different Genera of Magnoliaceae

To scientifically reflect the relatively evolutionary relationships among different genera of Magnoliaceae, 28 species having chloroplast complete genomes in NCBI were selected and calculated the evolutionary similarity and the phylogenetic similarity with the type of *Ginkgo biloba*, the results are shown in Table 6.

It can be seen from Table 6 that EVS between *Ginkgo biloba* and *Yulania diva*? is 0.0859 obvious higher than other genera and other species such as *Magnolia grandiflora*, *Liriodendron tulipifera* and *Michelia laevifolia*. So it can be concluded that *Yulania* Spach is the most primitive genus of Magnoliaceae. It is not supported that *Magnolia* L. is the most primitive genus in Hutchinson system and C. Y. Wu system (*Manglietia* Blum.=*Magnolia* L.).

### 5.4. Relatively Evolutionary Relationships Among Species of Genus Yulania

In order to determine the relatively evolutionary relationship among the species of genus of *Yulania*, the EVS and PHS between *Ginkgo biloba* and 10 species of *Yulania* Spach were calculated, and the results are shown in Table 7:

It can be seen from Table 7 that *Yulania puberula* and *Yulania cylindrica* have the closest relatively evolutionary relationships with *Ginkgo biloba*, and the evolutionary similarities are same as EVS=0.0255, but PHS between *Yulania puberula* and *Ginkgo biloba* is PHS=0.0713, which is higher than PHS= 0.0712 between *Yulania cylindrica* and *Ginkgo biloba*, so *Yulania puberula* has the closest evolutionary relationship and phylogenetic relationship with *Ginkgo biloba* among species of the genus of *Yulania* Spach.

So it can be concluded that Magnoliaceae Juss. are the most primitive family, *Yulania* Spach is the most primitive

genus and *Yulania puberula* is the most primitive species of Fructophyta.

**Table 6.** EVS and PHS of chloroplast genomes between *Ginkgo biloba* and different species of Magnoliaceae Juss.

Phylum	Species name and Genomic number of NCBI	EVL/17bp	EVS	PHL/17bp	PHS
Gymnospermophyta	<i>Ginkgo biloba</i> _JN867578.1	1153	1	138938	1
Fructophyta	<i>Yulania diva?</i> _NC023242.1	99	0.0859	9900	0.0713
Fructophyta	<i>Yulania puberula</i>	97	0.0841	9905	0.0713
Fructophyta	<i>Yulania cylindrica</i>	97	0.0841	9894	0.0712
Fructophyta	<i>Yulania salicifolia</i> _NC023240.1	97	0.0841	9909	0.0713
Fructophyta	<i>Magnolia grandiflora</i> _NC020318.1	97	0.0841	9941	0.0715
Fructophyta	<i>Magnolia dealbata</i> _NC023235.1	96	0.0833	9883	0.0711
Fructophyta	<i>Yulania shizhenii</i>	96	0.0833	9903	0.0713
Fructophyta	<i>Liriodendron tulipifera</i> _DQ899947.1	96	0.0833	9901	0.0713
Fructophyta	<i>Magnolia officinalis</i> _NC020316.1	95	0.0824	9906	0.0713
Fructophyta	<i>Yulania denudata</i> _JN867577.1	95	0.0824	9894	0.0712
Fructophyta	<i>Yulania liliiflora</i> _JX280397.1	95	0.0824	9658	0.0695
Fructophyta	<i>Yulania biondii</i> _KY085894.1	95	0.0824	9886	0.0712
Fructophyta	<i>Magnolia kwangsiensis</i> _HM775382.1	95	0.0824	9922	0.0714
Fructophyta	<i>Michelia laevifolia</i> _NC035956.1	95	0.0824	9909	0.0713
Fructophyta	<i>Liriodendron chinense</i> _NC030504.1	95	0.0824	9903	0.0713
Fructophyta	<i>Yulania acuminata</i> _JX280391.1	94	0.0815	9905	0.0713
Fructophyta	<i>Magnolia pyramidata</i> _NC023236.1	93	0.0807	9920	0.0714
Fructophyta	<i>Magnolia sinica</i> _NC023241.1	93	0.0807	9887	0.0712
Fructophyta	<i>Magnolia dandyi</i> _NC_037004.1	92	0.0798	9869	0.071
Fructophyta	<i>Magnolia tripetala</i> _NC024027.1	92	0.0798	9879	0.0711
Fructophyta	<i>Yulania kobus</i> _NC023237.1	92	0.0798	9877	0.0711
Fructophyta	<i>Michelia odora</i> _NC023239.1	92	0.0798	9868	0.071
Fructophyta	<i>Magnolia yunnanensis</i> _NC024545.1	92	0.0798	9896	0.0712
Fructophyta	<i>Magnolia glaucifolia</i> _NC037003.1	91	0.0789	9876	0.0711
Fructophyta	<i>Magnolia duclouxii</i> _NC037002.1	91	0.0789	9899	0.0712
Fructophyta	<i>Magnolia fordiana</i> _MF990562.1	91	0.0789	9871	0.071
Fructophyta	<i>Michelia cathartii</i> _NC023234.1	90	0.0781	9876	0.0711
Fructophyta	<i>Magnolia insignis</i> _MF990566.1	89	0.0772	9893	0.0712

