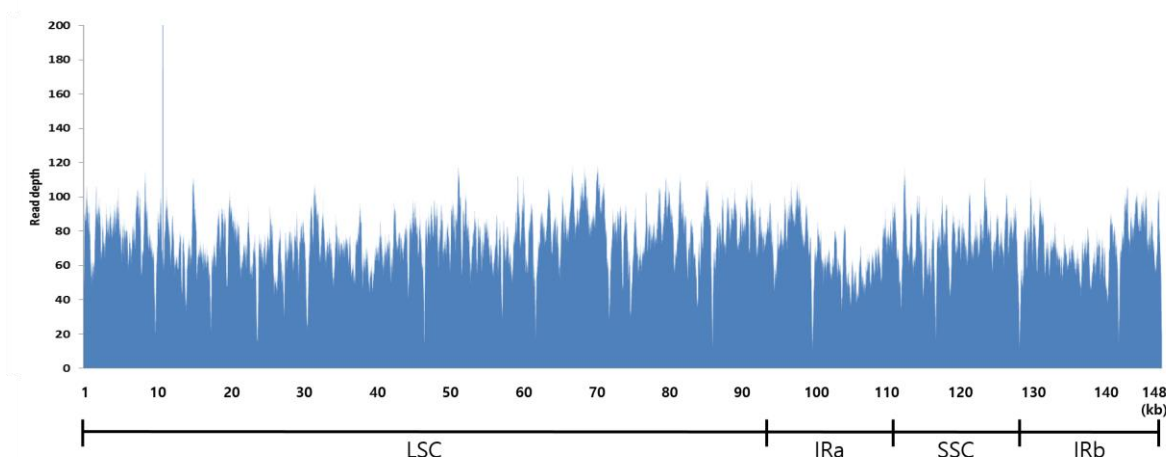


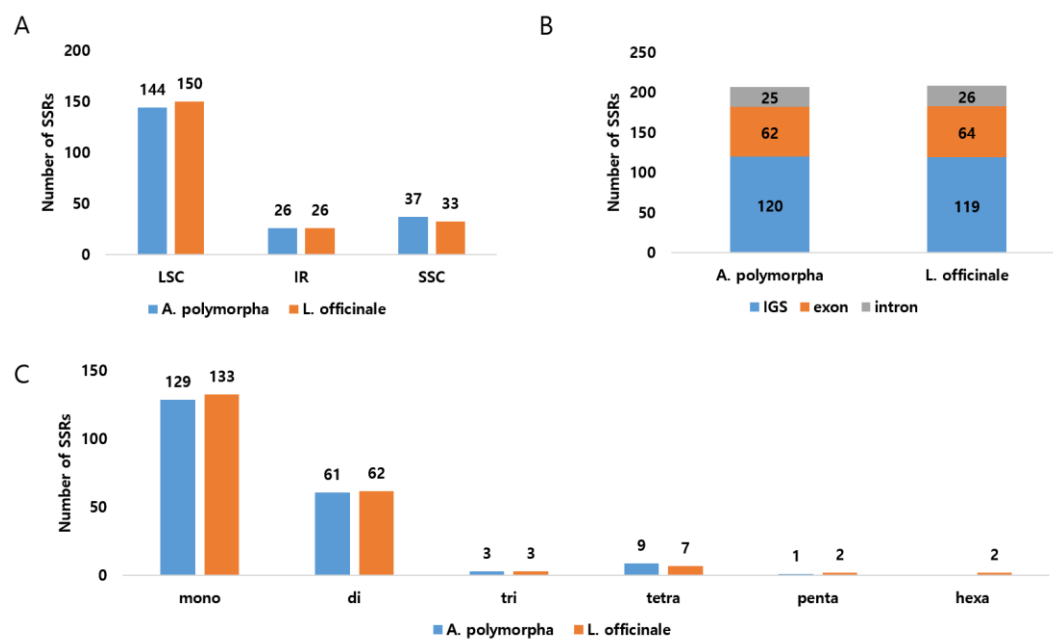
# Supplementary Materials: Sequencing and Comparative Analysis of the Chloroplast Genome of *Angelica polymorpha* and the Development of a Novel Indel Marker for Species Identification

