RESEARCH ARTICLE

Taylor & Francis

∂ OPEN ACCESS

() Check for updates

Development of Genomic Simple Sequence Repeat Markers for Evaluating Resources of Armillaira ostoyae and Their Transferability to Armillaira gallica

Sohee Kim 🝺 and Hwayong Lee 🝺

Department of Forest Science, Chungbuk National University, Cheongju, Republic of Korea

ABSTRACT

In this study, we aimed to develop simple sequence repeat (SSR) markers for evaluating resources in Armillaria ostoyae and examine their transferability to Armillaria gallica, related species. SSR markers were developed using the released A. ostoyae whole-genome sequence (GenBank assembly accession: GCA_900157425.1). The SSR regions were analyzed using the MISA (MIcroSAtellite identification tool) program. A total of 2319 SSR loci consisting of 922 (39.76%) mononucleotide, 763 (32.90%) trinucleotide, and 517 (22.29%) dinucleotide motifs were identified. Marker design involved an arbitrary choice of 150 SSR loci, considering motif abundance. A total of 22 strains of A. ostoyae were analyzed using the developed markers, and 105 markers were successfully amplified. The mean values of major allele frequency, number of alleles, expected heterozygosity, observed heterozygosity, and polymorphism information content (PIC) values were approximately 5.89, 5.4, 0.541, 0.255, and 0.504, respectively. A. gallica was analyzed, and 52 markers (49.5%) were successfully amplified to evaluate the transferability of the developed SSR markers. When these markers were used, the mean values of major allele frequency, number of alleles, expected heterozygosity, observed heterozygosity, and PIC were calculated to be approximately 0.615, 4.3, 0.517, 0.133, and 0.502, respectively. In conclusion, SSR markers were developed using the genome of A. ostoyae, and some of these markers exhibited transferability to A. gallica. These results can be used for resource evaluation of A. ostoyae and A. gallica.

1. Introduction

Armillaria, taxonomically belonging to the family Physalacriaceae within the phylum Basidiomycota, encompasses approximately 40 species worldwide [1]. They are white-rot fungi capable of decomposing lignin and parasitizing various coniferous and deciduous trees, woody vines, and even stumps [2].

These fungal species are pathogens of various plants, and their pathogenicity varies depending on the species [3]. Rhizomorphs are subterranean, cord-like structures measuring 1-5mm in diameter, composed of tightly packed hyphae surrounded by a melanized outer layer that provides protection against environmental stress and facilitates extension into the surrounding soil. This form of vegetative propagation enables Armillaria species to establish large genets that can persist in forest ecosystems for centuries or even millennia. Functionally, rhizomorphs facilitate efficient nutrient and water transport over long distances and play a critical role in host root colonization and infection [4-6].

Genotypes derived from vegetative propagation maintain stable habitats and exhibit high longevity, influencing multiple generations of host trees and potentially affecting forest structure and dynamics [7,8]. Additionally, Armillaria species can spread over long distances by wind through basidiospores [7]. These two dispersal strategies may affect population genetic structure; therefore, genetic markers are needed to reveal them at different spatial scales [7]. Assessment of the extent to which sexual and asexual reproduction influence population structure and disease transmission can help develop novel pathogen management strategies [9].

Armillaria species are also used in functional foods. Also known as honey mushroom, it has antioxidant [10], antibacterial [11], and anticancer [12] properties, and experiments using mice have revealed its potential to alleviate insomnia [6,13]. Molecular markers are widely used for the management of genetic resources. For example, they are essential tools for identifying varieties [14,15]. Additionally, molecular markers aid in

ARTICLE HISTORY

Received 29 July 2024 Revised 9 December 2024 Accepted 15 December 2024

KEYWORDS

Armillaria ostoyae; SSR marker; Armillaria gallica; transferability

CONTACT Hwayong Lee 🔯 leehy@chungbuk.ac.kr © 2025 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group on behalf of the Korean Society of Mycology.

This is an Open Access article distributed under the terms of the Creative Commons Attribution-NonCommercial License (http://creativecommons.org/licenses/bv-nc/4.0/). which permits unrestricted non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited. The terms on which this article has been published allow the posting of the Accepted Manuscript in a repository by the author(s) or with their consent.

the early selection and analysis of population structure [16]. Molecular markers are effective tools for evaluating genetic diversity because they are based on the genotypes of genetic resources and independent of environmental variations. Therefore, resource evaluation using molecular markers is necessary for the efficient utilization of *Armillaria* [17].

With the increasing importance of genetic information and advancements in molecular biology, there is a growing demand for genome analysis and genetic diversity assessments [18]. The main markers used for genetic diversity analysis include single nucleotide polymorphism (SNP), and simple sequence repeats (SSR). SSR consist of 1-6bp repeat sequences within the genome [19]. While incurring high initial development costs such as sequencing and primer design, SSR loci may possess high polymorphism information content (PIC) and harbor multiple alleles at each locus. Consequently, they are widely used for genetic diversity analysis, pedigree analysis, and population structure studies [20]. Comparative genetics has shown that SSR loci are highly conserved among closely related species, and the collinearity of common markers in comparative maps suggests that markers from one genus or species are present in other related genera/species [21,22]. Therefore, the application of SSR markers developed from one species to another by exploiting transferability, which allows the detection of marker sequences of related species using primer pairs designed based on sequences obtained from one species, has been successfully demonstrated in many species [23]. This approach eliminates the need to develop new markers for each species, making it economically efficient. Among the Armillaria, SSR markers were developed using several sequences of Armillaria mellea, Armillaria gallica, and Armillaria ostoyae [24], eight EST-based SSR markers for Armillaria luteo-virens were developed through 454 pyrosequencing [25], and 17 SSR markers were developed using 32 single-copy protein-coding genes of 12 Armillaria cepistipes samples [7]. In addition, Prospero and coauthors [7] isolated eight polymorphic SSR markers for A. cepistipes and confirmed that six markers were polymorphic in A. gallica, four in A. ostoyae, two in A. mellea, and one in Armillaria borealis. According to comparative genetics, A. gallica and A. cepistipes are closely related, with A. ostoyae being the next closest relative [26-28]. A. gallica is widely distributed in Korea and plays a significant role in forest ecosystems as a decomposer and a pathogen. However, the distribution of A. cepistipes is limited in Korea [29]. Therefore, this study focused on A. galliga [29]. We developed polymorphic SSR markers for *A. ostoyae* based on whole-genome sequences and tested their transferability to *A. gallica.*

2. Materials and methods

2.1. Armillaria strains

All *Armillaria* strains used in this study were obtained from the National Institute of Forest Science, Korea National Arboretum, and Forest Mushroom Research Institute. The study used 22 of the 40 strains of *A. ostoyae* (Table 1) and 16 strains of *A. gallica* (Table 2) from different locations in Korea. *A. ostoyae* and *A. gallica* were selected based on their *Armillaria* genet [30,31]. Mycelia of these strains were extracted and identified using the ITS1/ITS4 region.

2.2. SSR screen and primer design

We used the genome of A. ostoyae registered at NCBI (GenBank assembly accession: GCA_900157425.1), for SSR loci analysis. This Swiss genome was used as a reference for comparative genomic analysis in China [32]; and was utilized for analyzing the viruses in Czech samples [33], and a phylogenetic tree based on the whole genomes of Armillaria species showed that it was most closely related to samples from Vermont and Idaho in the United States [34]. We conducted SSR locus exploration using Microsatellite (MISA; https://webblast.ipk-gatersleben.de/ Finder misa/), setting the criteria based on SSR motifs as follows: dinucleotide repeats with a minimum of six repetitions, trinucleotide repeats with a minimum of five repetitions, and tetranucleotide repeats with a minimum of five or more repetitions. Considering the ratio of the number of motifs, 150 loci (60 dinucleotide repeats, 80 trinucleotide repeats, and 10 tetranucleotide repeats) were selected using a random number generation program (Random Number Generator: https://www.minzkn.com/random.html) (Table 3). Primers for SSR amplification were designed using Primer 3 PLUS program (https://www. bioinformatics.nl/cgibin/primer3plus/primer3plus.cgi) under the following conditions: primer length of 20 mer, Polymerase Chain Reaction (PCR) product size ranging from 150–200 bp, Melting Temperature (TM) set at 55°C, and a G/C ratio between 40% and 60%.

2.3. PCR and fragment analysis

Fungal strains were cultured on PDA (Potato Dextrose Agar) medium. Mycelia grown on PDA plates were fully harvested after 2 weeks, rapidly

Table 1. Information on Armillaria ostoyae strains used in this study.

No.	Strain name	Collecting location	Best match	Identity (%)
1	Nifos 321ª	10 Go Nishikagura 1 Sen, Asahikawa, Hokkaido	A. ostoyae (KT822292.1)	99.51
2	Nifos 846 ^a	Mt. Heibang Goesan-gun, Chungcheongbuk-do	A. ostoyae (KT822292.1)	99.75
3	Nifos 848 ^a	Mt. Odaesan, Jinbu-myeon, Pyeongchang-gun, Gangwon-do	A. ostoyae (KT822292.1)	99.4
4	Nifos 1230 ^a	Yeonggwimi-myeon, Hongcheon-gun, Gangwon-do	A. ostoyae (MG931931.1)	99.47
5	Nifos 1954 ^a	Yeonggwimi-myeon, Hongcheon-gun, Gangwon-do	A. ostoyae (KT822311.1)	96.26
6	Nifos 1957 ^a	Yeonggwimi-myeon, Hongcheon-gun, Gangwon-do	A. ostoyae (OK324328.1)	99.75
7	Nifos 2299 ^a	770 m, 165, Mt. Jungwhang Daehwa-myeon, Pyeongchang-gun, Gangwon-do	A. ostoyae (MG931931.1)	99.83
8	Nifos 2304ª	899 m, 164, Mt. Jungwhang Daehwa-myeon, Pyeongchang-gun, Gangwon-do	A. ostoyae (OP787670.1)	99.63
9	Nifos 2305 ^a	764 m, 165, Mt. Jungwhang Daehwa-myeon, Pyeongchang-gun, Gangwon-do	A. ostoyae (KT822292.1)	99.64
10	Nifos 2306 ^a	126, Mt. Jungwhang Daehwa-myeon, Pyeongchang-gun, Gangwon-do	A. ostoyae (OP787670.1)	99.63
11	Nifos 2307 ^a	125, Mt. Jungwhang Daehwa-myeon, Pyeongchang-gun, Gangwon-do	A. ostoyae (KT822292.1)	99.88
12	Nifos 2309 ^a	906 m, 164, Mt. Jungwhang Daehwa-myeon, Pyeongchang-gun, Gangwon-do	A. ostoyae (OP688126.1)	100
13	Nifos 2310 ^a	1109 m. 125, Mt. Jungwhang Daehwa-myeon, Pyeongchang-gun, Gangwon-do	A. ostoyae (KT822292.1)	99.87
14	Nifos 2311ª	1061 m, 125, Mt. Jungwhang Daehwa-myeon, Pyeongchang-gun, Gangwon-do	A. ostoyae (OP688126.1)	99.75
15	Nifos 2312 ^a	126, Mt. Jungwhang Daehwa-myeon, Pyeongchang-gun, Gangwon-do	A. ostoyae (MG931719.1)	99.58
16	Nifos 2313ª	124, Mt. Jungwhang Daehwa-myeon, Pyeongchang-gun, Gangwon-do	A. ostoyae (KT822292.1)	99.75
17	Nifos 2318 ^a	125, Mt. Jungwhang Daehwa-myeon, Pyeongchang-gun, Gangwon-do	A. ostoyae (KT822292.1)	98.02
18	20120925-72 ^b	Yongsanbong, Sapyeong 1-gil, Gagok-myeon, Danyang-gun, Chungcheonabuk-do	A. ostoyae (OP688126.1)	99.88
19	FMRI 7971 ^c	Mt. Balwang, Jinbu-myeon, Pyeongchang-gun, Gangwon-do	A. ostoyae (AB510896.1)	99.72
20	FMRI 7687°	Yeoju-si, Gyeonggi-do	A. ostoyae (MH550355.1)	99.04
21	KA15-0657 ^b	Mt. Mahwa, Hongcheon-gun, Gangwon-do	A. ostoyae (MG931722.1)	99.71
22	KA17-0855 ^b	Mt. Cheongok, Socheon-myeon, Bonghwa-gun, Gyeongsangbuk-do	A. ostoyae (MG696210.1)	96.91

The best match is the sequence identified from NCBI.

^aNational Institute of Forest Science.

^bKorea National Arboretum.

^cForest Mushroom Research Institute.

Table 2	Information	on Armil	laria aallica	strains	used in	this study.

No.	Strain name	Collecting location	Best match	Identity (%)
1	Nifos 569ª	57, Hoegi-ro, Dongdaemun-gu, Seoul	A. gallica (MG931780.1)	100
2	Nifos 570 ^a	57, Hoegi-ro, Dongdaemun-gu, Seoul	A. gallica (KY474051.1)	99.51
3	Nifos 847 ^a	Donghae-daero, Sonyang-myeon, Yangyang-gun, Gangwon-do	A. gallica (KY474051.1)	99.49
4	Nifos 997 ^a	Mt. Joryeong, Yeonpung-myeon, Goesan-gun, Chungcheongbuk-do	A. gallica (KY389173.1)	99.75
5	Nifos 1572 ^a	163 Mt. Gariwang, Daehwa-myeon, Pyeongchang-gun, Gangwon-do	A. gallica (KY474051.1)	99.39
6	Nifos 2010 ^a	Mt. Maebong, Daehwa-myeon, Pyeongchang-gun, Gangwon-do	A. gallica (KP162327.1)	99.62
7	Nifos 5063ª	Mt. Bukhan 375, Daeseomun-gil, Deogyang-gu, Goyang-si, Gyeonggi-do	A. gallica (KY474051.1)	99.51
8	FMRI-7088c	N. A	A. gallica (KY474051.1)	99.51
9	FMRI-7091c	N. A	A. gallica (KY474051.1)	99.75
10	FMRI-7930c	N. A	A. gallica (AY213570.1)	99.75
11	FMRI-7937c	Tapdong-gil, Jinbu-myeon, Pyeongchang-gun, Gangwon-do	A. gallica (AB716750.1)	99.51
12	FMRI-7135c	N. A	A. gallica (AY213570.1)	99.51
13	KA12-1405b	Nari Basin, Ulleung-gun, Gyeongsangbuk-do	A. gallica (MW947449.1)	99.02
14	KA13-1053b	Mt. Hwangmae Hapcheon-gun, Gyeongsangnam-do	A. gallica (KY474051.1)	99.88
15	KA13-1130b	Gwangneung Forest, Soheul-eup, Pocheon-si, Gyeonggi-do	A. gallica (AB510881.1)	99.63
16	KA17-0949b	Baeknokdam, Odeung-dong, Jeju-s	A. gallica (MW418538.1)	99.4

N. A: Not Available; the best match is the sequence identified from NCBI.

^aNational Institute of Forest Science.