**Table 7.** EVS and PHS between *Ginkgo biloba* and different species of *Yulania* Spach.

Species name and Genomic number of NCBI	EVL/17bp	EVS	PHL/17bp	PHS
<i>Ginkgo biloba</i> _JN867578.1	982	1	138938	1
<i>Yulania puberula</i>	25	0.0255	9905	0.0713
<i>Yulania cylindrica</i>	25	0.0255	9894	0.0712
<i>Yulania shizhenii</i>	24	0.0244	9903	0.0713
<i>Yulania diva?</i> _NC023242.1	24	0.0244	9900	0.0713
<i>Yulania salicifolia</i> _NC023240.1	24	0.0244	9909	0.0713
<i>Yulania liliiflora</i> _JX280397.1	23	0.0234	9658	0.0695
<i>Yulania biondii</i> _KY085894.1	23	0.0234	9886	0.0712
<i>Yulania acuminata</i> _JX280391.1	22	0.0224	9905	0.0713
<i>Yulania denudata</i> _JN867577.1	22	0.0224	9894	0.0712
<i>Yulania kobus</i> _NC023237.1	21	0.0214	9877	0.0711

**Table 8.** PHS and EVS of chloroplast genomes between *Yulania denudata* and different species of Magnoliaceae Juss.

Species name and cpDNA number of NCBI	PHL/17bp	PHS	EVL/17bp	EVS
<i>Yulania denudata</i> _JN867577.1	133206	1	4155	1
<i>Yulania cylindrica</i>	131736	0.99	4084	0.98
<i>Yulania puberula</i>	131551	0.99	4074	0.98
<i>Yulania shizhenii</i>	131460	0.99	4068	0.98
<i>Yulania liliiflora</i> _JX280397.1	129270	0.97	3979	0.96
<i>Yulania salicifolia</i> _NC023240.1	127070	0.95	3756	0.90
<i>Yulania diva?</i> _NC023242.1	126820	0.95	3722	0.90
<i>Yulania biondii</i> _KY085894.1	126313	0.95	3667	0.88
<i>Yulania kobus</i> _NC023237.1	125689	0.94	3632	0.87
<i>Yulania acuminata</i> _JX280391.1	123659	0.93	3505	0.84
<i>Magnolia yunnanensis</i> _NC024545.1	122609	0.92	3415	0.82
<i>Magnolia sinica</i> _NC023241.1	122465	0.92	3389	0.82
<i>Magnolia dealbata</i> _NC023235.1	121824	0.91	3366	0.81
<i>Magnolia fordiana</i> _MF990562.1	121647	0.91	3332	0.80
<i>Magnolia dandyi</i> _NC037004.1	121609	0.91	3325	0.80
<i>Magnolia insignis</i> _MF990566.1	121607	0.91	3329	0.80

Species name and cpDNA number of NCBI	PHL/17bp	PHS	EVL/17bp	EVS
Magnolia duclouxii_NC037002.1	121580	0.91	3332	0.80
Magnolia tripetala_NC024027.1	121578	0.91	3316	0.80
Michelia laevifolia_NC035956.1	121575	0.91	3328	0.80
Magnolia kwangsiensis_HM775382.1	121536	0.91	3361	0.81
Magnolia glaucifolia_NC037003.1	121499	0.91	3324	0.80
Magnolia grandiflora_NC020318.1	121332	0.91	3326	0.80
Magnolia pyramidata_NC023236.1	121260	0.91	3321	0.80
Michelia cathcartii_NC023234.1	121126	0.91	3307	0.80
Magnolia officinalis_NC020316.1	121121	0.91	3273	0.79
Michelia odora_NC023239.1	121014	0.91	3294	0.79
Liriodendron tulipifera_DQ899947.1	103965	0.78	2039	0.49
Liriodendron chinense_NC030504.1	103689	0.78	2009	0.48

**Table 9.** PHS and EVS of chloroplast genomes between *Magnolia fordiana* and different species of *Magnoliaceae* Juss.