Inkyu Park, Sungyu Yang, Wook Jin Kim, Jun-Ho Song, Hyun-Sook Lee, Hyun Oh Lee, Jung-Hyun Lee, Sang-Nag Ahn, and Byeong Cheol Moon\*

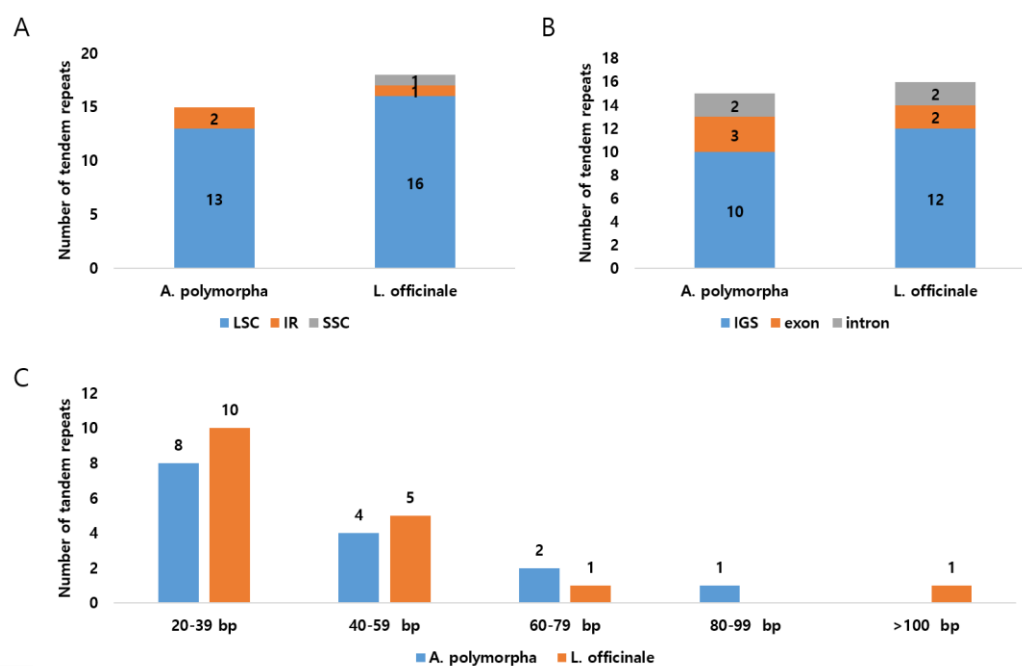


**Figure S1:** Distribution of paired-end reads mapped onto the complete chloroplast (CP) genome sequence of *A. polymorpha*.





**Figure S3:** Distribution of simple sequence repeats (SSRs) in the CP genomes of *A. polymorpha* and *L. officinale*. (A) Number of SSRs in CP genomes. (B) Number of SSRs in exons, introns and intergenic spacer (IGS) regions. (C) Number of different types of SSRs in CP genomes.



**Figure S4:** Analysis of tandem repeats in the CP genomes of *A. polymorpha* and *L. officinale*. (A) Distribution of tandem repeats in different regions of CP genomes. (B) Number of tandem repeats in IGS regions, exons, and introns. (C) Distribution of tandem repeats of variable lengths in CP genomes.