^bKorea National Arboretum.

^cForest Mushroom Research Institute.

frozen in liquid nitrogen, and ground into powder using a mortar and pestle. The crushed samples were subjected to DNA extraction using the GenEx^m

Plant kit (GeneAll, Seoul, Republic of Korea) The extracted DNA was then adjusted to a concentration of $20 \text{ ng/}\mu\text{L}$ using distilled water and used as

Marker name	SSR motif		SSR primer set $(5' \rightarrow 3')$	Product size (bp)
FEL-AO-001	(AC)8	F:	GTAATGGGCACTCGTGAAAC	151
551 4.0 000		R:	TGAGATACTGTCAGGGCACA	4.65
FEL-AO-002	(TC)6	F:		163
FFL-AO-003	(AT)7	К: F·		191
	(717)	R.	GCAACATGGGAATTTTTCTG	171
FEL-AO-004	(TG)6	F:	CGAGGAGATAGCGAAATTGA	195
		R:	AGCATGAACACCACCCTAAA	
FEL-AO-005	(GT)7	F:	TAAATTCCTTGCTCCCTTCC	163
		R:	GTGAGCCAGAAAAATGTGCT	151
FEL-AU-000	(CA)6	Г: D,		151
FEL-AO-007	(AG)7	F:	GATGAGATACGGGAGCAATG	155
		R:	TTACAACCAAGGGACGAGAG	
FEL-AO-008	(AT)8	F:	GCGTCGGTTTGTGTATGATT	183
		R:	TCTAGCCCGACATGTTCAGT	
FEL-AO-009	(TC)6	F:		156
FFL-AO-010	(GA)7	R: F·	GAAGCTCCATCAGCACAGTT	196
		R:	CTTCCTTCAACTTGCATCGT	150
FEL-AO-011	(AC)8	F:	CCAGATGCAACCAGAGAACT	176
		R:	TAAATTCCTTGCTCCCTTCC	
FEL-AO-012	(AT)6	F:	CTGTTAGCGTCAAAACGATG	180
	(AT)6	R:	AIGCIAICACCGIGICCAAI	165
FEL-AU-UIS	(AT)0	г. D.		105
FEL-AO-014	(TG)6	F:	GAGGGAGTATGGATGTCACG	151
		R:	TCCATCCATCACCCAATATC	
FEL-AO-015	(AC)8	F:	GGCACTCGTGGAACTAAGTG	199
	(10)	R:	TTGACAATTGTACGCAGTCG	100
FEL-AO-016	(AC)6	F:		198
FFL-AO-017	((G)6	R: F·	CGCTTTCCCTTTTTCTTCT	165
	(60)0	R:	GTCCAAACAAAAGCAGCAGT	105
FEL-AO-018	(CT)6	F:	GTTGCTTGCGGTCAATATCT	166
		R:	GTCGAGAGACGAGCAAACAT	
FEL-AO-019	(TG)10	F:	CTTGCTCCCTTCTGCACTTA	154
FEL-40-020	(46)8	К: F·		163
1 LL-AO-020	(AG)0	R.	CCACCATCAGCTCCTTTTTA	105
FEL-AO-021	(GT)6	F:	CTTGCTCCCTTCTGCACTTA	188
		R:	CCTGAGGAGAAATGTCATGG	
FEL-AO-022	(GT)8	F:	ATCGCGTTGCATTACTTAGC	157
	(AC)7	R:	GCAIGAACAACACCAAAA	100
FEL-AU-025	(AC)/	г. В-		100
FEL-AO-024	(GT)8	F:	ATCGCGTTGCATTACTTAGC	161
		R:	GCCTAGCGTGAACAACACTC	
FEL-AO-025	(GT)8	F:	ATCGCGTTGCATTACTTAGC	168
	(ΛC)	R:	AAGCATGGCCTAGTGTGAAC	175
FEL-AU-020	(AG)7	г. В·		175
FEL-AO-027	(AC)6	F:	GCGTGAACAACACCCTAATC	153
		R:	ATCGCGTTGCATTACTTAGC	
FEL-AO-028	(GT)10	F:	ATCGCGTTGCATTACTTAGC	198
	(16)0	R:	ATTACCGAGCACATCATCGT	171
FEL-AU-029	(AC)8	F: D.		171
FEL-AO-030	(AC)8	F:	GTAACGGGCACTCATGAAAC	189
		R:	ATCGCGTTGCATTACTTAGC	
FEL-AO-031	(AT)6	F:	ATGGCGAGGTAGGTTTTTCT	152
		R:	ACAAAGACCCCTCCATTCTC	407
FEL-AU-032	(GT)7	F:		187
FFI-AO-033	(CT)6	к: F·		170
//0 033	(01)0	R:	GGGAGAATGTTCAGCAGATG	
FEL-AO-034	(GT)8	F:	TTCCTTGCTCTTCCACAC	198
		R:	TAGAAATGGATACCGGCAGA	
FEL-AO-035	(AT)6	F:	TTCAAGTGAGCGCTATGTCA	192
		К:		

 Table 3. SSR loci selected from the whole genome of Armillaria ostoyae (GenBank assembly accession: GCA_900157425.1).