Species name and cpDNA number of NCBI	PHL/17bp	PHS	EVL/17bp	EVS
Magnolia fordiana_MF990562.1	133163	1	4187	1
Magnolia dandyi_NC037004.1	132460	0.99	4136	0.99
Magnolia glaucifolia_NC037003.1	132385	0.99	4134	0.99
Magnolia duclouxii_NC037002.1	129855	0.98	3955	0.94
Magnolia insignis_MF990566.1	129850	0.98	3942	0.94
Magnolia tripetala_NC024027.1	125593	0.94	3611	0.86
Magnolia officinalis_NC020316.1	124347	0.93	3534	0.84
Magnolia dealbata_NC023235.1	123825	0.93	3485	0.83
Magnolia yunnanensis_NC024545.1	123790	0.93	3481	0.83
Magnolia sinica_NC023241.1	123496	0.93	3445	0.82
Magnolia kwangsiensis_HM775382.1	123473	0.93	3479	0.83
Magnolia grandiflora_NC020318.1	123454	0.93	3500	0.84
Magnolia pyramidata_NC023236.1	123322	0.93	3462	0.83
Yulania acuminata_JX280391.1	122861	0.92	3429	0.82
Michelia laevifolia_NC035956.1	122773	0.92	3397	0.81
Yulania salicifolia_NC023240.1	122653	0.92	3417	0.82
Michelia odora_NC023239.1	122171	0.92	3349	0.80
Yulania diva?_NC023242.1	122135	0.92	3350	0.80
Yulania puberula	122115	0.92	3356	0.80
Yulania cylindrica	122078	0.92	3344	0.80
Yulania biondii_KY085894.1	122009	0.92	3339	0.80
Michelia cathcartii_NC023234.1	121998	0.92	3322	0.79
Yulania shizhenii	121947	0.92	3344	0.80
Yulania denudata_JN867577.1	121646	0.91	3331	0.80
Yulania kobus_NC023237.1	121557	0.91	3312	0.79
Yulania liliiflora_JX280397.1	121203	0.91	3359	0.80
Liriodendron tulipifera_DQ899947.1	105598	0.79	2126	0.51
Liriodendron chinense_NC030504.1	105223	0.79	2087	0.50

**Table 10.** PHS and EVS of chloroplast genomes between *Michelia odora* and different species of *Magnoliaceae* Juss.

Species name and cpDNA number of NCBI	PHL/17bp	PHS	EVL/17bp	EVS
Michelia odora_NC023239.1	133199	1	4146	1
Michelia laevifolia_NC035956.1	129813	0.97	3902	0.94
Michelia cathcartii_NC023234.1	125770	0.94	3607	0.87
Magnolia yunnanensis_NC024545.1	123016	0.92	3411	0.82
Magnolia sinica_NC023241.1	122776	0.92	3381	0.82
Magnolia dealbata_NC023235.1	122288	0.92	3370	0.81
Yulania acuminata_JX280391.1	122268	0.92	3373	0.81
Magnolia fordiana_MF990562.1	122169	0.92	3347	0.81
Magnolia dandyi_NC037004.1	122155	0.92	3345	0.81
Magnolia tripetala_NC024027.1	122090	0.92	3341	0.81
Magnolia duclouxii_NC037002.1	122078	0.92	3351	0.81
Yulania salicifolia_NC023240.1	122063	0.92	3362	0.81
Magnolia glaucifolia_NC037003.1	122048	0.92	3338	0.81
Magnolia insignis_MF990566.1	122030	0.92	3343	0.81
Magnolia kwangsiensis_HM775382.1	122021	0.92	3363	0.81
Magnolia pyramidata_NC023236.1	121652	0.91	3323	0.80
Yulania diva?_NC023242.1	121577	0.91	3314	0.80
Yulania puberula	121405	0.91	3308	0.80
Yulania cylindrica	121381	0.91	3303	0.80

Species name and cpDNA number of NCBI	PHL/17bp	PHS	EVL/17bp	EVS
Yulania biondii_KY085894.1	121340	0.91	3280	0.79
Yulania shizhenii	121311	0.91	3304	0.80
Magnolia grandiflora_NC020318.1	121033	0.91	3297	0.80
Yulania denudata_JN867577.1	121014	0.91	3294	0.79
Yulania kobus_NC023237.1	120843	0.91	3245	0.78
Magnolia officinalis_NC020316.1	120742	0.91	3258	0.79
Yulania liliiflora_JX280397.1	120661	0.91	3334	0.80
Liriodendron tulipifera_DQ899947.1	104128	0.78	2034	0.49
Liriodendron chinense_NC030504.1	104000	0.78	2010	0.48

Table 11. PHS and EVS of cpGenomes between *Liriodendron tulipifera* and different species of Magnoliaceae Juss.