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**Table S1:** Details of raw sequence reads and CP genome assembly of *A. polymorpha*.

| Parameter                    | Number of reads |
|------------------------------|-----------------|
| Input reads                  | 5,000,000       |
| Trimmed reads                | 4,307,210       |
| Total raw bases (bp)         | 1,255,000,000   |
| Trimmed bases (bp)           | 940,906,215     |
| Aligned reads                | 51,266          |
| Coverage (X)                 | 75              |
| Chloroplast genome size (bp) | 147,127         |

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**Table S2:** PCR-based sequence validation of junctions between the large single copy (LSC), small single copy (SSC), and inverted repeat (IRa and IRb) regions in the CP genome of *A. polymorpha*.

| Location | PCR-based<br>sequence (bp) | Start position<br>(bp) | End position<br>(bp) | Identity (%) |
|----------|----------------------------|------------------------|----------------------|--------------|
| LSC/IRa  | 376                        | 93,336                 | 93,711               | 100          |
| IRa/SSC  | 175                        | 111,453                | 111,572              | 100          |
| SSC/IRb  | 508                        | 128,855                | 129,362              | 100          |
| IRb/LSC  | 732                        | 146,942                | 546                  | 100          |

**Table S3:** List of genes and encoded proteins identified in the CP genomes of *A. polymorpha* and *L. officinale*.

| Gene group                           | Gene name                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|--------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Photosystem I                        | <i>psaA, B, C, I, J, ycf3<sup>2)</sup>, ycf4</i>                                                                                                                                                                                                                                                                                                                                                                                                        |
| Photosystem II                       | <i>psbA, B, C, D, E, F, H, I, J, K, L, M, N, T, Z</i>                                                                                                                                                                                                                                                                                                                                                                                                   |
| Cytochrome b6/f                      | <i>petA, B<sup>1)</sup>, D<sup>1)</sup>, G, L, N</i>                                                                                                                                                                                                                                                                                                                                                                                                    |
| ATP synthase                         | <i>atpA, B, E, F<sup>1)</sup>, H, I</i>                                                                                                                                                                                                                                                                                                                                                                                                                 |
| Rubisco                              | <i>rbcL</i>                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| NADH oxidoreductase                  | <i>ndhA<sup>1)</sup>, B<sup>1(3)</sup>, C, D, E, F, G, H, I, J, K</i>                                                                                                                                                                                                                                                                                                                                                                                   |
| Large subunit ribosomal proteins     | <i>rpl2<sup>1(3)</sup>, 14, 16<sup>1)</sup>, 20, 22, 23<sup>3)</sup>, 32, 33, 36</i>                                                                                                                                                                                                                                                                                                                                                                    |
| Small subunit ribosomal proteins     | <i>rps2, 3, 4, 7<sup>3)</sup>, 8, 11, 12<sup>2(3/4)</sup>, 14, 15, 16, 18, 19</i>                                                                                                                                                                                                                                                                                                                                                                       |
| RNA polymerase                       | <i>rpoA, B, C1<sup>1)</sup>, C2</i>                                                                                                                                                                                                                                                                                                                                                                                                                     |
| Unknown function protein-coding gene | <i>ycf1<sup>3)</sup>, 2, 15<sup>3)</sup></i>                                                                                                                                                                                                                                                                                                                                                                                                            |
| Other genes                          | <i>accD, ccsA, cemA, clpP<sup>2)</sup>, matK</i>                                                                                                                                                                                                                                                                                                                                                                                                        |
| Ribosomal RNAs                       | <i>rrn16<sup>3)</sup>, 23<sup>3)</sup>, 4.5<sup>3)</sup>, 5<sup>3)</sup></i>                                                                                                                                                                                                                                                                                                                                                                            |
| Transfer RNAs                        | <i>trnA-UGC<sup>1(3)</sup>, trnC-GCA, trnD-GUC, trnE-UUC, trnF-GAA, trnG-UCC<sup>1)</sup>, trnG-GCC, trnH-GUG, trnI-CAU, trnI-GAU<sup>1(3)</sup>, trnK-UUU<sup>1)</sup>, trnL-UAA<sup>1)</sup>, trnL-UAG, trnL-CAA<sup>3)</sup>, trnM-CAU, trnM-CAU, trnN-GUU<sup>3)</sup>, trnP-UGG, trnQ-UUG, trnR-ACG<sup>3)</sup>, trnR-UCU, trnS-GCU, trnS-GGA, trnS-UGA, trnT-GGU, trnT-UGU, trnV-UAC<sup>1)</sup>, trnV-GAC<sup>3)</sup>, trnW-CCA, trnY-GUA</i> |

<sup>1</sup> Genes containing a single intron.<sup>2</sup> Genes containing two introns.<sup>3</sup> Genes present as two copies in the IR regions.<sup>4</sup> Trans-spliced gene.