Tab	le	3.	Contin	nued

FEL-A0-036 (AC)6 F: CTAACGGCCACTCATACTTAGC 155 FEL-A0-037 (TG)12 F: TGCAGTCACTTACTTAGC 154 FEL-A0-038 (TG)8 F: ATGCGGTCACTTACTTAGC 154 FEL-A0-039 (GT)6 F: CGTGGACAACACCTTAGC 179 FEL-A0-040 (AG)7 F: ACGCGTTACATGCTCGC 179 FEL-A0-041 (AC)7 F: CGCATTACTGCTCACAGGGGACAT 122 FEL-A0-042 (GA)6 F: ATAGTCTCACAGGGGACACT 123 FEL-A0-043 (GG)7 F: GGCATTAGTGCTCACAGGGGCACACT 128 FEL-A0-044 (GA)6 F: CGCATTAGTGCACACTC 158 FEL-A0-043 (GG)7 F: GGCCATTAGTGCAGGCACT 158 FEL-A0-044 (GA)6 F: CCCCGGATTATCGCACACT 158 FEL-A0-044 (GA)7 F: GGCCATTGCATAGTGCACACT 158 FEL-A0-045 (AC)9 F: CCCCGGATTTCGATAGG 184 FEL-A0-046 (GT)6 F: CGCCATTGGCATGGGGA	Marker name	SSR motif		SSR primer set $(5' \rightarrow 3')$	Product size (bp)
R: ATCGCGTTGCATTACTTAGC FEL-A0-037 (TG)2 F: TGCATTCCAGTGCATACTTAGC 154 FEL-A0-038 (TG)8 F: ATCGCGTTGCATTACTTAGC 154 FEL-A0-039 (GT)6 F: CGTGAACAACACCCTAAACC 179 FEL-A0-040 (AG)7 F: ACGCGATTACTTAGTGCGTCCT 179 FEL-A0-041 (AC)7 F: GCCATTACTTGCTCCTGCT 182 FEL-A0-042 (GA)6 F: ATAGTGTTGCAGGGCACAT 182 FEL-A0-043 (GC)7 F: GCCATTACTAGGGCTCACT 182 FEL-A0-043 (GC)7 F: GCGCTAGTACTGCCGTGAT 170 R TGCATACTAGGCCAACT R TGCATACTAGCGCAACAT 183 FEL-A0-043 (GC)7 F: GCGGCTATACTAGCGTGATACT 151 FEL-A0-044 (AG)8 F: CCTGGATATCTACGAACAACT 188 FEL-A0-045 (AC)9 F: CGGGCATACAGCGTCCACCAAAAAAT 154 FEL-A0-047 (AG)7 F: GGGGCTACACGGTAACACACT 158 <td< td=""><td>FEL-AO-036</td><td>(AC)6</td><td>F:</td><td>GTAACGGGCACTCATGAAAC</td><td>185</td></td<>	FEL-AO-036	(AC)6	F:	GTAACGGGCACTCATGAAAC	185
PEL-MO-035 (10)12 F. INCARICARCE (TACINTICATING) (17.3) RELAD-038 (170)8 F. ATLCGCGTTACTATACTACC [154] FEL-AD-039 (GT)6 F. CGTGAACAACCCCTAAACC [179] FEL-AD-040 (A0)7 F. ACGCCAATTGGATACTACCATCG [182] FEL-AD-041 (A0)7 F. CGCCAACTTCTCTCCCTCTCCCTCTCCCTCCCTCCCCTC		(TC)12	R:	ATCGCGTTGCATTACTTAGC	175
Fell ACCGCGTICGATTAGCTIGGC 154 Fell AO-039 (GT)6 F: GCGTAMACACCCTAACCC 179 Fell AO-040 (AG)7 F: GCGCACATTIGTAATCCATCC 179 Fell AO-040 (AG)7 F: GCCATACATCACCCTCTAAT 182 Fell AO-041 (AG)7 F: GCCATACATCACTCCTCTCAAT 182 Fell AO-042 (GA)6 F: AAACTCAATGTCGACCTCGTGA 193 Fell AO-043 (GO)7 F: GCGTACATGTACTGACTGACT 182 Fell AO-044 (GA)6 F: CCCGTGATATGACGTATGG 170 Fell AO-044 (GA)6 F: CCCGTATGATATGACGTATG 188 Fell FC CAACCAATTGCAAGAAGACC 151 152 Fell AO-044 (GA)6 F: CCGCATGTATGACACT 158 Fell AO-045 (AC)9 F: CAACCAATTGCAAGAACACCT 154 Fell AO-047 (AG)7 F: CACCACTTGAATACACACACT<	FEL-AU-037	(10)12	F. R:	GTGGCCTAGTGTGAACAACA	175
R: CGTGAACAACCCCTAAACC FEL-A0-39 (G1)6 F: CGTCAATTGGATCACTGCT FEL-A0-39 (G1)7 F: CGCCATTAGTGACGACTGG 182 FEL-A0-404 (AC)7 F: CGCCATTAGTGACGACTGG 182 FEL-A0-041 (AC)7 F: CGCCATTAGTGACGACTGGGATG 193 FEL-A0-042 (GA)6 F: ATAGTTCTGGCTCCGGGATG 170 FEL-A0-043 (G3)7 F: GGCGCTAGTATTGCGGCACACT 151 FEL-A0-044 (GA)6 F: CCATGTATTGCAGCTGGATGGC 151 FEL-A0-044 (GA)6 F: CCATGTGATTGCAGGACACT 158 FEL-A0-045 (AC)9 F: CAAGCGTGGATGAGCACT 158 FEL-A0-046 (AT)6 F: CCATCTGTAGTGATGAGCACT 158 FEL-A0-047 (AG)7 F: CGAGCTGTGATAGACCACT 154 FEL-A0-048 (GT)8 F: CCTGCGATTGCAACATTAG 153 FEL-A0-049 (CG)6 F: CCCGCATAGCACACACACT 177 FEL-A0-049 (CG)6	FEL-AO-038	(TG)8	F:	ATCGCGTTGCATTACTTAGC	154
PEL-A0-040 (G1)6 P: CLCACAT TIGRATICATICC 17.9 RE ATGATCATGGGGTCATGG 182 FEL-A0-040 (A0]7 F: ACGCATTAGGGGTCATGG 182 FEL-A0-041 (A0]7 F: GCCATTGACTGGGTCATAGGGGTCATG 162 FEL-A0-042 (GA)6 F: MAGTTGTCAACTGGTTCTGGTATG 162 FEL-A0-043 (CG)7 F: GGCGTCAGTATCTGGGGAAGC 170 FEL-A0-044 (GA)6 F: CCGGTGAATGAGCAACC 151 FEL-A0-044 (GA)6 F: CCGGTGAATGAGCAACC 158 FEL-A0-046 (AT)9 F: CGGCGTATGAGGTGCAACG 158 FEL-A0-046 (AT)6 F: CCAGGTGTCCAACGAAAAAT 154 FEL-A0-048 (GT)8 F: CGGCCTAGCATGAAAAAAT 154 FEL-A0-048 (GT)8 F: CGGCCTGGAATGCACGAAAAAAT 154 FEL-A0-048 (GT)8 F: CGGCCTGGAATCACGAAAAAACCTCAGA 176 FEL-A0-049 (CG)6 F: CGCGCAATCACCAACAAACACCTCACGA 177 <td></td> <td></td> <td>R:</td> <td>CGTGAACAACACCCTAAACC</td> <td>470</td>			R:	CGTGAACAACACCCTAAACC	470
FEL-A0-040 IAG ACCECATINACTIAC ACTIGG 182 FEL-A0-041 (AC)7 F: CCCATINACTIACCACTGG 182 FEL-A0-042 (GA)6 F: TTAAACTCCTGACTCCCTTCC 182 FEL-A0-042 (GA)6 F: ATACTCTGACTCCCGTGA 193 FEL-A0-043 (CG)7 F: GCGTCACATTGCACTCCGTGAC 151 FEL-A0-044 (GA)6 F: CCCGGTGATATTGCGACTCCGTGAG 151 FEL-A0-044 (GA)6 F: CCCGGTGATATGCAAGGACC 151 FEL-A0-044 (GA)6 F: CCCGGTGGATATGCCAAGC 158 FEL-A0-044 (AC)9 F: CAAGGGTGGTGATGGACCGACACT 158 FEL-A0-046 (AT)6 F: CCCGCATTGCAGGTGCAAGCACT 154 FEL-A0-047 (AC)7 F: CAGGGGTTCCACCGAAAAGCT 154 FEL-A0-048 (GT)8 F: CATCCCCGTGAAAAAGCT 176 FEL-A0-050 (TC)6 F: AGCGCCTGAGGAACAACACT 176 FEL-A0-051 (AC)7 F: AGCGCCTCCCCCGAGGAAAAGAACT	FEL-AO-039	(GT)6	F:	GCCACAITIGIAAICCAICC	179
R: TTGATGCTCACAGGCACAT FEL-A0-041 (AC)7 F: GCCATGACTGCTCTCGAT 162 R: TATAACTCCTTGCTCCCTTCC FEL-A0-042 (GA)6 F: TATACTCCTGCTCCCTTCC FEL-A0-043 (GG)7 F: GGCCTCACTATCTGAGGACACT 170 FEL-A0-044 (GA)6 F: CCCCGTCAATTGCAGAGACC 151 FEL-A0-045 (AC)9 F: CAACGCTGGTAATGCAGAGACC 158 R: GGCATTGCATGAGAGACT 158 R: GGCATGGTAAAGCTCTCAACA FEL-A0-046 (AT)6 F: GCCGTGGTAATACTCACAATT 154 FEL-A0-047 (AG)7 F: GGGCTTCGATAACTTAGGAAAT 154 FEL-A0-048 (GT)8 F: GCCCCTGTCATATACTAGAAACT 153 FEL-A0-049 (CG)6 F: CACCACTTGCAAACAACACT 177 FEL-A0-049 (CG)6 F: CACCACTTGCAAACAACACT 177 FEL-A0-051 (AC)7 F: AGCGAAACAACACCTCCATTGCAGAACT 170 FEL-A0-053 (TC)9 F: CCGCAAACAACAACACCTCCATTGCACAC	FEL-AO-040	(AG)7	F:	ACGCGATTAAGTAGCAGTGG	182
FEL-AO-041 (AC)7 F: GCATTGATTGCTTCGTTCT 162 FEL-AO-042 (GA)6 F: TATACTCTTGCTCCTTCC FEL-AO-043 (CG)7 F: GGCGTCAGTATGTAGGAGACC 170 FEL-AO-044 (GA)6 F: CCGCTCAGTATGTAGGAGAAGC 170 FEL-AO-044 (GA)6 F: CCGCGTGTATGGAGACC 151 FEL-AO-044 (GA)6 F: CCGCGTGTATGGAGGACC 158 FEL-AO-045 (AC)9 F: CCAGCGTGTATGGAGCACC 158 FEL-AO-046 (AT)6 F: CCATGCGTGTATGGAGTACC 154 FEL-AO-047 (AG)7 F: GAGGTATGCACGGGTGAACC 176 FEL-AO-048 (GT)8 F: GATCTGCAGGTGAACACACT 177 FEL-AO-049 (CG)6 F: CACCACTTGTGACTCACGGAACACACT 177 FEL-AO-050 (TC)6 F: AGTTGGCAATGCACACAGACAT 176 FEL-AO-051 (AC)7 F: AGCAAACATGTCACAGGAACAT 177 FEL-AO-052 (AG)6 F: CGCATACGGTGAAAGCATACT 178			R:	TTGAATGCTCAGAGGGACAT	
FE IAAAC ICC I TOG LICCLI ICC FEL-AO-042 (GA)6 F. ATAGETIGGACCTCCGTGA 193 FEL-AO-043 (CG)7 F. GCGCTCAGTAITCGACGGTAIG 170 FEL-AO-044 (GA)6 F. CCCGTGAATAITGGACGTAACC 151 FEL-AO-045 (AC)9 F. CACAGCTGATAITGCAGGACACC 158 FEL-AO-046 (AT)6 F. CCGCGATAITGCACACAT FEL-AO-046 R. TCTCGCGATATCTCACACAT FEL-AO-046 (AT)6 F. GCATGTAGCACACAT FEL-AO-047 (AG)7 F. GAGGGTACCACACAT FEL-AO-048 (GT)8 F. GATCCCATGTAGACTACACAT FEL-AO-049 (GG)6 F. CCCCACACATGTAGCACACACT FFEL-AO-049 (GG)6 F. CCGCAAACAACACT FFEL-AO-049 (GG)6 F. CCCCACAGCATGACTACACAGACACT FFEL-AO-049 (GG)6 F. CCCCACAGCATGACTACACAGCACACT FFE FEL-AO-050 (TC)6 F. ACCCAAACAAACACCT FFE FFE ACCACATGATCACAGGAACACACT FFE FEL-AO-051 (AC)6 F. C	FEL-AO-041	(AC)7	F:	GCCATTGACTGCTCTCTGAT	162
Tel No Ora Ref TorCHACTGALCECCUM TorCHACTGALCECCUM Ref No Ora R TorCHACTGALCECCUM TorCHACTGALCECCUM FEL-A0-043 (CG)7 F. GGCGTCAGTATCTAGGCGACACT TorCHACTGALCECCUM FEL-A0-044 (GA)6 F. CCCCGTCAATTGALCGAAGCC TorCHACTGALCECUM FEL-A0-045 (AC)9 F. CAACGCTGTAATGACGCACT TS8 FEL-A0-046 (AT)6 F. CGATCTGCAAGCTCTCAAT FS8 FEL-A0-047 (AG)7 F. GAGGGTTCCACGAAATT TorCGCGATTGCAACGAACACT FEL-A0-048 (GT)8 F. CATCGCGTTGCATAACTAACTAGC TorCTGCGGTTGCATAACAACT FEL-A0-048 (GT)8 F. CACCACTTGTGAACTACTAGCACT TorCTGCGTTGCATACACGAACACT FEL-A0-050 (TC)6 F. CACCACTTGGTGACTACACGACACT TorCTGCTCTTCTCACCAC FEL-A0-051 (AC)7 F. AGGGAAATTAGGGTAACGACACT TorCTGCTCTTCTCACACCACACACACT FEL-A0-052 (AG)6 F. CTGCAAACAAGACCTCCATG TorCTGCTCTTCTCACACCACACACACCACT FEL-A0-053 (TC)9 F. CCATAAGGTAAGTTCACACACACT	FEL-40-042	(GA)6	R: F·		103
FEL-A0-043 (CG)7 F: GGCCTCAGTATICTGGCTATG 170 FEL-A0-044 (GA)6 F: CCCGCTGATATICTGGCGTATG 151 FEL-A0-045 (AC)9 F: CAGCGCTGTATATGAGCGCATC 151 FEL-A0-045 (AC)9 F: CAGCGCTGTATATGAGCACT 158 FEL-A0-046 (AT)6 F: CCCGCATTTCTAGCGGTCAACC 154 FEL-A0-047 (AG)7 F: GGGCTACTATAGCGCTCTGATTG 154 FEL-A0-047 (AG)7 F: GGGCGTACGAACACACT 154 FEL-A0-049 (CG)6 F: CACCACTTGGTGACTCAACGA 176 FEL-A0-049 (CG)6 F: GACCACTTGGACTCACAGCA 176 FEL-A0-050 (TC)6 F: AGCGAAACAACACT 176 FEL-A0-051 (AC)7 F: AGCGAAACAAACACCCCTCCATG 171 FEL-A0-052 (AG)6 F: CCGCACAACAAACAATCTGCCATGAGCAACA 175 FEL-A0-053 (TC)9 F: CCACACCTTGGACGGCAACA 170 FEL-A0-054 (CA)6 F: <td< td=""><td></td><td>(drijo</td><td>R:</td><td>TGCTACATGTACGGCACACT</td><td>175</td></td<>		(drijo	R:	TGCTACATGTACGGCACACT	175
R: ACACCAANTICCAAGAAAGC FEL-A0-044 (GA)6 F: CCCGGAATTICCAGGATACC 151 FEL-A0-045 (AC)9 F: CCAAGGCTGGTAATGGAGCACT 158 FEL-A0-046 (AT)6 F: GATACTGTCAAGGTCCAACG 158 FEL-A0-047 (AG)7 F: GAGGGTTTCCAACGAT 154 FEL-A0-047 (AG)7 F: GAGGGTTTCCAACGAT 154 FEL-A0-048 (GT)8 F: CATCGCATTGAACTACACT 154 FEL-A0-048 (GT)8 F: CATCGCATTGAACAACACT 154 FEL-A0-049 (CG)6 F: CATCACTTGAATCTACAGGAT 154 FEL-A0-050 (TT)6 F: CATCACTTGAATCTACAGGAT 176 FEL-A0-051 (AC)7 F: AGCAAAACAAGAACTTACTGCAGGAT 171 FEL-A0-053 (TC)9 F: CCACTAGGTGGTAAAGGCAGATG 175 FEL-A0-054 (CA)8 F: CTGTGGACTTACAGGCAGATG 170 FEL-A0-054 (CA)8 F: CTGTGGACTTCTACAGG 177 FEL-A0-	FEL-AO-043	(CG)7	F:	GGCGTCAGTATCTGGGTATG	170
FEL-R0-044 (GN)6 F: CCC001AAIRIGACGIARCC 151 FEL-R0-045 (AC)9 F: CAAGGCTGGTAATGAGCACT 158 FEL-R0-046 (AT)6 F: GCATGTAGGGTCCAAGG 154 FEL-R0-046 (AT)6 F: GCAGTGTAGGTCCGAAAAT 154 FEL-R0-047 (AG)7 F: GGAGGTATCCACCGAAAAT 154 FEL-R0-048 (GT)8 F: GATCGCGTGGATAACTTGAGT 154 FEL-R0-048 (GT)8 F: GATCGCGGGAAAACACT 77 FEL-R0-048 (GT)8 F: GATCGCCATGAACAACACT 77 FEL-R0-050 (TC)6 F: AGCGAAGACAAGAACCTCCATGA 776 FEL-R0-051 (AC)7 F: AGCAAAAGAGACTCCATGACAGAA 776 FEL-R0-053 (TC)9 F: CCACCAAGGTGATAGGTAAAGAACTG 776 FEL-R0-053 (TC)9 F: CGACAAGGTCATTGACAGAGAA 170 FEL-R0-053 (TC)9 F: CGACAAGGTCATTGACAGGGTA 175 FEL-R0-054 (CA)6 F: CTGGGAAG			R:	ACACCAAATTGCAAGAAAGC	151