Species name and cpDNA number of NCBI	PHL/17bp	PHS	EVL/17bp	EVS
Liriodendron tulipifera_DQ899947.1	133246	1	3618	1
Liriodendron chinense_NC030504.1	123803	0.93	2995	0.83
Magnolia tripetala_NC024027.1	105693	0.79	2153	0.60
Magnolia insignis_MF990566.1	105662	0.79	2128	0.59
Magnolia duclouxii_NC037002.1	105656	0.79	2133	0.59
Magnolia dealbata_NC023235.1	105651	0.79	2131	0.59
Magnolia kwangsiensis_HM775382.1	105629	0.79	2172	0.60
Magnolia fordiana_MF990562.1	105597	0.79	2125	0.59
Magnolia dandyi_NC037004.1	105550	0.79	2125	0.59
Magnolia glaucifolia_NC037003.1	105471	0.79	2116	0.58
Magnolia yunnanensis_NC024545.1	105464	0.79	2128	0.59
Magnolia sinica_NC023241.1	105336	0.79	2117	0.59
Magnolia pyramidata_NC023236.1	105308	0.79	2134	0.59
Magnolia officinalis_NC020316.1	105033	0.79	2110	0.58
Yulania acuminata_JX280391.1	104930	0.79	2089	0.58
Magnolia grandiflora_NC020318.1	104838	0.79	2116	0.58
Michelia laevifolia_NC035956.1	104757	0.79	2095	0.58
Yulania salicifolia_NC023240.1	104741	0.79	2100	0.58
Yulania diva?_NC023242.1	104483	0.78	2075	0.57
Michelia cathcartii_NC023234.1	104322	0.78	2043	0.56
Yulania biondii_KY085894.1	104249	0.78	2061	0.57
Yulania cylindrica	104133	0.78	2039	0.56
Michelia odora_NC023239.1	104130	0.78	2036	0.56
Yulania puberula	104126	0.78	2038	0.56
Yulania shizhenii	104103	0.78	2035	0.56
Yulania denudata_JN867577.1	103967	0.78	2041	0.56
Yulania kobus_NC023237.1	103946	0.78	2040	0.56
Yulania liliiflora_JX280397.1	103412	0.78	2054	0.57

## 6. Evolutionary System of Magnoliaceae Juss

The taxonomical system of Magnoliaceae Juss. has always been more controversial. Dandy system [11] had the biggest impact, which included 12 genera: Manglietia Blum., Magnolia L., Talauma Juss., Alcimandra Dandy, Aromadendron Blum., Pachylarnax Dandy, Kmeria (Pierre) Dandy, Elmerrillia Dandy, Michelia L., Paramichelia Hu, Tsoongiodendron Chun and Liriodendron L.. Based on the system, Y. H. Law system [12] increased 3 genera: Manglietiastrum Law, Dugandiodendron G. Lozano-Contreras, Parakmeria Hu et Cheng. N. H. Xia system [13] increased 5 genera: Houpoea N. H. Xia & C. Y. Wu, Oyama (Nakai) N. H. Xia & C. Y. Wu, Lirianthe Spach, Woonyoungia Law, Yulania Spach. Most of these genera were not supported by the phylogeny. Bailon system [14] and Nooteboom system [15] only included 2 genera: Magnolia L. and Liriodendron L., which were adopted by the NCBI

database.

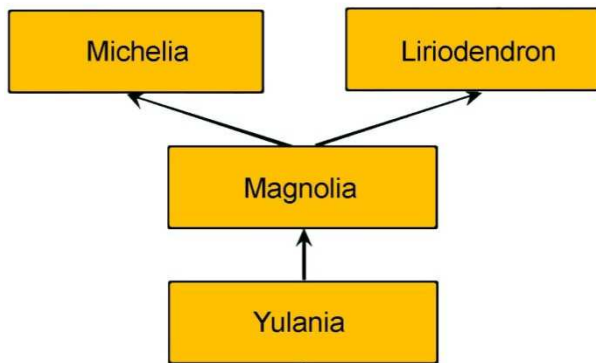
Traditional taxonomical and phylogenic system sometimes are inevitably partial and subjective [1]. To establish a scientific system, the PHS and EVS are analyzed based on the chloroplast complete genome of 28 species of Magnoliaceae using the types of 4 species respectively: Yulania denudata (Desr.) D. L. Fu, Magnolia fordiana (Oliver) Hu, Michelia odora (Chun) Nooteboom & B. L. Chen, Liriodendron tulipifera L., and the results are shown in Table 8 to 11.

It can be seen from Table 8 to 11 that using the types of Yulania denudata (Desr.) D. L. Fu, Magnolia fordiana (Oliver) Hu, Michelia odora (Chun) Nooteboom & B. L. Chen and Liriodendron tulipifera L. respectively, Magnoliaceae Juss. obviously include 4 natural genera: Yulania Spach, Magnolia L., Michelia L. and Liriodendron L., which all have the same boundaries:  $PHS(17bp) \geq 0.93$  (inner genus) and  $PHS(17bp) < 0.93$  (inter genera), and  $EVS(17bp) \geq 0.83$  (inner genus) and  $EVS(17bp) < 0.83$  (inter genera), except for Magnolia sinica (Y. W. Law) Nooteboom). For PHS being more easily calculated just need two samples, so