**Table S4:** List of intron-containing genes in the CP genomes of *A. polymorpha* and *L. officinale*.

| No | Gene            | Region | Exon I <sup>1</sup> | Intron I <sup>1</sup> | Exon II <sup>1</sup> | Intron II <sup>1</sup> | Exon III <sup>1</sup> |
|----|-----------------|--------|---------------------|-----------------------|----------------------|------------------------|-----------------------|
| 1  | <i>trnK-UUU</i> | LSC    | 37                  | 2523*                 | 35                   |                        |                       |
| 2  | <i>rps16</i>    | LSC    | 40                  | 855 (857)             | 197                  |                        |                       |
| 3  | <i>trnG-UCC</i> | LSC    | 23                  | 704                   | 48                   |                        |                       |
| 4  | <i>atpF</i>     | LSC    | 145                 | 722                   | 401                  |                        |                       |
| 5  | <i>rpoC1</i>    | LSC    | 435                 | 754                   | 1605                 |                        |                       |
| 6  | <i>ycf3</i>     | LSC    | 126                 | 720                   | 226                  | 778                    | 155                   |
| 7  | <i>trnL-UAA</i> | LSC    | 35                  | 504                   | 50                   |                        |                       |
| 8  | <i>trnV-UAC</i> | LSC    | 39                  | 591                   | 35                   |                        |                       |
| 9  | <i>rps12*</i>   | LSC    | 114                 |                       | 232                  |                        | 26                    |
| 10 | <i>clpP</i>     | LSC    | 71                  | 840                   | 292                  | 638                    | 231                   |
| 11 | <i>petB</i>     | LSC    | 6                   | 756                   | 642                  |                        |                       |
| 12 | <i>petD</i>     | LSC    | 8                   | 743                   | 475                  |                        |                       |
| 13 | <i>rpl16</i>    | LSC    | 9                   | 969                   | 399                  |                        |                       |
| 14 | <i>ndhB</i>     | IR     | 777                 | 684                   | 756                  |                        |                       |
| 15 | <i>trnI-GAU</i> | IR     | 37                  | 951                   | 35                   |                        |                       |
| 16 | <i>trnA-UGC</i> | IR     | 38                  | 817                   | 35                   |                        |                       |
| 17 | <i>ndhA</i>     | SSC    | 553                 | 1073                  | 540                  |                        |                       |

<sup>1</sup> Numbers represent the gene size (bp) in *A. polymorpha*; numbers in parentheses represent the gene size in *L. officinale*. \* The intron length of *trnK-UUU* includes *matK*.

**Table S5:** Codon-anticodon recognition patterns and codon usage in the CP genomes of *A. polymorpha* and *L. officinale*.

