

## ***Supplementary Material***

### **An Integrative Study of *Scrophularia takesimensis* Nakai in an Ovalbumin-Induced Murine Model of Asthma: The Effect on T Helper 2 Cell Activation**

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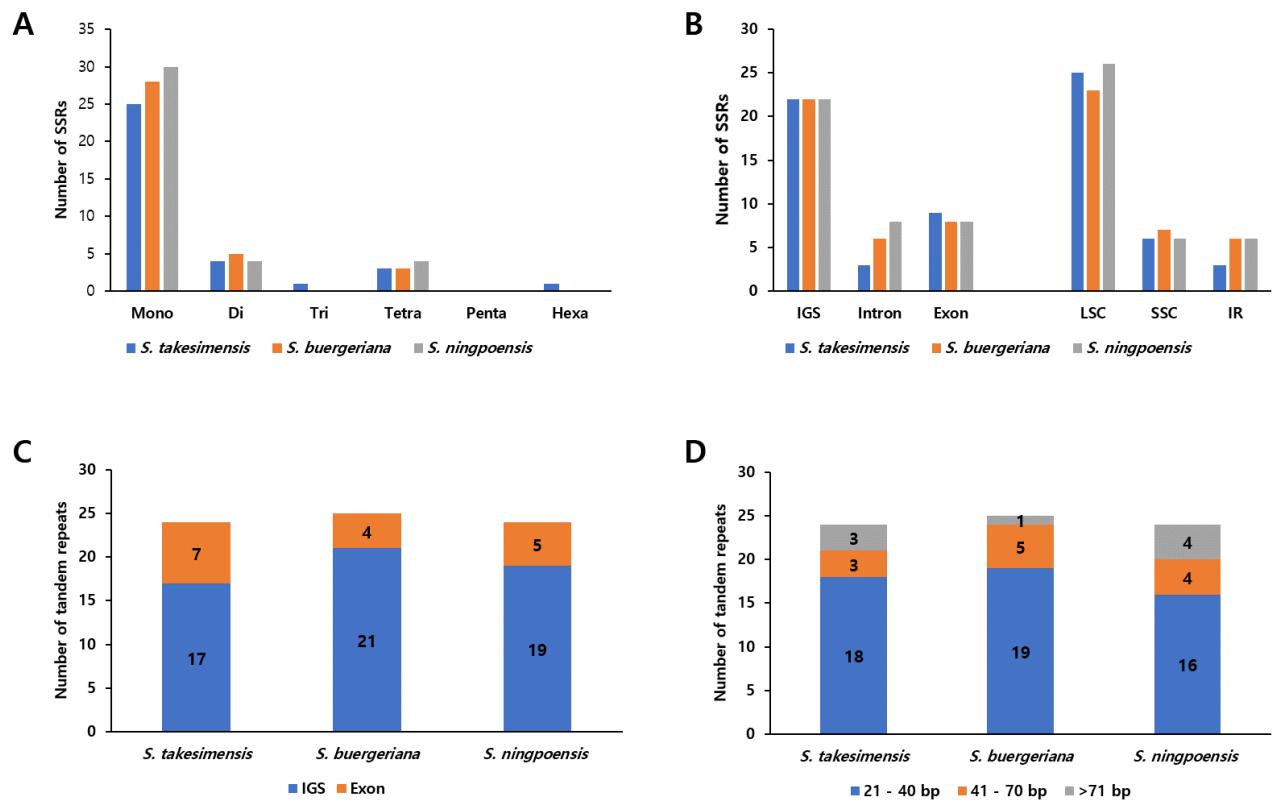
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Supplementary Figures and Tables

## Supplementary Material



**Fig. S1.** Voucher specimens of three *Scrophularia* species. **A.** *S. takesimensis* Nakai. **B.** *S. buergeriana* Miq. **C.** *S. ningpoensis* Hemsl.