PHS(17bp)=0.93 can be regarded as the generic boundary of Magnoliaceae. Based on the boundary, it can be concluded that *Manglietia* Blum., *Pachylarnax* Dandy, *Manglietiastrum* Law, *Parakmeria* Hu et Cheng, *Houpoea* N. H. Xia & C. Y. Wu, *Woonyoungia* Law, *Alcimandra* Dandy, and *Tsoongiodendron* Chun are not supported by chloroplast complete genomic evolutionomy. By means of morphological evolutionomy, it can be basically concluded that *Talauma* Juss., *Kmeria* (Pierre) Dandy, *Aromadendron* Blum., *Elmerrillia* Dandy, *Dugandiodendron* G. Lozano-Contreras, *Oyama* (Nakai) N. H. Xia & C. Y. Wu, *Lirianthe* Spach and *Paramichelia* Hu are not supported too.

According the evolutionary continuity principle, based on PHS and EVS of 28 species, the evolutionary system of Magnoliaceae Juss. can be established as Figure 2, which scientifically overcomes the partiality and subjectivity of traditional and phylogenetic system.



**Figure 2.** Evolutionary system of genera of Magnoliaceae Juss. based on the chloroplast genomic and morphological evolutionomy.

The genera of *Magnolia* L., *Michelia* L. and *Liriodendron* L. of Magnoliaceae Juss. were widely accepted by most of taxonomical system [2-8, 11-13, 15-19, 21-23], but the genus of *Yulania* Spach had been regarded as *Magnolia* L. by most botanical authorities [16-18]. As *Yulania* Spach was scientifically confirmed in 2001 [19], its species resources were also gradually identified [20-23].

## 7. Evolutionary Taxa of *Yulania* sect. *Yulania* Subsect. *Cylindrica*

### 7.1. *Yulania* Subsect. *Cylindrica* (Spongberg.) D. L. Fu, Subsect. Comb. Nov., Figures 3 to 5

*Magnolia* sect. *Cylindrica* S. A. Spongberg, in D. R. Hunt (ed.), *Magnolias & their allies*: 115. 1998. — *Yulania* sect. *Cylindrica* (Spongberg.) T. B. Zhao & Z. X. Chen, nom. illegit. (laps. cit.) in T. B. Zhao et al., *Shijie Yulanshu Zhiwu Ziyuan yu Zaipei Liyong*. 175.

Deciduous trees. Hornotini-branchlets reddish purple, often hairy. Leaves obovate, rarely elliptic, surface green, glabrous or sparsely puberulent, reticulate veins flat or depressed and rimous when dried, lower surfaces pallid green or glaucescent densely puberulent. Flower buds terminal, bracts membranous,

bractoid or peruloid. Flower precocious, often sepals 3 and tepals 6. Fruit aggregates cylindric, often curved or not.

Typus: *Yulania cylindrica* (Wils.) D. L. Fu, J. Wuhan Bot. Res., 19(3): 198. 2001; *Magnolia cylindrica* Wils. in J. Arnold Arbor. 8: 109. 1927.

Three species could be confirmed in this subsection: *Yulania puberula* D. L. Fu, sp. nov., *Yulania cylindrica* (Wils.) D. L. Fu, *Yulania shizhenii* D. L. Fu et F. W. Li, mainly distributed in Hubei, Anhui, Sichuan and other provinces of South China.

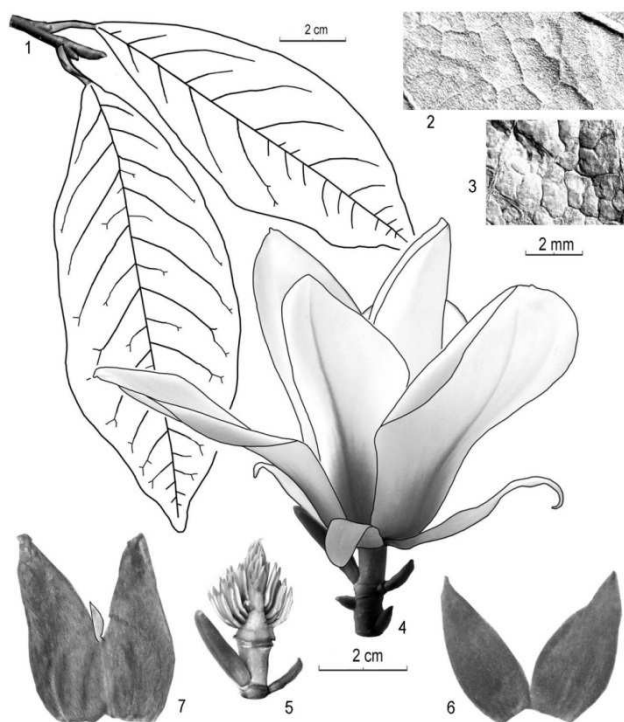
The species of this subsection are the most primitive taxa of fruit plants, and plays an important role in the study of origin and evolution of fruit plants.

