## Genetic authentication of

# Cynanchi Wilfordii Radix and Cynanchi Auriculati Radix by Using Conventional-PCR and Real-time PCR

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#### Abstract

The original plant species of Cynanchi Wilfordii Radix belong to the Asclepiadaceae family is differentially described in the national pharmacopoeia of Korea, China and Japan. Dried roots of this plant have been used for prevention and treatment of various diseases in Korea. Owing to the morphological similarities of the dried roots of this plant to those of *Cynanchum auriculatum*, which is often misidentified in Korean herbal medicine marketplace and distinguishing these two species is exceedingly difficult. The aim of this study was to compare the conventional-PCR method with the real-time PCR method for Detection of *Cynanchum wilfordii* and *C. auriculatum* DNA. According to the experimental results, both the conventional-PCR and the real-time PCR method were able to detect the *C. auriculatum* with more than 2% in mixture of *C.wilfordii* and *C. auriculatum*. In the monitoring results of 20 samples, *C.wilfordii* was detected in 19 samples and 1 sample(SP15) was pure *C. auriculatum*. 4 samples was mixture of *C. auriculatum* with *C.wilfordii*. Considering the unintentional mixture(3% or less), there was little difference between the two methods in the case of raw materials. Also in the case of the raw material, the conventional-PCR method.

## Materials and methods

## **Results & Discussion**



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#### Materials Table 1

- Samples were collected at random from Seoul Herbal Medicine Market, which were distributed as agricultural products (20 samples)
- ✓ Standard samples (*C.wilfordii* & *C.auriculatum*) received from MFDS

 Table 1. Information of Herbal Material for Becksuo Used in This Study

Number of Samples	Locality of Collected Samples	Material
13	Yeongju, Gyeongsangbuk-do	
3	Yeongcheon, Gyeongsangbuk-do	
2	Gangwon-do	<b>Dried Root</b>
1	Sangju, Gyeongsangbuk-do	
1	Not confirmed	

#### Method

MFDS guideline<sup>(1)</sup>

#### Analytical procedure Figure 1

- Sample roots were ground to powder by mixer and made into finer particles using No. 50 sieve (300 µm)
- The genomic DNA of each sample was extracted according to the

#### Sensitivity Figure 2

Sensitivity is expressed by Limits of Detection (LOD), which was assessed by analyzing depending on the mixed rate of *C. auriculatum*.



Figure 2. The Conventional-PCR and Real-time PCR detection of *C. auriculatum* adulteration into *C. wilfordii* presented in ratio of 0%, 1%, 2%, 5%, 10%, 20%, 50% and 100% (A) *C. wilfordii* specific primer, (B) *C. auriculatum* specific primer (*C. auriculatum* adulteration ratio 0% (Lane 1), 1% (Lane 2), 2% (Lane 3), 5% (Lane 4), 10% (Lane 5), 20% (Lane 6), 50% (Lane 7), 100% (Lane 8), Negative Control (Lane 9), Size Marker(M), (C) Amplification plot according 1% ~ 100% mixed rate

#### Monitoring Results of 20 samples in Comparative Analysis Table 3

 Table 3. Amplification results of samples using Conventional PCR and Real-time PCR

Conventional-PCR

Real-time PCR

manual for DNeasy<sup>®</sup> Plant Mini Kit (QIAGEN, Germany) and DNA concentration was determined by spectrophotometry (ScanDrop)
 ✓ Extracted DNA was amplified using 7500 Fast Real-Time PCR and Thermal Cycler (AERIS-BD048)