| Amino acid | Codon | <i>A. polymorpha</i> |                   | tRNA        |
|------------|-------|----------------------|-------------------|-------------|
|            |       | Count                | RSCU <sup>1</sup> |             |
| Phe        | UUU   | 798                  | 1.32              |             |
| Phe        | UUC   | 411                  | 0.68              | trnF-GAA    |
| Leu        | UUA   | 749                  | 1.96              | trnL-UAA    |
| Leu        | UUG   | 450                  | 1.18              | trnL-CAA    |
| Leu        | CUU   | 483                  | 1.26              |             |
| Leu        | CUC   | 154                  | 0.4               |             |
| Leu        | CUA   | 316                  | 0.83              | trnL-UAG    |
| Leu        | CUG   | 141                  | 0.37              |             |
| Ile        | AUU   | 875                  | 1.45              |             |
| Ile        | AUC   | 340                  | 0.56              | trnI-GAU    |
|            |       |                      |                   | trnI-CAU    |
| Ile        | AUA   |                      |                   | trn(f)M-CAU |
|            |       | 595                  | 0.99              | trnM-CAU    |
| Met        | AUG   | 512                  | 1                 | trnM-CAU    |
| Val        | GUU   | 474                  | 1.51              |             |
| Val        | GUC   | 147                  | 0.47              | trnV-GAC    |
| Val        | GUA   | 458                  | 1.46              | trnV-UAC    |
| Val        | GUG   | 176                  | 0.56              |             |
| Ser        | UCU   | 463                  | 1.75              |             |
| Ser        | UCC   | 251                  | 0.95              | trnS-GGA    |
| Ser        | UCA   | 294                  | 1.11              | trnS-UGA    |
| Ser        | UCG   | 167                  | 0.63              |             |
| Pro        | CCU   | 354                  | 1.57              |             |
| Pro        | CCC   | 163                  | 0.72              | trnS-GCU    |
| Pro        | CCA   | 237                  | 1.05              |             |
| Pro        | CCG   | 146                  | 0.65              |             |
| Thr        | ACU   | 467                  | 1.65              | trnP-UGG    |
| Thr        | ACC   | 210                  | 0.74              |             |
| Thr        | ACA   | 333                  | 1.18              |             |
| Thr        | ACG   | 123                  | 0.43              | trnT-GGU    |
| Ala        | GCU   | 569                  | 1.81              | trnT-UGU    |
| Ala        | GCC   | 198                  | 0.63              |             |
| Ala        | GCA   | 341                  | 1.09              |             |
| Ala        | GCG   | 147                  | 0.47              | trnG-UCC    |
| Tyr        | UAU   | 644                  | 1.61              | trnA-UGC    |

|      |     |     |      |          |
|------|-----|-----|------|----------|
| Tyr  | UAC | 157 | 0.39 |          |
| Stop | UAA | 43  | 1.61 |          |
| Stop | UAG | 21  | 0.79 | trnY-GUA |
| His  | CAU | 389 | 1.51 |          |
| His  | CAC | 126 | 0.49 |          |
| Gln  | CAA | 558 | 1.49 |          |
| Gln  | CAG | 191 | 0.51 |          |
| Asn  | AAU | 722 | 1.51 | trnH-GUG |
| Asn  | AAC | 233 | 0.49 | trnQ-UUG |
| Lys  | AAA | 774 | 1.5  |          |
| Lys  | AAG | 256 | 0.5  |          |
| Asp  | GAU | 677 | 1.59 | trnN-GUU |
| Asp  | GAC | 172 | 0.41 | trnK-UUU |
| Glu  | GAA | 801 | 1.49 |          |
| Glu  | GAG | 273 | 0.51 |          |
| Cys  | UGU | 175 | 1.51 | trnD-GUC |
| Cys  | UGC | 57  | 0.49 | trnE-UUC |
| Stop | UGA | 16  | 0.6  |          |
| Trp  | UGG | 377 | 1    |          |
| Arg  | CGU | 298 | 1.4  | trnC-GCA |
| Arg  | CGC | 87  | 0.41 | trnW-CCA |
| Arg  | CGA | 299 | 1.41 | trnR-ACG |
| Arg  | CGG | 109 | 0.51 |          |
| Ser  | AGU | 327 | 1.23 |          |
| Ser  | AGC | 89  | 0.34 |          |
| Arg  | AGA | 359 | 1.69 | trnR-UCU |
| Arg  | AGG | 124 | 0.58 |          |
| Gly  | GGU | 530 | 1.35 |          |
| Gly  | GGC | 176 | 0.45 | trnG-GCC |
| Gly  | GGA | 591 | 1.51 | trnG-UCC |
| Gly  | GGG | 268 | 0.68 |          |

**Table S6:** Details of palindromic repeats present in the LSC region of the CP genomes of *A. polymorpha* and *L. officinale*.