### 7.2. *Yulania Puberula* D. L. Fu, sp. Nov., Figure 3

Arbor decidua. Ramuli crassi, lenticellis rarioribus rotundis leviter protuberantibus, hornotini purpureo-rubri pubescentes et puberuli nitidi, ramuli abbreviati 3~5-nodi, internodiis ca. 3 mm longis leviter crassis pallide brunneis sparse puberulis. Gammae foliiferae conoideae vel ovoideo-conoideae 0.5~1.2 cm longae et 0.2~0.4 cm diam. dense pallide adpresso-flavo-pubescentes. Alabastra solitaria, terminalia, ovoidea circa 2.0 cm longa et 1.0 cm diam. extus dense pallide adpresso-flavo-villosa. Folia alterna tenuiter coriacea elliptica late oblanceolata vel oblanceolato-elliptica 6.5~10.5 cm longa et 2.0~3.5 cm lata apice acuminata vel acuta basi cuneata vel late cuneata margine integra supra viridia parte facile lateritoscentia in sicco glabra nitida nervis et nervulis impressis rimosus in sicco subtus pallide viridia, dense puberula, pilis 1.5~2.5 dmm longis, costis manifeste prominentibus dense puberulis, pilis usque ad 5.0 dmm longis, nervis lateralibus 10~15-jugis; petioli graciles 0.8~2.5 cm longi, dense puberuli, cicatriculis stipularum 2~3 mm longis interdum longitudine attingentibus 1/3 petiolorum partem aequantibus. Flores ante folia aperti, albi; pedicelli flavo-viriduli 0.8~1.2 cm longi et 0.7~0.8 diam. dense albi pubescentes vel villosi; bractae 1, peruli-morphis; sepala (1~3) alba carnea linearia, petala 6(~8) alba carnea spatulata vel spatulato-obovata, 7.0~10.0 cm longa et 3.5~6.0 cm lata extus costis roseolis basi vivido-purpureo-rubra. Stamina numerosa ca. 65 in quequo flore, 0.8~1.1 cm longa, pallide purpureo-rubra extus costis roseolis, thecis lateribus longitudinali-dehiscentibus, connetivis apice cum mucronibus triangulis ca. 1.5 mm longis; filamentis ca. 2.5 mm longis rectangularibus pallide purpureo-rubris; gynoecium subcylindricum ca. 1.6 cm longum, pistilla simplicia numerosa ca. 40~45 in quequo flore, glabra, ovariis pallide flavo-viridulis interdum pallide purpureo-rubris fasciatis protuberantis costis purpureo-rubris, stylis et stigmatibus extus pallide purpureo-rubris. Folliceta breviter cylindrica purpureo-rubra ca. 5.0 cm longa et 2.8 cm diam. saepe curvata; semina depresso-globosa 0.7 mm longa et 0.7 cm lata.

Hubei: D. L. Fu2018032601 (Holotypus, hic designatus, CAF) branchlets with flower, were collected from Mountain Wudang at alt. about 970 m on Mar. 26, 2018, by D. L. Fu, and D. L. Fu 2017100801 (Paratypus, CAF), branchlets with fruit,

flower buds and leaves were collected from the same position on Oct. 08, 2017.



**Figure 3.** *Yulania puberula* D. L. Fu, *sp. nov.* 1. branchlet with leaves; 2. lower surface of leaf (to show densely alba puberulent); 3. upper surface of leaf (reticulate veins depressed and rimous when dried); 4. flower; 5. flower with tepals removed to show gynoecium and androecium; 6. perule; 7. bract (peruloid). (drawn by D. L. Fu)

The chloroplast complete genome of this new species is mostly similar to *Y. cylindrica* (Wils.) D. L. Fu and PHS = 0.992.

The main typici-evolutionary characters including diagnostic differences and particularities of the new species are that the hornotini-branchlets reddish purple, leaves thin corious, elliptic or oblanceolati-elliptic, reticulate veins depressed and rimous when dried, lower surfaces densely puberulent; Flower precocious, sepals 3 and tepals 6, bract 1, peruloid. That the leaves oblanceolati-elliptic, reticulate veins depressed and rimous when dried, bract peruloid are also the new typci-evolutionary characters of the species, which can be used to distinguish to similar species *Yulania cylindrica* (Wils.) D. L. Fu [16-23], *Y. shizhenii* D. L. Fu et W. F. Li [20] and other species of the genus. Furthermore the leaf reticulate veins depressed and rimous when dried and bract peruloid are also the most primitive morphological signs in fruit plants.

**Distribution:** The species is mainly distributed in Hubei province of China.

The species is the most primitive fruit plants and will play an important role in researching the Evolutionomy of Magnoliaceae Juss. even that of Fructophyta D. L. Fu & H. Fu, but it is very rare in population, so the authors intensively proposed that the species should be protected as first level protection.