FEL-A0-045 (AC)9 F: CAAGGCTGGTAATGAGCACT 158 R: GATACTGTCAGGGTCAAGC FEL-A0-046 (AT)6 F: GGATACTGTCAGGTCGAAGC FEL-A0-046 (AT)6 F: GGATACTGTCAGGTGGATAGC 154 FEL-A0-047 (AG)7 F: GGAGGTATCCACGAAAAT 154 FEL-A0-048 (GT)8 F: GGATCGCCGGAAAAAT 154 FEL-A0-049 (CG)6 F: CACCACTTGGTAAACTAG 177 FEL-A0-050 (TC)6 F: AGCGAGATCCACCACAACAA 176 FEL-A0-051 (AC)7 F: AGCGAAGTTCACAGGTC 171 FEL-A0-051 (AC)7 F: AGCGAACTCACACACACAC 176 FEL-A0-051 (AC)7 F: CGCAAACAAGAACCTCCATTG 171 FEL-A0-052 (AG)6 F: CGGCAAAACAAGAACCTCCATTG 173 FEL-A0-053 (TC)9 F: CCACATGGTGGTAAGGTAA 150 FEL-A0-054 (CA)8 F: CTGGGAAGTCTTCCAAGGCAAGATACT 173 FEL-A0-055 (AG)6	FEL-AU-044	(GA)6	F: R·	TCCGCATTTTCTAAGGGACT	121
R:GATACTGTCAGGGTCAGAGCFEL-A0-046(AT)6F:GCATGTAGGTTCAGAGTTGG188R:TTCTGGGATTCTCCAACATFEL-A0-047(AG)7F:GAGGGTATCCACCACAT154FEL-A0-048(GT)8F:GATCGCCATGAACTTAG163R:GCCCTAGCATGAACACACCTFEL-A0-049(CG)6F:CACCACTTGTGACTCACGTC177FEL-A0-049(CG)6F:CACCACTGTGTACTCACGTC177FEL-A0-050(TC)6F:AGCGAGATCCATCACGACACACACACACACACACACACAC	FEL-AO-045	(AC)9	F:	CAAGGCTGGTAATGAGCACT	158
FEL-A0-046 (AT)6 F: GCATGTAGGTTCTGGATTGG 188 FEL-A0-047 (AG)7 F: GAGGGTATCCACGGAAAAAT 154 FEL-A0-048 (GT)8 F: GACCGCTTGCATACCTTAG 163 FEL-A0-049 (CG)6 F: CACCACTTGGATGACTACACTA 177 FEL-A0-049 (CG)6 F: CACCACTTGTGAGTCACCTC 177 FEL-A0-050 (TC)6 F: AGCCAGATCCATCACAGAACAT 176 FEL-A0-051 (AC)7 F: AGCAAACAAGACTCTACACGA 176 FEL-A0-052 (AG)6 F: CGGCAAAACAAGAATCTACACGA 175 FEL-A0-053 (TC)9 F: CGCAAAACAAGAATCTGACAGA 150 FEL-A0-053 (TC)9 F: CGCATAGGTGAAGATACTG 173 FEL-A0-053 (TC)9 F: CGCATAGGTGAAGGTCAG 175 FEL-A0-055 (AG)6 F: CTGGCAAAGATGCGACAGA 175 FEL-A0-055 (AG)6 F: CTGCAATCGTGAGGCACT 200 FEL-A0-055 (AG)6 F: CTGGCAACAAGA			R:	GATACTGTCAGGGTGCAAGC	
FEL-A0-047 (AG)7 F: GAGGGTATCCACGAAAAT 154 FEL-A0-048 (GT)8 F: GAGGGTATCCACGCAAAAT 154 FEL-A0-048 (GT)8 F: GACCCATTGAAGCTCTGAT 163 FEL-A0-049 (CG)6 F: CACCACTTGGACTACACTG 177 FEL-A0-050 (TC)6 F: AGCGAACACACACGCCACTGACAGAAAC 176 FEL-A0-051 (AC)7 F: AGCCAAACAAACACTCCATGACAGAAC 176 FEL-A0-052 (AG)6 F: CGGCAAAAGAAACCTCCATGACAGAAC 176 FEL-A0-052 (AG)6 F: CGGCAAAAGGTAAACTTGACACAC 175 FEL-A0-053 (TC)9 F: CCACTAGGGTAAGGTCAGA 176 FEL-A0-054 (CA)8 F: CTGACAGGTAGGTCAGAGGTAA 175 FEL-A0-055 (AG)6 F: CTGACAGGTAGGTCAGAGTAGA 170 FEL-A0-055 (AG)6 F: CTGACAGTGTCTTTGCATGCAGA 170 FEL-A0-057 (AC)6 F: GTGCCATGTGCAGGCTTGCAA 174 FEL-A0-058 (TC)7 F:	FEL-AO-046	(AT)6	F:	GCATGTAGGTTCTGGATTGG	188
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	FEL-AO-047	(AG)7	к: F:	GAGGGTATCCACCGAAAAAT	154
FEL-A0-048 (GT)8 F: GATCGCGTTGCATAACTTAG 163 R: GGCCTAGCATGAACAACACT FEL-A0-049 (CG)6 F: CACCACTTGTGACTCACGTC 177 FEL-A0-050 (TC)6 F: AGCGAAGTCTACACGACACT 176 R: TATTGGGCAAACAACACAGAC 176 177 FEL-A0-051 (AC)7 F: AGCGAAACCAACGAGACACT 171 R: TTCCTTGCTCTCTCACCACAGAC 176 177 171 FEL-A0-052 (AG)6 F: CGGCAAAACAACACCTCCATTG 171 FEL-A0-053 (TC)9 F: CCACATAGTGCTGAAGGGTA 175 FEL-A0-053 (TC)9 F: CGCATAGGTGAAGGTA 173 FEL-A0-054 (CA)8 F: CTGTGAGCTAGAGGTA 170 FEL-A0-055 (AG)6 F: CTGTGAGCTCTTTCATGCAGAGGTT 170 FEL-A0-057 (AC)6 F: GTCCATCTTTTCAGAGGGGTTTG 170 FEL-A0-058 (AT)6 F: TTCCATGAACAAGGGGCTTTCA 173 FEL-A0-059 (TC)8 F:		()	R:	CTCGCATTTGAAGCTCTGAT	
R:GGCCTAGCATGAACAACACTFEL-A0-049(CG)6F:CACCACTTGGACTCACGTC177FEL-A0-050(TC)6F:AGCGAGATCCATCACAGAAC176FEL-A0-051(AC)7F:AGCAAACAAGACCTCCATTG171R:TTCCTTCCTCTCTCTCCACCGFEL-A0-052(AG)6F:CGGCAAAGATATTGGACTCAGGTAA150FEL-A0-052(AG)6F:CGGCAAAGATATTGGACTAGFEL-A0-053175FEL-A0-053(TC)9F:CCACACTTTCCAGGCTAAAGGTAT153FEL-A0-054(CA)8F:CTGATGGATCAGFEL-A0-054FEL-A0-055(AG)6F:CTGATGGATGGAGTCAG170FEL-A0-055(AG)6F:CTGATGGATGGAGTGG170FEL-A0-056(TC)7F:AACAATGTAGAGGGGGTTG170FEL-A0-057(AC)6F:GTCCCATGTCTCTTGCAGAGT174FEL-A0-058(AT)6F:TTCCATGACACAAGCACATC181FEL-A0-059(TC)8F:AGGGATACTGGGAGAGT173FEL-A0-060(AG)6F:GAAGGAATCATGAGAGTGGTGAA174FEL-A0-061(GAC)5F:TCTATCACGGCTCTCTGTC191FEL-A0-061(GAC)5F:ATGGATACAGGAGCGTAAGGAGT181FEL-A0-063(CTA)5F:ACATCAGGATCGGAGAGAGT174FEL-A0-064(GAC)5F:AGAGGATACACAGGACACATC181FEL-A0-066(GAC)5F:AGAGGATCATCAGGAGTGGAGAG174FEL-A0-066(GAC)5F:AGAGGGATCATCAGGAGTGGAGAGAG174FEL-A0-066(GA	FEL-AO-048	(GT)8	F:	GATCGCGTTGCATAACTTAG	163
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	FEL_00_049	((()))	R:	GGCCTAGCATGAACAACACT	177
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	FEL-AU-049	(CG)0	F. R:	GAATCTCCCATGACGAACAT	177
$\begin{tabular}{ c $	FEL-AO-050	(TC)6	F:	AGCGAGATCCATCACAGAAC	176
HELAO-051 (AC)/ F: AGGAAACAAGACCICCATIG 171 R: TTCCTTGCTCCTTCCACACC 710 710 710 710 FEL-AO-052 (AG)6 F: CGGCAAAAGATATTGGGTAA 150 R: GTCGTCAGGCAAGATACTG 75 75 75 FEL-AO-053 (TC)9 F: CCACTAGGGTGATAGGTCAG 75 FEL-AO-054 (CA)8 F: CTGAGCACTTCACAGGCTC 200 R: CTGTGGAGCTCTTTCATGCACGACTC 200 78 710 76 FEL-AO-055 (AG)6 F: CTGATGATGAGGGACTC 200 71 74 74 74 74 FEL-AO-056 (TC)7 F: ATGCCATGATGAGGAGGTTGGGA 74 75			R:	ATTTGGGCAAATCTACACGA	
FEL-A0-052 (AG)6 F: CGGCAAAAGATATGGGTAA 150 FEL-A0-053 (TC)9 F: CGCAAAAGATATGG 175 FEL-A0-053 (TC)9 F: CCACTAGGTGCTGAAGGGTA 175 FEL-A0-054 (CA)8 F: CTGAGACTTTCCACGAGGTCA 200 FEL-A0-055 (AG)6 F: CTGAGACTTTCCACGGAGCTC 200 R: CTGTGGAGGCTTTTCCATGGCAGGTGT 173 176 170 176 FEL-A0-056 (TC)7 F: AACAATGTAGAGGGGCGGTTTG 170 174 FEL-A0-057 (AC)6 F: CTGACACTCTATCAAGGTGGTGGTGG 174 174 FEL-A0-058 (AT)6 F: TTCCCATGACAAGGCCATTAC 181 181 FEL-A0-059 (TC)8 F: AGGCGTCTCTCCTCTGTCTCACA 173 FEL-A0-060 (AG)6 F: GAAGGGAATCATGACGAGGTGAG 174 FEL-A0-061 (GAC)5 F: TCTATCACGGACCTTACA 173 FEL-A0-061 (GAC)5 F: TCATATGACAGGTGGAGGGTGAG 174	FEL-AO-051	(AC)7	F: D.		1/1
FEL-A0-053(TC)9F: F: CCACTAGGTCCTGAAGGTA CCACTAGGTCCTGAAGGGTA TCACGGTGCTGAAGGGTA FEL-A0-054175 R: GCGATACGTTCCACGAGCTTFEL-A0-054(CA)8F: F: CTGACCTTTCCATGGCACTC200 R: CTGACACTTTCCATGGCACTCFEL-A0-055(AG)6F: F: CTGATGCTCTCTTTGGCATGT170 R: R: ACAATGTAGAGGCGGGTTTGFEL-A0-056(TC)7F: R: ACAATGTAGAGGCGGCTTTG170 R: R: CATAAGAAGTGGTCGTCGCAAFEL-A0-057(AC)6F: 	FEL-AO-052	(AG)6	F:	CGGCAAAAGATATTGGGTAA	150
$\begin{array}{cccc} FEL-AO-053 & (TC)9 & F: & CCACTAGGTGCTGAAGGGTA & 175 \\ & & GCGATACGGTGATAGGTCAG & \\ FEL-AO-054 & (CA)8 & F: & CTGGACACTTTCCACGAGCTT & 153 \\ & & CTGTGGAGCTCTTTCATGCT & \\ FEL-AO-055 & (AG)6 & F: & CTGATTGATGGACGGACTC & 200 \\ & & & TTGTCTTCCTTTTGGCATGT & \\ FEL-AO-056 & (TC)7 & F: & AACAATGTAGAGGCGGTTTG & 170 \\ & & ATGCCATCATCAAGGCTGGT & 174 \\ & & ATGCCATCATCAAGGCTGGG & 174 \\ FEL-AO-057 & (AC)6 & F: & GTCCCATGTCTCTTTGGATG & 174 \\ & & CATAAGAAGTGGTGCGTGCAA & \\ FEL-AO-058 & (AT)6 & F: & TCCCAAAGCACACTC & 181 \\ & & & TCCAAAATTCGGACCTTACA & \\ FEL-AO-059 & (TC)8 & F: & AGCGTCTCTCTTGTCTCA & 173 \\ & & & TGTTTGGTATAGGGGTGGAG & \\ FEL-AO-060 & (AG)6 & F: & GAAGGGAATCATGACGAGTG & 163 \\ FEL-AO-061 & (GAC)5 & F: & TCCATGACCGAGG & 163 \\ FEL-AO-061 & (GAC)5 & F: & TCTATCACCGGCTCAGA & \\ FEL-AO-062 & (TGG)6 & F: & ATGGATAGCAGTGAGA & 197 \\ FEL-AO-063 & (CTA)5 & F: & TCATCACGGACGCAGG & 197 \\ FEL-AO-064 & (CGT)5 & F: & TCCATGAGCTGAGG & 197 \\ FEL-AO-065 & (CAT)5 & F: & TCCATGAGCTCAT & 161 \\ & & & CAGCGTACATCTTTGGTT & \\ FEL-AO-066 & (GAC)5 & F: & TCCAATATGCCGAGGTGATGAG & 174 \\ FEL-AO-066 & (GAC)5 & F: & TCCAATATGCCAGCTCCAT & 161 \\ & & & CAGCGTACGTCATTGGGTT & \\ FEL-AO-066 & (GAC)5 & F: & ATGGATAGCCAGGTCGATGAG & 174 \\ FEL-AO-066 & (GAC)5 & F: & ATGGATAGCCAGGTCCAT & 161 \\ & & & CAGCGTACGTCCTTCTAT & \\ FEL-AO-066 & (GAC)5 & F: & AGGCGTCAGTCCAT & 161 \\ & & & & CAGCGTACGTCCAT & 161 \\ & & & & CAGCGTACGGTTGGTTG & \\ FEL-AO-066 & (GAC)5 & F: & AGGCACCAGGGCGGTGG & 170 \\ & & & & & & & & & \\ FEL-AO-066 & (GAC)5 & F: & AGGCACCAGGGCGTTGG & 170 \\ & & & & & & & & & & \\ FEL-AO-066 & (GAC)5 & F: & AGGCACCCAGGAGGAGT & 170 \\ & & & & & & & & & \\ FEL-AO-067 & (AGA)5 & F: & AGGCACCCAGGCAGGGGTG & 170 \\ & & & & & & & & & \\ FEL-AO-068 & (TGG)6 & F: & & & & & & \\ FEL-AO-069 & (CAA)5 & F: & & & & & & & \\ FEL-AO-069 & (CAA)5 & F: & & & & & & & \\ FEL-AO-069 & (CAA)5 & F: & & & & & & & & \\ FEL-AO-069 & (CAA)5 & F: & & & & & & & & \\ FEL-AO-070 & (CAT)5 & F: & & & & & & & & \\ FEL-AO-070 & (CAT)5 & F: & & & & & & & & \\ FEL-AO-071 & (TCC)5 & F: & & & & & & & & \\ $			R:	GTCGCTCAGGCAAGATACTG	
R:GCGATACGGTGATAGGTGATAGGTGAGGFEL-AO-054(CA)8F:CTGATGACCTTTCCAGGAGCTT153R:CTGTGGAGCTCTTTCATGCT200R:TTGTCTTCCTTTTGGATGT200R:TTGTCTTCCTTTTGGATGT170R:AAGAGTGAGAGCGGGTTTG170R:ATGCCATCTATCAAGGTTGG174FEL-AO-056(TC)7F:ACAATGTAGAGCGGGTTTG174FEL-AO-057(AC)6F:GTCCCATGTCTTTCGATG174R:CATAAGAAGTGGTGGTGGCAAFEL-AO-058(AT)6F:TCCAAGAAGTGGCGTGGCAAFEL-AO-059(TC)8F:AGCGTCTTCCTTGTGTTCA173R:TGCTTGGTATAGGGGTGGAGGFEGAAGGGAATCATGACGAGG163FEL-AO-060(AG)6F:GAAGGGAATCATGACGAGTG163FEL-AO-061(GAC)5F:TCTATCACCGGCTTCTGGTGT191FEL-AO-062(TGG)6F:CTGGATACATCATGAGGTGAGG197FEL-AO-063(CTA)5F:TCATCGGAACGGAATCATTGAGGTT161FEL-AO-064(CGT)5F:TCAATGGGAGCCAAAAFFEL-AO-066(GAC)5F:AGAGGCACTCAGAGGTGATGG174FEL-AO-066(GAC)5F:AGGCACTCAGAGGAGGAGT170R:CGGGCATTAGGAGTGGTGGTGGTFGGTGGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	FEL-AO-053	(TC)9	F:	CCACTAGGTGCTGAAGGGTA	175
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	FEL_AO_054	(CA)8	R:	GCGATACGGTGATAGGTCAG	152
FEL-AO-055 (AG)6 F: CTGATTGATTGACGGACTC 200 R: TTGTCTTCCTTTTGCATGT TTG FEL-AO-056 (TC)7 F: AACAATGTAGAGGCGGTTTG 170 R: CATAAGAAGGTAGAGGCGGGTTG 174 FEL-AO-057 (AC)6 F: GTCCCATGTCTCTTGGATG 174 FEL-AO-058 (AT)6 F: CATAAGAAGTGGTGTGGAA 174 FEL-AO-059 (TC)8 F: AGCGTCTCTCTTGGATA 173 FEL-AO-060 (AG)6 F: GAAGGAATCATGAGGAGTGAG 174 FEL-AO-061 (GAC)5 F: TTGCTTCGTGTCTGCATT 173 FEL-AO-061 (GAC)5 F: TTCCATCACGGCTTCTTGTG 191 FEL-AO-062 (TGG)6 F: ATGGATGGAGGGATCAAAAA 170 FEL-AO-063 (CTA)5 F: TCCAATGTGAGGAGTGAAAAA 170 FEL-AO-066 (GAC)5 F: ACATTCACAGTCGAGACCATACA 181 FEL-AO-066 (GAC)5 F: ACATTCACATTGGATAGAGTTGA 199 FEL-AO-066 (GAC)5 F: ACATTCACAGGGAGTCAAAAA 161 FEL-AO-066 <td>1 22-70-034</td> <td>(CA)0</td> <td>R:</td> <td>CTGTGGAGCTCTTTCATGCT</td> <td>172</td>	1 22-70-034	(CA)0	R:	CTGTGGAGCTCTTTCATGCT	172
R: TIGTCTTCCTTTGGCATGT FEL-A0-056 (TC)7 F: AACAATGTAGAGGCGGTTG 170 R: ATGCCATGTACAAGGTTGG 174 R: CATAAGAAAGTGGTCGTGCAA 174 FEL-A0-057 (AC)6 F: GTCCCATGTCTCTTTGGATG 174 R: CATAAGAAAGTGGTCGTGCAA 181 R: 174 FEL-A0-058 (AT)6 F: TTCCATGACACAAGCACCATC 181 R: TGTTTCGTATAGGGACTCTTACA 173 R: 161 FEL-A0-059 (TC)8 F: AGGGTCTCTCCTGTGTCTACA 173 R: TGTTTCGTATAGGGGTCGAGG 163 R: 163 FEL-A0-060 (AG)6 F: GAAGGGAATCATGACGAGGTG 163 R: CCGCGCATACATCATGACGAGGTGAGAG 197 R: RCCGGCATACACGAGTCGATGAGG 197 FEL-A0-061 (GAC)5 F: TCCATGGAGCGCGATGAGG 197 R: RCGGGATCGGTGGAGGAGAGAGGTCGT 198 FEL-A0-062 (TGG)6 F: ATGGATAGCAGGTCGATGAGG 197 R: GCATGGAGGCGAAGAGGTCGATGAGG 197 FEL-A0-064 (CGT)5 F: <td>FEL-AO-055</td> <td>(AG)6</td> <td>F:</td> <td>CTGATTGATTGGACGGACTC</td> <td>200</td>	FEL-AO-055	(AG)6	F:	CTGATTGATTGGACGGACTC	200