| Species              | Position                                           | Loop<br>(bp) | Position                                  | Repeat<br>unit<br>length<br>(bp) | Repeat unit sequence                     |
|----------------------|----------------------------------------------------|--------------|-------------------------------------------|----------------------------------|------------------------------------------|
| <i>A. polymorpha</i> | IGS <sup>1</sup> ( <i>trnH</i> -GUG, <i>psbA</i> ) | 6            | IGS ( <i>rnH</i> -GUG, <i>psbA</i> )      | 31                               | TGAAATATAAAAAGAAGAAATACCGCCCTCTTG        |
|                      | IGS ( <i>psbM</i> , <i>trnD</i> -GUC)              | 490          | IGS ( <i>trnE</i> -UUC, <i>trnT</i> -GGU) | 39                               | AAAAGGGAAAGATGATTGATGTACTTATTGAATCTGTCTG |
|                      | IGS ( <i>trnT</i> -GGU, <i>psbD</i> )              | 62           | IGS ( <i>trnT</i> -GGU, <i>psbD</i> )     | 26                               | TTATCATCCTACTAAATTAGAATTTA               |
|                      | IGS ( <i>psbE</i> , <i>petL</i> )                  | 0            | IGS ( <i>psbE</i> , <i>petL</i> )         | 32                               | TCTTTCTTACTTTACTTGTTGCTTGTCAGTGT         |
|                      | IGS ( <i>psbT</i> , <i>psbN</i> )                  | 3            | IGS ( <i>psbT</i> , <i>psbN</i> )         | 21                               | TTGAAGTAATGAGTCCCCCAA                    |
| <i>L. officinale</i> | IGS ( <i>trnH</i> -GUG, <i>psbA</i> )              | 13           | IGS ( <i>rnH</i> -GUG, <i>psbA</i> )      | 24                               | AAAAAAGCAATACCGCCCTCTTG                  |
|                      | IGS ( <i>psbM</i> , <i>trnD</i> -GUC)              | 490          | IGS ( <i>trnE</i> -UUC, <i>trnT</i> -GGU) | 39                               | AAAAGGGAAAGATGATTGATGTACTTATTGAATCTGTCTG |
|                      | IGS ( <i>trnT</i> -GGU, <i>psbD</i> )              | 62           | IGS ( <i>trnT</i> -GGU, <i>psbD</i> )     | 26                               | TTATCATCCTACTAAATTAGAATTTA               |
|                      | IGS ( <i>psbE</i> , <i>petL</i> )                  | 10           | IGS ( <i>psbE</i> , <i>petL</i> )         | 27                               | TCTTTCTTACTTTACTTGTTGCTTGTC              |
|                      | IGS ( <i>psbT</i> , <i>psbN</i> )                  | 3            | IGS ( <i>psbT</i> , <i>psbN</i> )         | 21                               | TTGAAGTAATGAGTCCCCCAA                    |
|                      | Intron ( <i>petB</i> , <i>petB</i> )               | 9            | Intron ( <i>petB</i> , <i>petB</i> )      | 20                               | TAAATCGAAAGAAAGGTTTG                     |

41 <sup>1</sup>IGS, intergenic spacer.