**Fig. S2.** The distribution of the repeat sequences in *Scrophularia* chloroplast genomes. (A) Distribution of single se-quence repeats (SSRs) types. (B) The number of SSRs in genomic regions. (C) Distribution of tandem repeats in ge-nomic regions. (D) Distribution of lengths of the tandem repeats

**Table S1 Raw and trimmed read data**

Scientific name	Input reads	Trimmed reads	Total raw bases	Trimmed bases		
<i>S. takesimensis</i>	226,428,024	221,287,500	97.73%	34,190,631,624	32,595,043,159	95.33%

**Table S2 Genome assembly information for *S. takesimensis* chloroplast genomes**

Scientific name	Aligned reads (#)	Coverage (x)	Cp genome length (bp)
<i>S. takesimensis</i>	29,525,085	8,000	152,420

**Table S3 Genes in the chloroplast genomes of *S. takesimensis* species**

Group of genes	Name of genes
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)</sup><sup>3)</sup>, C, D, E, F, G, H, I, J, K</i>
Large subunit ribosomal proteins	<i>rpl2<sup>1)</sup><sup>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)</sup><sup>3)</sup><sup>4)</sup>, 14, 15, 16<sup>1)</sup>, 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<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)</sup><sup>3)</sup>, trnC-GCA, trnD-GUC, trnE-UUC, trnF-GAA, trnfM-CAU, trnG-GCC, trnG-UCC<sup>1)</sup>, trnH-GUG, trnI-CAU<sup>3)</sup>, trnI-GAU<sup>1)</sup><sup>3)</sup>, trnK-UUU<sup>1)</sup>, trnL-CAA<sup>3)</sup>, trnL-UAA<sup>1)</sup>, trnL-UAG, 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-GAC<sup>3)</sup>, trnV-UAC<sup>1)</sup>, trnW-CCA, trnY-GUA</i>

1) Gene containing a single intron, 2) gene containing two introns, 3) two gene copies in IRs, 4) trans-splicing gene

**Table S4 Genic introns in *S. takesimensis* chloroplast genomes**

	Gene	Region	exon I	intron I	exon II	intron II	exon III
1	trnk-UUU	LSC	37	37	2509	35	
2	rps16	LSC	39	44	846	223	
3	trnG-UCC	LSC	23	23	684	47	
4	rpoC1	LSC	435	144	722	411	
5	ycf3	LSC	126	435	757	1620	
6	trnL-UAA	LSC	37	128	707	227	726
7	trnV-UAC	LSC	39	37	488	50	
8	rps12	LSC	114	38	584	37	
9	clpP	LSC	69	114		232	
10	petB	LSC	6	69	730	291	634
11	petD	LSC	8	6	722	642	
12	rpl16	LSC	9	8	734	475	
13	rpl2	LSC	393	9	883	399	
14	ndhB	IR	777	393	664	435	
15	trnI-GAU	IR	42	777	679	756	
16	trnA-UGC	IR	38	42	945	35	
17	ndhA	SSC	552	38	813	35	

**Table S5 Voucher specimen information for floral micromorphology, palynology, and chloroplast genomes, DNA barcode analysis used in this study**

No.	Species	Collection information	Coordinates	Collector collection no. (Herbarium acronym)
1		Deogyusan Mt., Seolcheon-myeon, Muju-gun, Jeollabuk-do, Korea	35°51'27.9"N 127°43'18.9"E	B. Choo & Y. Ji KIOM200901002023 (KIOM) <sup>C, M, P, D</sup>
2	<i>S. takesimensis</i>	Cheonhwangsan Mt., Icheon-ri, Sangbuk-myeon, Ulju-gun, Ulsan, Korea	35°33'29.4"N 128°58'26.4"E	S.C. Ko KIOM201601018272 (KIOM) <sup>M, P, D</sup>
3		Baegunsan Mt., Gwangyang-si, Jeollanam-do, Korea	35°03'06.1"N 127°35'31.8"E	Y. Ji & B. Moon KIOM201101004181 (KIOM) <sup>M, P</sup>

**Table S6 Chloroplast genomes from NCBI used for phylogenetic analysis**

No.	Tribe	Taxon	GenBank accession number
1		<i>Scrophularia takesimensis</i>	KP718628
2		<i>Scrophularia dentata</i>	KT428154
3		<i>Scrophularia takesimensis</i>	NC_026202
4		<i>Scrophularia buergeriana</i>	NC_031437
5	Scrophulariaceae	<i>Scrophularia dentata</i>	NC_036942
6		<i>Scrophularia henryi</i>	NC_036943
7		<i>Scrophularia ningpoensis</i>	NC_053823
8		<i>Scrophularia cephalantha</i>	NC_057296
9		<i>Verbascum phoeniceum</i>	NC_050920
10		<i>Verbascum chinense</i>	NC_051533