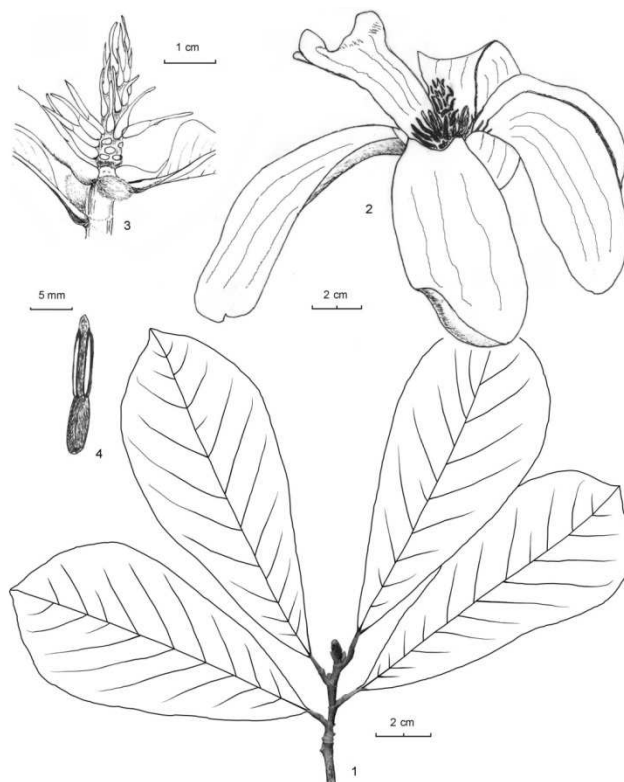
### 7.3. *Yulania Shizhenii* D. L. Fu et F. W. Li, *sp. Emend.*, **Figure 4**

Bull. Bot. Res. (Haerbin), 30 (4): 387-389. 2010, p.p. excl. paratypus; T. B. Zhao et al., *Shijie Yulanshu Zhiwu Ziyuan yu Zaipei Liyong*: 258-259. 2013. — *Yulania kobus* var. *shizhenii* T. B. Zhao et Z. X. Chen, in *Shijie Yulanshu Zhiwu Zhongzhi Ziyuan Zhi*: 67-68. 2013. — *Yulania liliiflora* var. *shizhenii* T. B. Zhao et Z. X. Chen, in *Henan Yulan Zaipei*: 226-227. 2015.

Characteres specifiici peculiare prioritatum et evolutionales typici: Ramuli graciles cum limbo-cicatricibus petiolorum hornotini purpureo-rubri. Folia longe obovata membranacea subtus dense puberula, petiolis base dilatatis. Flores ante folia aperti; sepala 3 et tepala 6; stamina alba, filamentis latiora quam antheris.

The main typici-evolutionary characters: the branchlets slender with eave scars of petioles, hornotini-branchlets reddish-purple; leaves long obovate, membranous and the lower surfaces densely puberulent; petiole bases enlargement; Flower precocious, sepals 3 and tepals 6, stamens white and filaments wider than anthers.

**Typus:** D. L. Fu 200103161 (Holotypus, CAF), D. L. Fu 2017110501 (Epitypus, hic designatus, CAF). The types were collected from Chengdu city of Sichuan province of China and kept at Chinese Academy of Forestry (CAF).



**Figure 4.** *Yulania shizhenii* D. L. Fu et F. W. Li, *sp. emend.* 1. branchlet with leaves (drawn by H. Fu); 2. flower; 3. gynoecium and androecium; 4. stamen. (from Bull. Bot. Res.)

This species is named for commemorating Li Shizhen, a great pharmacologist and botanist of ancient China.

**Distribution:** The species is distributed in Sichuan province

of China.

The species is an excellent ornamental tree species with the pure white flowers, open in early spring. Its flower buds into Chinese medicine, called Xinyi. As one of the most primitive taxa, it should be recommended for inclusion in the national first-level list of protected plants for its small number of populations and very important role in the origin and evolution of fruit plants.

#### 7.4. *Yulania cylindrica* (Wils.) D. L. Fu, Figure 5

J. Wuhan Bot. Res., 19(3): 198. 2001; Xia Nianhe et al., Flora of China vol. 7: 75. 2008; ———*Magnolia cylindrica* Wils. in J. Arnold Arbor. 8: 109. 1927. Typus: R. C. Ching 2949 (A, collected from Mountain Huang in Anhui province of China).

*Yulania fragarigynandria* T. B. Zhao, Z. X. Chen et H. T. Dai, in T. B. Zhao et al. Shijie Yulanshu Zhiwu Ziyuan yu Zaipei Liyong: 236-237. 2013. Type: 200504041(HEAC); T. B. Zhao et al. Shijie Yulanshu Zhiwu Zhongzhi Ziyuan Zhi: 78-79. 2013; T. B. Zhao et al., Henan Yulan Zaipei: 270-271. 2015.