**Table S7:** List of *A. polymorpha* and *L. officinale* accessions used in this study.

| No. | Species              | Collection information                                    | Voucher number   | Coordinates                   | GenBank accession number | Marker test |
|-----|----------------------|-----------------------------------------------------------|------------------|-------------------------------|--------------------------|-------------|
| 1   | <i>L. officinale</i> | Ilcheongungjaebaeji, Bonghwa-gun, Gyeongsangbuk-do, Korea | KIOM201501014665 | 36°48'01.9"N<br>128°57'47.2"E | NC039760                 | o           |
| 2   |                      | Subi-myeon, Yeongyang-gun, Gyeongsangbuk-do, Korea        | KIOM201701018797 | 36°47'39.8"N<br>129°12'19.6"E |                          | o           |
| 3   |                      | Subi-myeon, Yeongyang-gun, Gyeongsangbuk-do, Korea        | KIOM201701018796 | 36°47'39.8"N<br>129°12'19.6"E |                          | o           |
| 4   |                      | Yeongyang-eup, Yeongyang-gun, Gyeongsangbuk-do, Korea     | KIOM201501014665 | 36°40'32.0"N<br>129°06'46.2"E |                          | o           |
| 5   |                      | Yeongyang-eup, Yeongyang-gun, Gyeongsangbuk-do, Korea     | KIOM200601000207 | 36°40'32.0"N<br>129°06'46.2"E |                          | o           |
| 6   |                      | Yeongyang-eup, Yeongyang-gun, Gyeongsangbuk-do, Korea     | KIOM200601000208 | 36°40'32.0"N<br>129°06'46.2"E |                          | o           |
| 7   |                      | Subi-myeon, Yeongyang-gun, Gyeongsangbuk-do, Korea        | KIOM201701018769 | 36°47'39.8"N<br>129°12'19.6"E |                          | o           |
| 8   |                      | Subi-myeon, Yeongyang-gun, Gyeongsangbuk-do, Korea        | KIOM201701018770 | 36°47'39.8"N<br>129°12'19.6"E |                          | o           |
| 9   |                      | Subi-myeon, Yeongyang-gun, Gyeongsangbuk-do, Korea        | KIOM201701018771 | 36°47'39.8"N<br>129°12'19.6"E |                          | o           |
| 10  |                      | Subi-myeon, Yeongyang-gun, Gyeongsangbuk-do, Korea        | KIOM201701018795 | 36°47'39.8"N<br>129°12'19.6"E |                          | o           |
| 11  |                      | Subi-myeon, Yeongyang-gun, Gyeongsangbuk-do, Korea        | KIOM201701018617 | 36°47'39.8"N<br>129°12'19.6"E |                          | o           |
| 12  |                      | Subi-myeon, Yeongyang-gun, Gyeongsangbuk-do, Korea        | KIOM201301005868 | 36°47'39.8"N<br>129°12'19.6"E |                          | o           |
| 13  | <i>A. polymorpha</i> | Wonju-si, Gangwon-do, Korea                               | KIOM201501014664 | 37°20'17.6"N<br>128°02'27.5"E | MH260705                 | o           |
| 14  |                      | Seoha-myeon, Hamyang-gun, Gyeongsangnam-do, Korea         | KIOM201501015521 | 35°38'39.7"N<br>127°44'12.2"E |                          | o           |

|    |                                                         |                  |                               |   |
|----|---------------------------------------------------------|------------------|-------------------------------|---|
| 15 | Yeonpung-myeon, Goesan-gun,<br>Chungcheongbuk-do, Korea | KIOM201701020170 | 36°42'55.1"N<br>128°03'07.5"E | o |
| 16 | Changjuk-dong, Taebaek-si, Gangwon-<br>do, Korea        | KIOM201701020255 | 37°13'50.7"N<br>128°56'17.1"E | o |
| 17 | Wicheon-myeon, Geochang-gun,<br>Gyeongsangnam-do, Korea | KIOM201501015376 | 35°42'53.8"N<br>127°47'45.7"E | o |
| 18 | Gohan-eup, Jeongseon-gun, Gangwon-<br>do, Korea         | KIOM201501015172 | 37°12'14.3"N<br>128°54'31.1"E | o |
| 19 | Dunnae-myeon, Hoengseong-gun,<br>Gangwon-do, Korea      | KIOM201001003015 | 37°29'28.6"N<br>128°14'52.1"E | o |
| 20 | Jinbu-myeon, Pyeongchang-gun,<br>Gangwon-do, Korea      | KIOM200901002083 | 37°47'58.0"N<br>128°32'35.2"E | o |
| 21 | Jinbu-myeon, Pyeongchang-gun,<br>Gangwon-do, Korea      | KIOM200901002084 | 37°47'58.0"N<br>128°32'35.2"E | o |

44 **Table S8:** List of primers used for the validation of the CP genome sequence of *A. polymorpha*.