$\begin{tabular}{ c c c c c c c c c c c c c c c c c c c$			R:	TTGTCTTCCTTTTGGCATGT	170
$\begin{array}{ccccc} FEL AO-057 & (AC) G & F: & GTCCCATCITTCGATG & 174 \\ R: & CATAAGAAGTGGTCGTGCAA & \\ FEL AO-058 & (AT) G & F: & TTCCATGACACAAGCACATC & 181 \\ R: & TCCAAAATTCGGACCTTACA & \\ FEL AO-059 & (TC) S & F: & AGCGTCTCCTTGTCTTCA & 173 \\ FEL AO-060 & (AG) G & F: & GAAGGGAATCATGAGGGGGGGGGGGGGGGGGGGGGGGGG$	FEL-AO-056	(1C)7	F: p.		170
FEL-AO-058(AT)6F:TTCCATAGAAGTGGTCGTGCAA TTCCATGACACAAGCACATC181R:TCCAAAATTCGGACCTTACAR:TCCAAAATTCGGACCTTACAFEL-AO-059(TC)8F:AGCGTCCTCCTCTGTGTCTCA173R:TGTTTCGTATAGGGGTGAGG163FEL-AO-060(AG)6F:GAAGGGAATCATGACGAGTG163FEL-AO-061(GAC)5F:TCTATCACCGGCTTCTTGTC191R:CCGCGATACATCATGACGAGTG197FEL-AO-062(TGG)6F:AGATGCTGGTAGGACCAAAAFEL-AO-063(CTA)5F:TCATCGGAGCGTAAGTCCT199R:ACATTCACATTCGGATCCAT161FEL-AO-064(CGT)5F:TCCAATATGCCAGGTTGCAT161R:CAGCGTACCGTCCTTTGTG181FEL-AO-066(GAC)5F:TCCAATATGCCAGGTTGCCTAT161R:CAGCGGCATTAGAGTTGCCTAGGGTTG181FEL-AO-066(GAC)5F:AGAGGGTGCCTAGGGTTGGTAG174FEL-AO-067(AGA)5F:AGCGGCACTAGAAGCTCGTAG170R:CGAGCAAGCTCTGTAGCAT170R:CGAGCAAGCTCTGGATGA170FEL-AO-068(TGG)6F:CGTAGGACGACGACGACAAGAC196FEL-AO-069(CAA)5F:AGAATTGCAAACCGATAGG187FEL-AO-070(CAT)5F:AGAATTGCAAACCGATCAGGTGGATG164FEL-AO-071(TCC)5F:GGGTGGAGGAGCAAGATCTCC192R:CTATGACGACTCGCTGGATT192R:CTATGACGACTCGCTGGATT	FEL-AO-057	(AC)6	F:	GTCCCATGTCTCTTTCGATG	174
FEL-A0-058(AT)6F:TTCCATGACACAGCACATC181R:TCCAAAATTCGGAGCCTTACAFEL-A0-059(TC)8F:AGCGTCTCTCCTTGTCTTCA173R:TGTTTGGATAGGGGTCGAGFEL-A0-060(AG)6F:GAAGGGAATCATGAGCGAGTG163R:TTCCCTTCTGTGCTATTCCAR:TTCCCTTGTGCTATTCCAFEL-A0-061(GAC)5F:TCTATCACCGGGTTGATTCCA191R:CCGCGATACATCATTGAGTTR:CCGCGATACATCATTGAGT191FEL-A0-062(TGG)6F:ATGGATAGCAGGTGATGAG197R:AGATGCTGGTAGGCACAAAAR:AGATGCTGGTAGGCACAAAA199FEL-A0-063(CTA)5F:TCATCGGAGGTCAATGCAT161FEL-A0-064(CGT)5F:ACATTCACATTCGGATCCAT161FEL-A0-065(CAT)5F:AATAGGGTTGCCTAGGGTTG181R:CAGCGTACCGTCCTTTCATR:GACGGGCATTAGAGGTTGCAT170FEL-A0-066(GAC)5F:ATAGCGACAGAGGAGAGAT170R:CGAGCAAGCTCTGTATCCATR:CGAGCAAGCTCTGTATCCAT196FEL-A0-067(AGA)5F:AGAATTGCAAAACCGATACGGAGGAGAT170R:CGAGCAAGCTCTGTATCCATR:GATCTCACCGAAGCTCGAGGGCGAA196R:ATAGCGACACAGCGACTGGGACGR:AAATTGCGACCATCGGCTGTC192FEL-A0-070(CAT)5F:AGAATTGCAAAACCGATACGGTGGTC192R:CTATGACGACTGACACTGAAGGTCTAAGGACTCC192R:CTATGACGACTCGCTGGATTFEL-A0-071(TCC)5F:GGGTGAAGTCACTGCT			R:	CATAAGAAGTGGTCGTGCAA	
$\begin{tabular}{ c c c c c c c c c c c c c c c c c c c$	FEL-AO-058	(AT)6	F:	TTCCATGACACAAGCACATC	181
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	FEL-AO-059	(TC)8	к: F:	AGCGTCTCTCCTTGTCTTCA	173
FEL-AO-060 (AG)6 F: GAAGGGAATCATGACGAGTG 163 R: TTCCCTTCTGTGCTATTCCA TTCCCTTCGTGCTATTCCA 191 FEL-AO-061 (GAC)5 F: TCTATCACCGGCTTCTTGTC 191 R: CCGCGATACATCATTGAGTT 197 R: CCGCGATACATCATTGGAGTGAG 197 R: AGATGCTGGAGGCACAAAA 197 FEL-AO-063 (CTA)5 F: TCATCGGAGCGAGACACAAAA FEL-AO-064 (CGT)5 F: ACATTCACATTCGGATCCAT 191 FEL-AO-064 (CGT)5 F: CAGCGTACCGTCTCTTTCAT 199 R: CAGCGTACCGTCTCTTTCAT 161 181 181 FEL-AO-066 (GAC)5 F: AATAGGGTTGCTAGGGTTGGT 181 FEL-AO-066 (GAC)5 F: AGGCACTCAGAACGTCGTAG 174 R: GACGGGCATTAGAGGTTCAA R: 174 170 FEL-AO-068 (TGG)6 F: CGTTAGGACAGAGGAGAGAGAT 170 R: GACTCACCGAATCATCGGATCG 187 181 174 FEL-AO-069 (CAA)5 F: ATTAGCGACAGGACAGGAGAGAGAT 170		(1-)-	R:	TGTTTCGTATAGGGGTCGAG	
R:TICCCTTICTGIGGTATTCCAFEL-AO-061(GAC)5F:TCTATCACCGGGTTCTTGTC191R:CCGCGATAGCAGGAGGAGGAG197R:AGATGCTGGTAGGCAGAGAG197R:AGATGCTGGTAGGCACAAAAA197FEL-AO-063(CTA)5F:TCATCGAGGGCAAAGCTCT199R:ACATTCACATTCGGATCCCAT161R:CAGCGTACCGTCCCTT161R:CAGCGTACCGTCCCAT161R:CAGCGTACCGTCCCAT161R:CAGCGTACCGTCCCTTTCAT161FEL-AO-065(CAT)5F:AATAGGGTTGCCTAGGGTTG181FEL-AO-066(GAC)5F:AGGCACTCAGAACGTCGTAG174R:GTTTTGGTGTTGGTGTGGTR:GACGGGCATTAGAGTTCCAA170FEL-AO-067(AGA)5F:ATTAGCGACAGGGAGAGAGAT170R:CGAGCAAGCTCTGTGATACAT166R:GATCTCACCGAATCTGGGTCA196FEL-AO-068(TGG)6F:CGAGCAAGCTCTGTGGTGCA196FEL-AO-069(CAA)5F:ATGATTAGCGTCGATACG187FEL-AO-070(CAT)5F:ATCGACGCATGACTCAAAGT164R:AAATATAGCGGACCATGTCGR:AAATATAGCGGACCATGTCG192FEL-AO-071(TCC)5F:GGGTGGAGGTCAAAGTATCC192R:CTATGACGACTCGCGCGGTGGATT164R:CTATGACGACTCGCGGTGGATT	FEL-AO-060	(AG)6	F:	GAAGGGAATCATGACGAGTG	163
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	FEL-40-061	(GAC)5	R: F·		101
FEL-AO-062 (TGG)6 F: ATGGATAGCAGGTCGATGAG 197 R: AGATGCTGGTAGGCACAAAA		(dire)s	R:	CCGCGATACATCATTGAGTT	121
R:AGATGCTGGTAGGCACAAAAFEL-AO-063(CTA)5F:TCATCGGAGCGTAAGTCTCT199R:ACATTCACATTCGGATCCAT161R:CAGCGTACCGTCCAT161R:CAGCGTACCGTCCTTTCAT161R:CAGCGTACCGTCCTTTCAT181FEL-AO-065(CAT)5F:AATAGGGTGCCTAGGGTGG181R:GTTTTGGTGTTGGTGTTGGT181FEL-AO-066(GAC)5F:AGCGGCATTAGAGTGTCGAG174FEL-AO-067(AGA)5F:ATAGCGACAGGGAGAGAT170FEL-AO-068(TGG)6F:CGTTAGGATCATCTGGGTCA196R:CAGACGACCTCGGATGGATG187R:AGAATTGCAAAACCGATACG187FEL-AO-069(CAA)5F:ATGATTAGCGTCGATCGTC187FEL-AO-070(CAT)5F:ATCGACGACTCAAAGTCAAGT164FEL-AO-071(TCC)5F:GGGTGGAGGTCAAAGTATCC192R:CTATGACGACTCGCGTCGTCGR:CTATGACGACTCGCGGTCAGATT192	FEL-AO-062	(TGG)6	F:	ATGGATAGCAGGTCGATGAG	197
$\begin{array}{c c c c c c c c c c c c c c c c c c c $			R:	AGATGCTGGTAGGCACAAAA	100
FEL-AO-064(CGT)5F:TCCAATATGTCCAGCTCCAT161R:CAGCGTACCGTCCTTTTCATFEL-AO-065(CAT)5F:AATAGGGTTGCCTAGGGTTG181R:GTTTTGGTGTTGGTGTGGTR:GACGGCATTAGAGTTCCAA174FEL-AO-066(GAC)5F:AGGCACTCAGAACGTCGTAG174R:GACGGGCATTAGAGTTTCAAR:GACGGGCATTAGAGTTTCAA170FEL-AO-067(AGA)5F:ATTAGCGACAGGGAGAGAGAT170R:CGAGCAAGCTCTGTATCCATR:CGAGCAAGCTCTGGATCACCAT196FEL-AO-068(TGG)6F:CGTTAGGATCATCTGGGTCA196R:GATCTCACCGAATCTGGATCATFEL-AO-069(CAA)5F:AGAATTGCAAAACCGATACG187FEL-AO-070(CAT)5F:ATCGACGACTCTGAAGT164R:AAATATAGCGGACCATGTCGFEL-AO-071(TCC)5F:GGGTGGAGGTCAAAGTATCC192R:CTATGACGACTCGCTGGCTGGCTGC	FEL-AU-063	(CTA)5	F: R·		199
FEL-AO-065(CAT)5R:CAGCGTACCGTCTCTTTCATFEL-AO-066(GAC)5F:AATAGGGTTGGTGGTGGTGGT181R:GTTTTGGTGTTGGTGTGGTGTGGTR:GACGGCATTAGAGTTCCAA174FEL-AO-067(AGA)5F:ATTAGCGACAGGGAGGAGAGAT170R:CGAGCAAGCTCTGTATCCATR:CGAGCAAGCTCTGTGATCCAT196FEL-AO-068(TGG)6F:CGATCTCACGAATCTGGGTCA196FEL-AO-069(CAA)5F:AGAATTGCAAAACCGATACG187FEL-AO-070(CAT)5F:ATCACGACGCATGACTCAAGT164R:AAATATAGCGGACCATGTCGR:AAATATAGCGGACCATGTCG192FEL-AO-071(TCC)5F:GGGTGGAGGTCAAAGTATCC192R:CTATGACGACTCGCTGGCTGGATT164164164	FEL-AO-064	(CGT)5	F:	TCCAATATGTCCAGCTCCAT	161
$ \begin{array}{cccc} \mbox{FeL-AO-065} & (CAT)5 & F: & AATAGGGTTGCCTAGGGTTG & 181 \\ R: & GTTTTGGTGTTGGTGTTGGT \\ \mbox{FeL-AO-066} & (GAC)5 & F: & AGGCACTCAGAACGTCGTAG & 174 \\ R: & GACGGCATTAGAGTTTCAA \\ \mbox{FeL-AO-067} & (AGA)5 & F: & ATTAGCGACAGGGAGGAGAT & 170 \\ R: & CGAGCAAGCTCTGTATCCAT \\ \mbox{FeL-AO-068} & (TGG)6 & F: & CGTTAGGATCATCTGGGTCA & 196 \\ R: & GATCTCACCGAATCTGGATG \\ \mbox{FeL-AO-069} & (CAA)5 & F: & AGAATTGCAAACCGATACG & 187 \\ R: & ATGATTAGCGTCGGTCA & 164 \\ R: & ATGATTAGCGTCGAACTCTGGC \\ \mbox{FeL-AO-070} & (CAT)5 & F: & ATCGACGCATGACTCAAAGT & 164 \\ \mbox{FeL-AO-071} & (TCC)5 & F: & GGGTGGAGGTCAAAGTATCC & 192 \\ \mbox{R:} & CTATGACGACTCGCTGGATT \\ \end{array} $			R:	CAGCGTACCGTCTCTTTCAT	
R:GTTTGGGTTGGGTGGTGGTGGTFEL-AO-066(GAC)5F:AGGCACTCAGAACGTCGTAG174R:GACGGGCATTAGAGTTTCAAFEL-AO-067(AGA)5F:ATTAGCGACAGGGAGGAGAT170R:CGAGCAAGCTCTGTATCCATFEL-AO-068(TGG)6F:CGTTAGGATCATCTGGGTCA196R:GATCTCACCGAATCTGGATGR:AGAATTGCAAAACCGATACG187FEL-AO-069(CAA)5F:AGAATTGCAAAACCGATACG187R:ATGATTAGCGTCGGTCTGTCR:AAATATAGCGGACCATGACT164FEL-AO-070(CAT)5F:GGGTGGAGGTCAAAGTATCC192R:CTATGACGACTCGCTGGATTR:CTATGACGACTCGCTGGATT	FEL-AO-065	(CAT)5	F:	AATAGGGTTGCCTAGGGTTG	181
R: GACGGGCATTAGAGGTTCAA FEL-AO-067 (AGA)5 F: ATTAGCGACAGGGAGGAGAT R: CGAGGCATTAGAGCTCTGTATCCAT FEL-AO-068 (TGG)6 F: CGTTAGGATCATCTGGGTCA FEL-AO-069 (CAA)5 F: AGAATTGCAAAACCGATACG FEL-AO-070 (CAT)5 F: ATGATTAGCGTCGACCATGTCG FEL-AO-071 (TCC)5 F: GGGTGGAGGTCAAAGTACC R: CTATGACGACTCGCGTCGATT	FEI -AQ-066	(GAC)5	K: F:		174
FEL-AO-067(AGA)5F:ATTAGCGACAGGGAGAGAT170R:CGAGCAAGCTCTGTATCCATFEL-AO-068(TGG)6F:CGTTAGGATCATCTGGGTCA196R:GATCTCACCGAATCTGGATGFEL-AO-069(CAA)5F:AGAATTGCAAAACCGATACG187R:ATGATTAGCGTCGGTCTGTCR:ATGATTAGCGTCGGTCTGTCFEL-AO-070(CAT)5F:ATCGACGCATGACTCAAAGT164R:AAATATAGCGGACCATGTCGFEL-AO-071(TCC)5F:GGGTGGAGGTCAAAGTATCC192R:CTATGACGACTCGCTGGATTK:CTATGACGACTCGCTGGATT192		(0) (0)0	R:	GACGGGCATTAGAGTTTCAA	., .
R: CGAGCAAGCTCTGTATCCAT FEL-AO-068 (TGG)6 F: CGTTAGGATCATCTGGGTCA 196 R: GATCTCACCGAATCTGGATG 196 FEL-AO-069 (CAA)5 F: AGAATTGCAAAACCGATACG 187 R: ATGATTAGCGTCGGTCTGTC 164 FEL-AO-070 (CAT)5 F: AAATATAGCGGACCATGACTG 192 FEL-AO-071 (TCC)5 F: GGGTGGAGGTCAAAGTATCC 192 R: CTATGACGACTCGCTGGATT 192	FEL-AO-067	(AGA)5	F:	ATTAGCGACAGGGAGGAGAT	170
FEL-AO-069 (CAA)5 F: CGTAGGAICATCIGGGTCA 196 FEL-AO-070 (CAT)5 F: AGAATTGCAAAACCGATACG 187 R: ATGATTAGCGTCGGTCTGTC 164 R: AAATATAGCGGACCATGTCG 164 FEL-AO-071 (TCC)5 F: GGGTGGAGGTCAAAGTATCC 192 R: CTATGACGACTCGCTCGGATT 192			R:	CGAGCAAGCTCTGTATCCAT	104
FEL-AO-069 (CAA)5 F: AGAATTGCAAAACCGATACG 187 R: ATGATTAGCGTCGGTCGTGC 164 FEL-AO-070 (CAT)5 F: ATCGACGCATGACTCAAAGT 164 R: AAATATAGCGGACCATGTCG 164 R: AAATATAGCGGACCATGTCG 192 R: CTATGACGACTCGCTGGATT 192 R: CTATGACGACTCGCTGGATT 192	1 EL-AU-000	(000)0	г: R·	GATCTCACCGAATCTGGATG	190
R: ATGATTAGCGTCGGTCTGTC FEL-AO-070 (CAT)5 F: ATCGACGCATGACTCAAAGT 164 R: AAATATAGCGGACCATGTCG 164 FEL-AO-071 (TCC)5 F: GGGTGGAGGTCAAAGTATCC 192 R: CTATGACGACTCGCTGGATT	FEL-AO-069	(CAA)5	F:	AGAATTGCAAAAACCGATACG	187
FEL-AO-070 (CAT)5 F: ATCGACGCATGACTCAAAGT 164 R: AAATATAGCGGACCATGTCG 164			R:	ATGATTAGCGTCGGTCTGTC	
FEL-AO-071 (TCC)5 F: GGGTGGAGGTCAAAGTATCC 192 R: CTATGACGACTCGCTGGATT	FEL-AO-070	(CAT)5	F:	ATCGACGCATGACTCAAAGT	164
R: CTATGACGACTCGCTGGATT	FEL-AO-071	(TCC)5	к: F:	AAAIAIAGCGGACCAIGICG GGGTGGAGGTCAAAGTATCC	192
			R:	CTATGACGACTCGCTGGATT	