*Yulania gynophora* T. B. Zhao, Z. X. Chen et J. Zhao, in T. B. Zhao et al. Shijie Yulanshu Zhiwu Ziyuan yu Zaipei Liyong: 288-289. 2013. Type: 200203131(HEAC); T. B. Zhao et al. Shijie Yulanshu Zhiwu Zhongzhi Ziyuan Zhi: 79-80. 2013; T. B. Zhao et al., Henan Yulan Zaipei: 269-270. 2015.

*Yulania varians* T. B. Zhao, Z. X. Chen et Z. F. Ren, in T. B. Zhao et al. Shijie Yulanshu Zhiwu Ziyuan yu Zaipei Liyong: 289-291. 2013. Type: 201303222(HEAC); in T. B. Zhao et al. Shijie Yulanshu Zhiwu Zhongzhi Ziyuan Zhi: 82-83. 2013; in T. B. Zhao et al., Henan Yulan Zaipei: 272-273. 2015.

*Yulania anhueiensis* T. B. Zhao, Z. X. Chen et J. Zhao, in T. B. Zhao et al. Shijie Yulanshu Zhiwu Ziyuan yu Zaipei Liyong: 302-303. 2013. Type: 200503301(HEAC); in T. B. Zhao et al. Shijie Yulanshu Zhiwu Zhongzhi Ziyuan Zhi: 78-79. 2013; in T. B. Zhao et al., Henan Yulan Zaipei: 268-269. 2015.

*Magnolia glabrata* auct. Non Law et R. Z. Zhou ined.: Y. H. Liu, Magnolias of China: pict.(top-left, p.61). 2004.

*Yulania axilliflora* auct. non(T. B. Zhao et al.) D. L. Fu: T. B. Zhao et al., Henan Yulan Zaipei: t.74(6). 2015.

The main typici-evolutionary characters: Fruit aggregates cylindric, often short and thick, and not curved, the follicles dehiscing by dorsal suture or not, but the apical portions falling away individually or in irregular masses leaving the seeds suspended on persistent central axes [17]. It can be clearly distinguished from other species of *Yulania*.

The species was described and illustrated as some new species such as *Yulania fragarigynandria* T. B. Zhao, Z. X. Chen et H. T. Dai [21-23], *Yulania gynophora* T. B. Zhao, Z. X. Chen et J. Zhao [21-23], *Yulania varians* T. B. Zhao, Z. X. Chen et Z. F. Ren [21-23] and *Yulania anhueiensis* T. B. Zhao, Z. X. Chen et J. Zhao [21-23], which all were synonyms of *Yulania cylindrica* (Wils.) D. L. Fu.

Distribution: The species is distributed in Anhui, Zhejiang, Jiangxi, Fujian, Hubei and Henan province of China, in broad-leaved forest at an altitude of 600~1600 m.

The species with white or whitish-purple flowers and red fruits, very beautiful, is an excellent ornamental tree species in

urban and rural areas; Flower buds is used as Chinese medicine for "Xinyi", and is also an excellent spice plant resource.



**Figure 5.** *Yulania cylindrica* (Wils.) D. L. Fu. 1. branchlet with leaves and fruit. (from Rare and Endangered Plants in China).

## 8. Conclusion

Scientifically overcoming the limitation of Phylogeny sometimes being partial and subjective, typical algorithm for the genomic evolutionomy, is a scientifically new method and new tool to solve the puzzle of evolutionomy of fruit plants. Based on the results of chloroplast genomic analyses, it can be concluded that Fructophyta are originated from Ginkgoopsida of Gymnospermophyta, not from Cycadopsida thought by the euanthium-theory or Chlamydropsermopsida thought by the pseudoanthium-theory, which will create a new situation in the development of evolutionomy of Fructophyta D. L. Fu & H. Fu.

Among some representative species of Fructophyta, *Ginkgo biloba* has the closest relatively evolutionary relationship with *Yulania puberula* indicating that the new species is the relatively most primitive species of fruit plants. It is consistent with the research results of morphological evolutionomy, but it is not consistent with the current people's cognition. Therefore, it will certainly promote the research of re-understanding of the evolutionomy of fruit plants and promote the development of the evolutionomy of Fructophyta D. L. Fu & H. Fu.

Based on the results of evolutionomic analyses of chloroplast genomes and morphology, the evolutionary system of Magnoliaceae includes 4 natural genera: *Yulania* Spach, *Magnolia* L., *Michelia* L. and *Liriodendron* L., whose boundaries all are PHS(17bp)=0.93 (chloroplast complete genomes). This will create a new situation in the scientific classification of Magnoliaceae Juss. and will also promote the development of the evolutionomy of Fructophyta D. L. Fu & H. Fu.

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