| Primer name | Primer sequence (5'→3')   | Junction |
|-------------|---------------------------|----------|
| LIGLF       | GGATCCTCGCGGACAGAAAA      | LSC/IRa  |
| LIGLR       | CGTGTCTGGTACTGCATGGT      |          |
| LIGISF      | ACAATTCTAACTAGCCCTAATGGTC | IRa/SSC  |
| LIGISR      | TCAAATCTGTAGGTAGTGGGCG    |          |
| LIGSIF      | ACGCCTTTGAACACGCATAG      | SSC/IRb  |
| LIGSIR      | AGAGGTTGAACAGAAAATAGACCG  |          |
| LIGILF      | GATCTGCAGGGTCCCAAATGA     | IRb/LSC  |
| LIGILR      | ACTTTGATCCAACGGAGCCC      |          |

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**Table S9:** List of CP genomes downloaded from NCBI for phylogenetic analysis.

| Order      | Family     | No. | Taxon                                                   | GenBank accession number |
|------------|------------|-----|---------------------------------------------------------|--------------------------|
| Apiales    | Apiaceae   | 1   | <i>Angelica acutiloba</i>                               | NC029391.1               |
|            |            | 2   | <i>Angelica dahurica</i>                                | NC029392.1               |
|            |            | 3   | <i>Angelica decursiva</i>                               | KT781591.1               |
|            |            | 4   | <i>Angelica gigas</i>                                   | NC029393.1               |
|            |            | 5   | <i>Angelica nitida</i>                                  | MF594405.1               |
|            |            | 6   | <i>Arracacia xanthorrhiza</i>                           | KY117235.1               |
|            |            | 7   | <i>Glehnia littoralis</i>                               | KT153022.1               |
|            |            | 8   | <i>Ledebouriella seseloides</i>                         | KT153021.1               |
|            |            | 9   | <i>Peucedanum insolens</i>                              | NC033344.1               |
|            |            | 10  | <i>Seseli montanum</i>                                  | KM035851.1               |
|            |            | 11  | <i>Ligusticum tenuissimum</i>                           | NC029394.1               |
|            |            | 12  | <i>Ligusticum officinale</i>                            | NC039760.1               |
|            |            | 13  | <i>Daucus carota</i>                                    | NC008325.1               |
|            |            | 14  | <i>Anthriscus cerefolium</i>                            | NC015113.1               |
|            |            | 15  | <i>Tiedemannia filiformis</i> subsp. <i>greenmannii</i> | HM596071.1               |
|            |            | 16  | <i>Coriandrum sativum</i>                               | NC029850.1               |
|            |            | 17  | <i>Bupleurum latissimum</i>                             | NC033346.1               |
|            |            | 18  | <i>Bupleurum falcatum</i>                               | NC027834.1               |
|            |            | 20  | <i>Anethum graveolens</i>                               | NC029470.1               |
|            |            | 21  | <i>Petroselinum crispum</i>                             | NC015821.1               |
|            |            | 22  | <i>Foeniculum vulgare</i>                               | NC029469.1               |
|            | Araliaceae | 23  | <i>Eleutherococcus senticosus</i>                       | JN637765.1               |
|            |            | 24  | <i>Fatsia japonica</i>                                  | NC027685.1               |
|            |            | 25  | <i>Kalopanax septemlobus</i>                            | NC022814.1               |
|            |            | 26  | <i>Metapanax delavayi</i>                               | NC022812.1               |
|            |            | 27  | <i>Schefflera delavayi</i>                              | NC022813.1               |
|            |            | 28  | <i>Aralia undulata</i>                                  | NC022810.1               |
|            |            | 29  | <i>Panax ginseng</i>                                    | AY582139.1               |
|            |            | 30  | <i>Panax notoginseng</i>                                | NC026447.1               |
| Dipsacales | Adoxaceae  | 31  | <i>Adoxa moschatellina</i>                              | NC034792.1               |
|            |            | 32  | <i>Tetradoxa omeiensis</i>                              | NC034793.1               |

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