Preparation of Samples

**DNA** Extraction

Polymerase Chain Reaction

Figure 1. Procedure of PCR analysis

 Table 2. Information of species-primer sets used in this study

Species	Primer Sequences(5'→3')		SP13	SP13 +	SP13 + -	SP13 + - +	SP13 + - + +
C. wilfordii	ATA TTA TAT TCT AAA ATT AGA T		SP14	SP14 +	SP14 + -	SP14 + - +	SP14 + - + +
	ΔΛΑ ΤΩΑ ΑΤΤ ΤΑΑ ΑΛΑ ΤΤΟ ΑΑΤ ΑΟΑ		SP15	SP15 -	SP15 - +	SP15 - + +	SP15 - + + -
C. auriculatum	GTT CTA TTT CTA TTT ATT TTT AT		SP16	SP16 +	SP16 + -	SP16 + - +	SP16 + - + +
PAC	TCT GCC CTA TCA ACT TTC AAT GGT A		SP17	SP17 +	SP17 + -	SP17 + - +	SP17 + - + +
Real-time PCR <i>C. wilfordii</i>	AAT TTG CGC GCC TGC TGC CTT CCT T		SP18	SP18 +	SP18 + +	SP18 + + +	SP18 + + + +
	CAA AAA AGC CCG TAG		SP19	SP19 +	SP19 + -	SP19 + - +	SP19 + - + +
C. auriculatum	CTT GTT CCA ATT ATT CC		SP20	SP20 +	SP20 + -	SP20 + - +	SP20 + - + +
	AAT GAG AAA AGT TTC TG		<sup>+</sup> : Detected, <sup>-</sup>	+: Detected, -: Not detecte	*: Detected, -: Not detected	*: Detected, -: Not detected	*: Detected, <sup>-</sup> : Not detected
	SpeciesC. wilfordiiPACC. wilfordiiC. auriculatum	SpeciesPrimer Sequences(5'→3')C. wilfordiiATA TTA TAT TCT AAA ATT AGA T CTC TAT TTC TAT TTC TATC. auriculatumAAA TGA ATT TAA AAA TTC AAT ACA GTT CTA TTT CTA TTT ATT TTT ATPACTCT GCC CTA TCA ACT TTC AAT GGT A AAT TTG CGC GCC TGC TGC CTT CCT TC. wilfordiiGCG TAT ATG TAG AAA CC 	SpeciesPrimer Sequences(5' $\rightarrow$ 3')SP13C. wilfordiiATA TTA TAT TCT AAA ATT AGA T CTC TAT TTC TAT TTC TATSP14C. auriculatumAAA TGA ATT TAA AAA TTC AAT ACA GTT CTA TTT CTA TTT ATT ATTSP15PACTCT GCC CTA TCA ACT TTC AAT GGT A AAT TTG CGC GCC TGC TGC CTT CCT T SP18SP17C. wilfordiiGCG TAT ATG TAG AAA CC CAA AAA AGC CCG TAGSP19C. auriculatumCTT GTT CCA ATT ATT CC AAT GAG AAA AGT TTC TGSP20*: Detected, T*: Detected, T	SpeciesPrimer Sequences(5'3')SP13+C. wilfordiiATA TTA TAT TCT AAA ATT AGA T CTC TAT TTC TAT TTC TATSP14+C. auriculatumAAA TGA ATT TAA AAA TTC AAT ACA GTT CTA TTT CTA TTT ATT ATT TT CTA TTT CTA TTT ATT AAT TTG CGC GCC TGC TGC CTT CCT T CAA AAA AGC CCG TAGSP15-PACTCT GCC CTA TCA ACT TTC AAT GGT A AAT TTG CGC GCC TGC TGC CTT CCT T CAA AAA AGC CCG TAGSP17+C. wilfordiiGCG TAT ATG TAG AAA CC CAA AAA AGC CCG TAGSP19+C. auriculatumCTT GTT CCA ATT ATT CC AAT GAG AAA AGT TTC TGSP20+*: Detected, :: Not detected	SpeciesPrimer Sequences(5'→3')SP13+-C. wilfordiiATA TTA TAT TCT AAA ATT AGA T CTC TAT TTC TAT TTC TAT CTC TAT TTC TAT TTC TAT GTT CTA TTT CTA TTT CTA TT GTT CTA TTT CTA TTT ATT PACSP14+-MAA TGA ATT TAA AAA TTC AAT ACA GTT CTA TTT CTA TTT ATT TTC GCC CTA TCA ACT TTC AAT ACA GTT CTA TTT CTA TTT ATT PACSP16+-PACTCT GCC CTA TCA ACT TTC AAT GGT A AAT TTG CGC GCC TGC TGC CTT CCT T CAA AAA AGC CCG TAGSP17+-C. wilfordiiGCG TAT ATG TAG AAA CC CAA AAA AGC CCG TAGSP19+-C. auriculatumCTT GTT CCA ATT ATT CC AAT GAG AAA AGT TTC TGSP20+-*: Detected, :: Not detected	SpeciesPrimer Sequences(5'→3')SP13+-+C. wilfordiiATA TTA TAT TCT AAA ATT AGA T CTC TAT TTC TAT TTC TAT CTC TAT TTC TAT TTC TAT GTT CTA TTT CTA TTT CTA TT GTT CTA TTT CTA TTT ATT PACAAA TGA ATT TAA AAA TTC AAT AGA GTT CTA TTT CTA TTT ATT TTT AT TTG CGC GCC TGC TGC CTT CCT T C. wilfordiiSP13+-+PACTCT GCC CTA TCA ACT TTC AAT GGT A AAT TTG CGC GCC TGC TGC CTT CCT T C. wilfordiiGCG TAT ATG TAG AAA CC CAA AAA AGC CCG TAGSP17+-+C. wilfordiiGCG TAT ATG TAG AAA CC CAA AAA AGC CCG TAGSP19+-+C. auriculatumCTT GTT CCA ATT ATT CC AAT GAG AAA AGT TTC TGSP20+-+*: Detected, ': Not detected	SpeciesPrimer Sequences(5'→3')SP13+-++C. wilfordiiATA TTA TAT TCT AAA ATT AGA T CTC TAT TTC TAT TTC TAT CTC TAT TTC TAT TTC TAT GTT CTA TTT CTA TTT CTA TTT AT PACAAA TGA ATT TAA AAA TTC AAT ACA GTT CTA TTT CTA TTT CTA TTT ATT TTG CGC GCC TGC TGC CTT CCT T C. wilfordiiAAA TGA ATT TAG AAA CC CCAA AAA AGC CCG TAGSP13+-++PACTCT GCC CTA TCA ACT TTC AAT GGT A AAT TTG CGC GCC TGC TGC CTT CCT T C. wilfordiiGCG TAT ATG TAG AAA CC CAA AAA AGC CCG TAGSP17+-++SP18++++++++C. auriculatumCTT GTT CCA ATT ATT CC AAT GAG AAA AGT TTC TGSP20+-++*: Detected, :: Not detected