Tab	e	3.	Continued.
1010	-	•••	continuctur

				Product
Marker name	SSR motif		SSR primer set $(5' \rightarrow 3')$	size (bp)
FEL-AO-072	(CTC)6	F:	ATTCCGTTTCTCCTTGCTCT	191
		R:	GIAITIGCGIGGGIACCIGI	101
FEL-AU-U/S	(ACG)5	г. р.		101
FEL-AO-074	(CAA)8	F:	GACGATTGTCGGTGTAAAGC	195
	(2.1.1)0	R:	CTGGGATAGGAAAAGGTCGT	
FEL-AO-075	(CTC)5	F:	CAGGTACATTGGGTCGAGAT	193
		R:	TCATTTTGAAACTCCCTGCT	
FEL-AO-076	(GAC)6	F:	TGTCTCCTCCAATGACGATT	158
FEL-40-077	(CGT)5	К: F·		185
	(cdi)5	R:	TCCGTGCTTACCTTGTCTTC	105
FEL-AO-078	(TGG)5	F:	TTAACCATGATGCTCGAAGG	192
		R:	CCCAACTTCTTTCACCCTTT	
FEL-AO-079	(GAC)7	F:	TGAAGAGAAGTCGGGAGTTG	195
		R:	GIAICCAGGGGAIICGAGAG	100
FEL-AU-000	(CAG)/	г. R•	CATTTICCTICACAGGTIGG	102
FEL-AO-081	(CGT)9	F:	ATGGCCGCTGGTAATACATA	157
		R:	TTCATTGAAGAGCTGGTTCC	
FEL-AO-082	(TCC)6	F:	GAGAATGAGCCCACCAATTA	182
FFL 40 000		R:	CGGTTTGAGTATGGGAGTGT	477
FEL-AO-083	(AIG)6	F: D.		1//
FFI-AO-084	(CGT)6	F:	GAGATCCTTAGACGCGGTTT	165
	(201)0	R:	ATCGCCTCATCCTCCTCTAT	105
FEL-AO-085	(CAC)5	F:	GACGGCTGATAAGACAGTGG	185
		R:	CGGTATGATCTGCTCTCGTT	
FEL-AO-086	(ACT)6	F:	ACTTAATAGGGACCGCTTGC	183
FEL-40-087	(GGT)6	К: F·		165
	(001)0	R:	ACCACGCTTCATGAGAAGAA	105
FEL-AO-088	(ATC)6	F:	CAATTGCGTGGGATTTCTAT	185
		R:	CAAGGTGGGAAGAGCCTTAT	
FEL-AO-089	(TGG)6	F:	AGGAAAGGCTGATGGGATAC	195
		R:	ATGATGTGAACCGGTTTGAG	100
FEL-AU-090	(GAA)5	F: R·		199
FEL-AO-091	(ACG)5	F:	CAGCGATATCAGGGTCAATC	181
		R:	GGCCCTCCATCAGAGTAAAG	
FEL-AO-092	(ACC)5	F:	ATGTGAACGGTCCGATATTC	171
		R:	GGGATTGACGGTGGTAAGTA	105
FEL-AU-095	(100)5	г. R•	GCCACACGTTTCCAATATCT	195
FEL-AO-094	(GAC)5	F:	CCACGTTCAAAAGTTCGAGT	181
		R:	GAAGCGTGCGGAATAAATAA	
FEL-AO-095	(CCG)5	F:	CGCCATATAGAGCAACCACT	199
		R:	CATTACCCTTCGGCTTCTTT	160
FEL-AU-090	(CAC)5	F: R·		162
FEL-AO-097	(ACG)5	F:	AACGCTGATAGACGCTTGAC	188
		R:	TTCTACCATTGAACCCGGTA	
FEL-AO-098	(CGC)5	F:	ATCTGCAGAGGCTTGTTCAC	196
		R:	TCGTAGTGATTGGTGCACTG	150
FEL-AU-099	(CGT)5	F: R·		150
FEL-AO-100	(GGA)5	F:	GACCCTGGATGATTGCATTA	192
	. ,	R:	TCGTGGTTAAGGTGCAAGAT	
FEL-AO-101	(TCG)5	F:	AGCGTACCTTTGTCAACGTC	168
FEL 40 400		R:	TGGCATGAAAGTCTTCATCA	1.62
FEL-AO-102	(1CG)5	F: D.		162
FFI-AO-103	(AAT)5	F:	GCATGGAGTCTCAGAGGAAG	195
	····,-	R:	GCTCGAGTTGAACCTTCTCA	
FEL-AO-104	(TCA)6	F:	TGAATGCCCATCAAGGTACT	170
	(1	R:	ACATCCGTCCATGCAGTAAT	
FEL-AU-105	(AGT)5	F:		197
FFI -AQ-106	(CAT)5	К: F·	ϤϹΑΑΙΑϹϹΤΙϤϹΤΙϤΙϹϤΑΙ ϚϚ <u>Ϭ</u> ΤΤϚΤΤϚΑΤϚΑΔΤ <u></u> ΓΓ	190
. 12 /10 100		R:	CAGTGTGGGGAAGTTGGAGTC	170
FEL-AO-107	(TCT)9	F:	TGCACTCACACTTGGCATAC	183
		R:	AGATGAAGAGTACGCGATGG	

Table 3. Continued.

Marker name	SSR motif		SSR primer set $(5' \rightarrow 3')$	Product
	(TTC)7	с.		102
FEL-AU-100	(110)/	F. R·		105
FEL-AO-109	(CGG)5	F:	GAACGTGGGCTGAGACTCTA	168
		R:	TGACCCAAGCTCAAGGATTA	
FEL-AO-110	(CAT)5	F:	CTGGATTGCCTTATCACCAC	175
		R:	GTGACATGAGGGTGAATTGG	175
FEL-AU-TTT	(1CG)5	F: D.		1/5
FEL-AO-112	(TCA)6	F:	CTCTGCCTGCACTCTTGATT	157
	(10,1)0	R:	AGTTGCAGCGTGGAAGTTAC	107
FEL-AO-113	(TCC)5	F:	CCATTCTTCGGGAACAACTA	198
		R:	TGGCTATCGCTAATTCGTGT	
FEL-AO-114	(CTA)5	F:	CTCTGCTCCACTTCAGGTGT	197
	(CTC)5	К: с.		161
FEL-AU-TTJ	(CIG)5	г. В·		101
FEL-AO-116	(CCG)7	F:	ATACCTGCCCTTCCATTACC	191
		R:	GCGTCTTCTTCTGAGCTGAC	
FEL-AO-117	(CAT)9	F:	CAACGTTCTCAACCGTTTTC	165
	(676) -	R:	GGCTAGATTTCTACGCCACA	470
FEL-AO-118	(CTC)5	F:	GCACIGGACCAIGAAIICIC	179
FFL_00_110	(ATC)5	К: F·	ΤGAIACAAI IGCCGAGGAAC	173
	(AIC)5	R:	TGCCTCGGTACCACTATCTC	175
FEL-AO-120	(ATG)5	F:	TTGGGTAGCGAAGTATGGAG	168
		R:	TATGTCCTGTTGGAGGATCA	
FEL-AO-121	(GTG)5	F:	TGCACACCAGCTAAGATGAA	153
		R:	CCTGAAACAACCCCAGTATG	100
FEL-AU-122	(GAC)6	F: D-		188
FEL-AO-123	(GTG)7	F:	TGCAAGAAAATGTCGATACG	164
	()	R:	CAAAACGGTATGAGCCTTTG	
FEL-AO-124	(ACC)5	F:	CGTCCAGCCTACTTGAATGT	189
		R:	CAATAATGGGACGAAACGAC	
FEL-AO-125	(TGG)6	F:	CGATGTTCGAATCTCCTGAC	153
		R:		107
FEL-AU-120	(CAC)/	F. R·	CATCICGICGICGICTITICI	197
FEL-AO-127	(TGA)7	F:	TGGAGGTCAGGGATGATCTA	159
		R:	GGGATTCTTCTGGCTCCTTA	
FEL-AO-128	(ATG)6	F:	GGGTGTGTGAGTGGTTTAGC	158
		R:	CTGTCGATGACACTGATCCA	160
FEL-AU-129	(GTG)6	F: D-		160
FEL-AO-130	(ACA)5	F:	GCTCAAGCGAGAGAGAGAGAG	190
		R:	CGTTTGAGGAGGAGAAGGAT	
FEL-AO-131	(GTC)5	F:	GTTTCCCGCACTTCTCTTCT	175
	(R:	AACTGCAGAGACACCGAGAC	
FEL-AO-132	(GCA)6	F:	GCATAIGGCAAGIGTICCTT	160
FFL-AO-133	(GAA)6	F.	CGACGACGAAGATGATACAG	199
122710 100		R:	CAGCATCGATTTCCTGTTCT	
FEL-AO-134	(AGG)7	F:	GCATCGGAGAACATCTCATC	164
		R:	GTTGCCGTCTAGATCGATTG	
FEL-AO-135	(TTC)5	F:	AATGCACAAAGCTGGTTCTC	190
FEL_AO_136	(TGC)5	R: 5	GAAACCGIACCACCAAAGIG	174
1 LL-AO-150	(100)5	г. R•	CTICGTTIGGACAGTCAGGT	174
FEL-AO-137	(GAT)5	F:	CACGACGAGTCCAGAAAGTT	163
		R:	TGGACTTCCAGAAACGCTAC	
FEL-AO-138	(TTC)6	F:	GTATCTCCGCAGTGAGGAAC	193
FEL AO 130		R:	GCAAACACCATCAAACCTCT	100
FEL-AU-139	(100)/	F: D,	GILGEILEIILGACIALICA	100
FFI-AO-140	(TCA)8	F:	GTGCGTTTCTTCAAGGTCAT	185
	(3, 90	R:	GCGAGAATTCAATGTTCAGG	
FEL-AO-141	(CATT)5	F:	GTCATGATGCCTGCAGTAGA	189
	(0.0-1)-	R:	ACCTTGATTTGCCCAGATTT	
FEL-AO-142	(GGTA)7	F:	AAGGAAGATGTGGTGACAGC	168
FEL-40-143		К: F	ϤΤΙΔΟΤΙΔΟΙΟΑΟΔΟΔΟΑ ΤΤΔΔΤΤΔΩΩΩΩΩΩΑΔΟΔΟΔΟΑ	107
		R.	CTGAGGCAAGCATCAAGATT	172
		n.		