	C. wilfordii	C. auriculatum	PAC	C. wilfordii	C. auriculatum
SP1	+	_	+	+	-
SP2	+	-	+	+	-
SP3	+	-	+	+	-
SP4	+	-	+	+	-
SP5	+	-	+	+	-
SP6	+	+	+	+	+
SP7	+	-	+	+	-
SP8	+	-	+	+	-
SP9	+	+	+	+	+
SP10	+	-	+	+	-
SP11	+	+	+	+	-
SP12	+	-	+	+	-
SP13	+	-	+	+	-
SP14	+	-	+	+	-
SP15	-	+	+	-	+
SP16	+	-	+	+	-

## Conclusion

✓ Both the conventional-PCR and the real-time PCR method were able to detect the C. auriculatum with more than 2% in mixed samples.

- C. wilfordii was detected in 19 samples and 1 sample(SP15) was pure C. auriculatum, 4 samples was mixture of C. auriculatum with C.wilfordii.
- In the case of the raw material, the conventional-PCR method detected the C. auriculatum at a detection level similar to the real-time PCR

### Reference

(1) MFDS Guideline : Detection of Cynanchum wilfordii and C. auriculatum DNA using conventional-PCR and real-time PCR(2015, 2016, 2017)

(2) Kyu-Heon Kim et al., : Development of Primer Sets for the Detection of Polygonum multiflorum, Cynanchum wilfordii and C. auriculatum. J. Food Hyg. Saf.,

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