Marker name	SSR motif		SSR primer set $(5' \rightarrow 3')$	Product size (bp)
FEL-AO-144	(GGTA)5	F:	GGAATTGTCAGGGTGTTGAG	154
		R:	CCACACACTGCCGTGTAATA	
FEL-AO-145	(TTCC)5	F:	GTCGCGGTACAAAGAGAAGA	152
		R:	GTAGCTGGATCCTTGTTGGA	
FEL-AO-146	(ACCT)5	F:	TCATCCATCAGGGTCTGTCT	156
		R:	GCTTCGATCTTGATGAGGAG	
FEL-AO-147	(GGTA)5	F:	TGAAGTTGGACTTTCGCTGT	195
		R:	GCAAGTGATGGTGGTCATGT	
FEL-AO-148	(TAGA)5	F:	ATAAGCATGGGCTGATCAAA	200
		R:	GGGTATTGCTTATTCCACCA	
FEL-AO-149	(CTTC)6	F:	CTTTTAAGGAGCCACAACGA	165
		R:	AAGCCGGCATTTATTACCTC	
FEL-AO-150	(CTTC)5	F:	CGGACGTCGTTATGTTTCTT	172
		R:	CCCACAAAACAGCCAGAATA	

Table 3. Continued.

template DNA for PCR reactions. The PCR reaction mixture was prepared by mixing 15µL of GainBlue™ Hot Start Master Mix, 2× (Gainbio, Daejeon, Republic of Korea), 3 µL of each forward and reverse primer (5 pmol), 10.5 µL of distilled water, and 1.5 µL of DNA, resulting in a total volume of 30 µL. The PCR conditions involved pre-denaturation at 95°C for 3 min, followed by denaturation at 95 °C for 30 s, annealing at 55 °C for 30 s, and extension at 72 °C for 20s. This process was repeated for 35 cycles, followed by a final extension at 72°C for 20min. The amplified PCR products were electrophoresed on 2% agarose gel to confirm amplification. Subsequently, fragment sizes were analyzed using the PROSize 2.0 software (Advanced Analytical Technologies, Ankeny, IA, USA) on a Fragment Analyzer (Advanced Analytical Technologies, Ankeny, IA, USA). Transferability was tested by genotyping 16A. gallica isolates using 150 SSR loci.

2.4. Data analysis

Using the data obtained from the Fragment Analyzer, genetic diversity was estimated based on the following parameters. Major allele frequency (M_{AF}) indicates the relative frequency of alleles, expected heterozygosity $(H_{\rm F})$ represents the expected level of heterozygosity calculated under genetic equilibrium conditions, and observed heterozygosity (H_0) reflects the observed level of heterozygosity calculated from the actual populations. PIC is commonly used to measure genetic diversity arising from polymorphisms in the presence of two or more alleles at specific loci in a population [35]. PIC represents the information content of the DNA markers, whereas the number of alleles (NA) reflects the average number of observed alleles per locus [35]. The parameters mentioned above were analyzed using Power Maker V3.25 program. Based on these results, an unweighted pair group method with arithmetic mean

(UPGMA) tree was constructed using the shared allele method.

3. Results and discussion

3.1. SSR distribution

Using the A. ostoyae genome, 2319 SSR loci were identified. Among these, mononucleotide motifs were the most frequent (39.8% of SSR loci). Among the mononucleotide motifs, T (40.8%), A (37.8%), and C (10.9%) were the most abundant in the same order [36]. This pattern is similar to previous studies on SSR loci in nine fungal species (Aspergillus nidulans, Cryptococcus neoformans, Encephalitozoon cuniculi, Fusarium graminearum, Magnaporthe grisea, Neurospora crassa, Saccharomyces cerevisiae, Schizosaccharomyces pombe, Ustilago matdis), where mononucleotide motifs were the most abundant and A/T repeats accounted for >80% of the repeats [36]. Similar findings have been reported in other fungal species, such as Schizophyllim commune, Copricopsis cinerea, Laccaria bicolor, Pleurotus ostreatus where the proportion of A/T repeats is overwhelmingly high [37-40]. Following mononucleotide motifs, trinucleotide motifs were the next most abundant, with 763 loci (32.90%). Compared to previous studies, trinucleotide motifs were found to be abundant in N. crassa with 4,084 motifs, in M. grisea with 1,573 motifs, and in U. maydis with 865 motifs, following mononucleotide motifs [41]. Similarly, trinucleotide motifs are prevalent in S. commune, C. cinerea, L. bicolor, and P. ostreatus [37-40]. Trinucleotide motifs were the second most abundant, accounting for 33.86% of the total in Leptosphaeria maculans, the causal agent of blackleg disease [42], Similarly of A. bisporus SSR loci revealed trinucleotide motifs as the most abundant, with 898 loci identified, reflecting a pattern similar to the findings of this study [43]. The third most abundant motif was dinucleotides, with 517 loci

Table 4. Diversity statistics from selected 105 SSR markers used for analyzing 22 Armillaria ostoyae strains.

	in selected i	os son manters asea		indina ostojac strains.	
Marker	$M_{\rm AF}$	N	H₅	Ho	PIC
	0.500				
FEL-AO-001	0.500	6	0.685	0.571	0.650
FEL-AO-002	0.300	6	0.751	0.300	0.709
FEL_AO_003	0.286	9	0.800	0 143	0 773
	0.200	3	0.000	0.145	0.773
FEL-AO-004	0.368	8	0.796	0.053	0.774
FEL-AO-006	0.818	4	0.318	0.000	0.302
FFI -AO-009	0.523	5	0.632	0.636	0.576
	0.520	4	0.616	0.056	0.550
FEL-AO-010	0.528	4	0.010	0.030	0.552
FEL-AO-012	0.571	2	0.490	0.000	0.370
FEL-AO-013	0.667	2	0.444	0.000	0.346
FEL_AO_014	0 795	6	0 358	0.045	0 347
	0.7 75	0	0.550	0.045	0.547
FEL-AU-UT5	0.545	6	0.617	0.182	0.564
FEL-AO-017	0.500	5	0.667	0.000	0.622
FFI-AO-018	0.432	6	0.669	0.136	0.612
	0.455	6	0 704	0.500	0.662
FEL-AU-024	0.455	0	0.704	0.300	0.002
FEL-AO-025	0.595	6	0.571	0.190	0.518
FEL-AO-027	0.405	7	0.748	0.333	0.715
FFI - 40-029	0 444	6	0.690	0 278	0.642
	0.111	0	0.000	0.270	0.012
FEL-AU-030	0.262	9	0.799	0.286	0.770
FEL-AO-031	0.700	6	0.485	0.150	0.460
FEL-AO-032	0.342	7	0.756	0.211	0.719
EEL_AO_033	0.471	0	0 720	0 176	0.602
	0.471	3	0.720	0.170	0.092
FEL-AO-035	0.571	9	0.639	0.286	0.617
FEL-AO-036	0.500	4	0.546	0.100	0.444
FFI-AO-037	0.286	10	0.819	0.619	0.796
EEL_AO_038	0 705	5	0347	0364	0322
	0.7.7.5	-	0.347	0.310	0.322
FEL-AU-039	0.341	/	0.788	0.318	0.760
FEL-AO-042	0.667	6	0.523	0.048	0.493
FFI - 40-043	0 762	2	0 363	0.000	0 297
	0.722	2	0.303	0.000	0.741
FEL-AU-045	0.275	0	0.778	0.455	0.741
FEL-AO-046	1.000	1	0.000	0.000	0.000
FEL-AO-048	0.909	3	0.169	0.091	0.163
FFI-AO-049	0 250	10	0.850	0.455	0.834
	0.250	10	0.050	0.100	0.054
FEL-AU-050	0.625	3	0.531	0.100	0.468
FEL-AO-052	0.571	4	0.598	0.238	0.546
FEL-AO-053	0.705	6	0.485	0.318	0.465
FEL_AO_054	0.523	8	0.683	0364	0.657
	0.525	8	0.005	0.504	0.037
FEL-AO-055	0.679	5	0.508	0.071	0.478
FEL-AO-057	0.357	7	0.732	0.810	0.690
FEL-AO-058	0.381	7	0.730	0.333	0.688
FEL_A0_060	0.682	1	0.479	0.001	0.427
FEL-AO-000	0.082	4	0.479	0.091	0.427
FEL-AO-063	0.886	2	0.201	0.045	0.181
FEL-AO-064	0.750	3	0.394	0.091	0.344
FFI-AO-066	0.600	7	0.613	0.000	0.594
	0.610	, .	0.015	0.000	0.551
FEL-AU-007	0.019	5	0.576	0.000	0.544
FEL-AO-070	0.295	10	0.822	0.773	0.801
FEL-AO-071	0.295	11	0.790	0.682	0.762
FEL_AO_073	0 568	6	0.632	0 182	0.602
	0.500	0	0.052	0.102	0.002
FEL-AU-U/S	0.619	3	0.526	0.190	0.455
FEL-AO-076	0.310	9	0.814	0.429	0.791
FEL-AO-077	0.607	4	0.556	0.143	0.499
FFL-AO-078	0 533	6	0 647	0 200	0.606
	0.333	7	0.017	0.200	0.000
FEL-AU-079	0.477	/	0.714	0.591	0.685
FEL-AO-080	0.310	10	0.819	0.857	0.797
FEL-AO-081	0.275	10	0.826	0.500	0.805
FFI-AO-082	0.636	4	0 524	0 273	0 465
	0.614	т А	0.527	0.275	0.403
	0.014	4	0.550	0.227	0.503
FEL-AO-084	0.295	9	0.823	0.364	0.803
FEL-AO-086	0.905	4	0.178	0.095	0.172
FFI-AO-089	0 786	4	0 366	0 190	0 346
	0.706	т С	0.000	0.120	0.0-0
FEL-AU-U92	0./80	0	0.3/3	0.238	0.361
FEL-AO-093	0.682	6	0.502	0.545	0.471
FEL-AO-094	0.976	2	0.046	0.048	0.045
FEL-AO-095	0 750	3	0 394	0.045	0 344
	0.055	-			
FEL-AU-099	0.955	2	0.087	0.000	0.083
FEL-AO-100	0.475	5	0.635	0.300	0.568
FEL-AO-101	0.909	3	0.168	0.091	0.160
FEL-AO-102	0.667	- 7	0 444	0.000	0 346
	0.007	2	0.777	0.000	0.540
FEL-AU-103	0.625	6	0.570	0.400	0.538
FEL-AO-104	0.524	4	0.591	0.571	0.515
FEL-AO-106	0.909	2	0.165	0.000	0.152
EEL_AO_107	0.600	- -	0.103	0.000	0.460
	0.090	5	0.491	0.429	0.400
FEL-AU-109	0.452	5	0.646	0.333	0.580
FEL-AO-110	0.864	3	0.244	0.091	0.228
FFI-AO-111	0.659	4	0 510	0 182	0 461
	0.614	7	0.510	0.102	0 56 4
FEL-AU-112	0.014	/	0.590	0.318	0.564
FEL-AO-113	0.682	6	0.496	0.364	0.459
FEL-AO-114	0.600	4	0.545	0.100	0.476
FEI - AO-115	0.810	4	0 331	0.095	0 313
	0.010	7	0.001	0.025	0.00
ILL-AU-IIU	0.000	O	0.051	0.102	0.000

Table 4. Continued.

Marker	M _{AF}	N _A	H _E	H _o	PIC
FEL-AO-117	0.452	6	0.713	0.524	0.675
FEL-AO-118	0.773	2	0.351	0.091	0.290
FEL-AO-119	0.619	4	0.505	0.095	0.418
FEL-AO-120	0.738	4	0.426	0.286	0.394
FEL-AO-121	0.500	3	0.522	0.182	0.407
FEL-AO-122	0.386	6	0.707	0.545	0.657
FEL-AO-124	0.225	8	0.826	0.300	0.803
FEL-AO-125	0.433	5	0.709	0.200	0.665
FEL-AO-127	0.857	2	0.245	0.095	0.215
FEL-AO-129	0.452	6	0.693	0.381	0.647
FEL-AO-130	0.591	6	0.582	0.636	0.532
FEL-AO-131	0.909	2	0.165	0.000	0.152
FEL-AO-132	0.909	3	0.169	0.000	0.163
FEL-AO-133	0.432	5	0.635	0.636	0.565
FEL-AO-134	0.714	5	0.467	0.095	0.444
FEL-AO-135	0.818	5	0.319	0.045	0.304
FEL-AO-136	0.886	4	0.210	0.136	0.202
FEL-AO-137	0.786	4	0.366	0.143	0.346
FEL-AO-139	0.295	8	0.822	0.455	0.800
FEL-AO-140	0.477	6	0.682	0.591	0.637
FEL-AO-142	0.952	2	0.091	0.000	0.087
FEL-AO-143	0.325	10	0.808	0.600	0.784
FEL-AO-145	0.500	6	0.670	0.591	0.627
FEL-AO-146	0.658	5	0.533	0.158	0.503
FEL-AO-147	0.238	8	0.841	0.476	0.822
FEL-AO-148	0.977	2	0.044	0.045	0.043
MAX	1.000	11.000	0.850	0.857	0.834
MIN	0.225	1.000	0.000	0.000	0.000
Mean	0.589	5	0.541	0.255	0.504

 M_{AF} : major allele frequency; N_{A} : number of alleles; H_{0} : observed heterozygosity; H_{E} : expected heterozygosity; PIC: polymorphism information content.

(22.29%), followed by tetranucleotides with 83 loci (3.58%) and hexanucleotides with 29 loci (1.25%). Pentanucleotide repeats were the least abundant, with only five loci (0.22%).

3.2. Amplified SSR

In this study, from the 150 SSR loci considered in *A. ostoyae*, 105 were successfully amplified, whereas 45 failed to amplify or showed nonspecific PCR products.

3.3. SSR polymorphism

Using the 105 successfully amplified SSR loci, we analyzed 22 strains of A. ostoyae. The M_{AE} values ranged from 0.225 (FEL-AO-124) to 1.000 (FEL-AO-046), with an average of 0.589. Only one if the 105 loci analyzed (FEL-AO-046) was monomorphic, as indicated by $N_A = 1$, $H_E = 0$, $H_O = 0$, and PIC = 0. The remaining loci were polymorphic, with N_A ranging from 2 to 11 (FEL-AO-071) and an average of 5.4 alleles per locus. $H_{\rm E}$ ranged from 0.000 (FEL-AO-046) to 0.850 (FEL-AO-080), with an average of 0.541. $H_{\rm O}$ was 0.000 (observed in 14 loci) to 0.857 (FEL-AO-080), with an average 0.255. The PIC values ranged from 0.000 (FEL-AO-046) to 0.834 (FEL-AO-049), with an average of 0.504; 19 loci exhibited a PIC value of 0.7 or higher (Table 4). These highly polymorphic markers provide robust tools for studying genetic variation and assessing population dynamics in *Armillaria* species [44,45]. In UPGMA clustering analysis, the 22 strains were broadly divided into four groups (Figure 1).

Compared with SSR markers for the analysis of other Armillaria species, NA of eight EST-based SSR markers developed from 404 A. luteo-virens resources from 23 wild populations ranged from 4 to 15 with an average of 8.75, H_o ranged from 0.451-0.485 with an average of 0.472, and $H_{\rm E}$ ranged from 0.513 to 0.549 with an average 0.525 and SSR markers of A. cepistipes from 25 resources each from the Swiss population and the Ukrainian population were as follows: N_A ranged from 1 to 8 with an average of 4.68, H_0 ranged from 0.04 to 0.84 with an average of 0.478, and $H_{\rm E}$ ranged from 0.20 to 0.84 with an average of 0.601 [36]. Although a direct comparison is difficult because the resources were different, the SSR marker developed using A. ostoyae in this study had a lower H_0 than that in the previous study.

3.4. Transferability of A. ostoyae *SSR markers to* A. gallica

Among the 105 SSR loci tested, 52 were successfully amplified in *A. gallica*. The transferability of 20 *Pinus koraiensis* SSR markers was assessed across 7 closely related species (45%) [46]. Of the 600 markers developed for *Myrica rubra*, 91.14% were successfully amplified in *Myrica adenophora*, while *Myrica nana* showed a success rate of 89.87%, and



Figure 1. UPGMA dendrogram of 22 Armillaria ostoyae strains based on shared allele method. Numbers on the branches indicate genetic distance values, and numbers in parentheses represent strain numbers.

Myrica cerifera exhibited a transferability rate of 46.84% [47]. Similarly, among 78 EST-SSR markers developed for Triticun aestivum, the transferability to Hordeum vulgare was 55% [47]. In the genus Armillaria, eight SSR markers for A. cepistipes, six markers for A. galiica, four markers for A. ostoyae, one marker for A. borealis, and two markers for A. mellea were polymorphic, confirming the cross-species PCR amplification [36]. The results of this study further indicate the potential transferability of gSSR markers developed from A. ostoyae to the related A. gallica. Upon evaluating the diversity of amplified markers in A. gallica, the M_{AF} ranged from a minimum of 0.214 (FEL-AO-136) to a maximum of 1.000 (FEL-AO-102, FEL-AO-118), with a mean of 0.615. The N_A ranged from 1 (FEL-AO-102, FEL-AO-118) to 10 (FEL-AO-114), with an average of 4.3 alleles. The $H_{\rm E}$ ranged from a minimum of 0.000 (FEL-AO-102 and, FEL-AO-118) to a maximum of 0.860 (FEL-AO-136), with a mean of 0.517, while the H_{Ω} was 0.000 at 19 loci, with the highest value of 0.563 observed in FEL-AO-001. The PIC value ranged from 0.000 (FEL-AO-102, FEL-AO-118) to 0.844 (FEL-AO-136), with a mean of 0.475; six loci exhibited a PIC value of 0.7 or higher (Table 5). The successful cross-species amplification of SSR markers between A. ostoyae and A. gallica suggested a degree of genetic conservation between these species, highlighting their potential transferability to related species [48]. This observed transferability sets the stage for future research that incorporates broader genomic data to explore further the genetic structure and evolutionary dynamics of these species [48]. Furthermore, UPGMA clustering identified five distinct groups, indicating clear genetic differentiation the among individuals (Figure 2). This distinct

Table 5. Diversity statistics from selected 52 SSR markers used for analyzing 16 Armillaria gallica strains.

Table St Diversity statist	ies nom selected a		sea for analyzing	le fillinana gan	
Marker	M _{AF}	N _A	H _E	Ho	PIC
FEL-AO-001	0.438	7	0.701	0.563	0.655
FFI-AQ-006	0.625	4	0.555	0.000	0.510
FFI-AO-012	0.909	2	0.165	0.000	0 1 5 2
FFI-AO-013	0.750	3	0.406	0.000	0 371
FFI-AO-014	0.750	3	0.406	0.000	0.371
FEL-AO-018	0.464	4	0.620	0.000	0.546
FEL-40-035	0.404	3	0.518	0.214	0.451
FEL-AO-042	0.000	5	0.510	0.200	0.505
	0.000	5	0.002	0.007	0.505
	0.230	2	0.015	0.230	0.780
	0.000	2	0.430	0.000	0.337
	0.023	4	0.539	0.000	0.405
	0.505	2	0.570	0.000	0.490
	0.400	4	0.684	0.133	0.624
FEL-AO-064	0.625	4	0.525	0.063	0.459
FEL-AO-071	0.594	5	0.594	0.375	0.554
FEL-AO-073	0.893	2	0.191	0.071	0.173
FEL-AO-075	0.500	4	0.564	0.0/1	0.4/0
FEL-AO-077	0.844	3	0.271	0.063	0.248
FEL-AO-080	0.313	9	0.828	0.313	0.810
FEL-AO-082	0.750	2	0.375	0.000	0.305
FEL-AO-083	0.594	5	0.576	0.063	0.525
FEL-AO-084	0.625	6	0.578	0.000	0.553
FEL-AO-092	0.656	4	0.525	0.313	0.486
FEL-AO-093	0.344	6	0.740	0.438	0.698
FEL-AO-095	0.917	2	0.153	0.000	0.141
FEL-AO-099	0.563	4	0.578	0.000	0.510
FEL-AO-100	0.500	5	0.653	0.000	0.602
FEL-AO-102	1.000	1	0.000	0.000	0.000
FEL-AO-104	0.625	4	0.539	0.000	0.483
FEL-AO-110	0.781	5	0.375	0.125	0.357
FEL-AO-111	0.500	3	0.620	0.000	0.548
FEL-AO-112	0.594	7	0.619	0.188	0.599
FEL-AO-113	0.800	4	0.347	0.133	0.329
FEL-AO-114	0.429	10	0.770	0.429	0.752
FEL-AO-115	0.750	3	0.401	0.357	0.359
FEL-AO-118	1.000	1	0.000	0.000	0.000
FEL-AO-120	0.433	4	0.633	0.267	0.560
FEL-AO-122	0.455	6	0.711	0.273	0.673
FEL-AO-125	0.375	5	0.727	0.250	0.682
FFI-AQ-127	0.594	4	0.561	0.063	0.498
FFI-AQ-129	0.400	4	0.660	0.000	0.596
FEL-AO-130	0.429	7	0.737	0 357	0 705
FFI-AO-131	0.594	5	0.547	0.125	0.475
FFL-AO-132	0.467	9	0.742	0.767	0.723
FEL-ΔΩ-133	0.407	4	0.525	0.063	0.725
FEL-ΔΟ-134	0.050	3	0.325	0.005	0.400
FEL_AO_134	0.760	3	0.240	0.000	0.227
FEL-AO-135	0.709	2	0.379	0.000	0.545
FEL-ΔΩ-142	0.214	2	0.000	0.429	0.044
	0.009	2	0.190	0.000	0.1/0
	0.045	5	0.331	0.145	0.521
	0.394	2	0.394	0.125	0.004
FEL-AU-148	0./33	4	0.429	0.133	0.393
	1.000	10	0.860	0.563	0.844
	0.214	1 20	0.000	0.000	0.000
iviean	0.615	4.38	0.517	0.133	0.475

 $M_{\rm AF}$: major allele frequency; $N_{\rm A}$: number of alleles; $H_{\rm o}$: observed heterozygosity; $H_{\rm E}$: expected heterozygosity; PIC: polymorphism information content.

clustering pattern demonstrates that the developed SSR markers are effective in detecting genetic diversity [49], making them valuable tools for further population genetics studies.

4. Conclusion

In the present study, we identified SSR loci in the whole genome of *A. ostoyae* and developed 150 SSR markers to evaluate *Armillaria*. Of these, 105 markers were successfully amplified and analyzed. We assessed the potential transferability of the related

species, *A. gallica* and confirmed its transferability using 52 of 105 markers (49.5%).

These markers are expected to serve as valuable tools for evaluating genetic diversity, analyzing population structure, efficiently selecting traits within the *Armillaria* genus, and in other related studies. Further investigations are required to determine the transferability of these markers to other closely related species and their practical applications. Future research should focus on validating these markers across a broad range of *Armillaria* species and investigating their utility in ecosystem management, disease control, and breeding for advantageous traits.



Figure 2. UPGMA dendrogram of 16 Armillaria gallica strains based on based on shared allele method. Numbers on the branches indicate genetic distance values, and numbers in parentheses represent strain numbers.

Acknowledgments

The authors thank National Institute of Forest Science, Forest Mushroom Research Institute, and Korea National Arboretum for providing the isolate, used as a reference in this study.

Author contributions

S.K.: Conceptualization, methodology, investigation, formal analysis, visualization, and writing—original draft. H.L.: Conceptualization, data curation, supervision, and writing—original draft, reviewing, and editing. All authors have read and agreed to the published version of the manuscript.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This work was supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government (MSIT) (NRF-2022R1F1A1074607).

ORCID

Hwayong Lee (b) http://orcid.org/0000-0003-4526-2082 Sohee Kim (b) http://orcid.org/0009-0006-5083-4451

References

- Baumgartner K, Coetzee MP, Hoffmeister D. Secrets of the subterranean pathosystem of *Armillaria*. Mol Plant Pathol. 2011;12(6):515–534. doi: 10.1111/j.1364-3703.2010.00693.x.
- [2] Volk TJ. A nomenclatural study of Armillaria and Armillariella species. Synopsis Fungorum. 1995;8:1–121.
- [3] Sipos G, Prasanna AN, Walter MC, et al. Genome expansion and lineage-specific genetic innovations in the forest pathogenic fungi *Armillaria*. Nat Ecol Evol. 2017;1(12):1931–1941. doi: 10.1038/s41559-017-0347-8.
- [4] Guillaumin JJ, Mohammed C, Anselmi N, et al. Geographical distribution and ecology of the *Armillaria* species in western Europe. Eur J For Pathol. 1993;23(6– 7):321–341. doi: 10.1111/j.1439-0329.1993.tb00814.x.
- [5] Tsykun T, Rigling D, Prospero S, et al. Diversity and ecology of *Armillaria* species in virgin forests in the Ukrainian Carpathians. Mycol Prog. 2012;11(2):403– 414. doi: 10.1007/s11557-011-0755-0.
- [6] Heinzelmann R, Dutech C, Tsykun T, et al. Latest advances and future perspectives in *Armillaria* research. Can J Plant Pathol. 2019;41(1):1–23. doi: 10.1080/07060661.2018.1558284.
- [7] Tsykun T, Rellstab C, Dutech C, et al. Comparative assessment of SSR and SNP markers for inferring the population genetic structure of the common fungus *Armillaria cepistipes*. Heredity. 2017;119(5):371–380. doi: 10.1038/hdy.2017.48.
- [8] Bendel M, Kienast F, Rigling D. Genetic population structure of three *Armillaria* species at the landscape scale: a case study from Swiss *Pinus mugo* forests. Mycol Res. 2006;110(6):705–712. doi: 10.1016/j.mycres.2006.02.002.

- [9] Langrell SRH, Lung-Escarmant B, Decroocq S. Isolation and characterization of polymorphic simple sequence repeat loci in *Armillaria ostoyae*. Mol Ecol Notes. 2001;1(4):305–307. doi: 10.1046/j.1471-8278.2001.00119.x.
- [10] Erbiai E, da Silva EH, Saidi LP, et al. Chemical composition, bioactive compounds, and antioxidant activity of two wild edible mushrooms *Armillaria mellea* and *Macrolepiota procera* from two countries (Morocco and Portugal). Biomolecules. 2021;11(4):575. doi: 10.3390/biom11040575.
- [11] Engels B, Heinig U, Grothe T, et al. Cloning and characterization of an *Armillaria gallica* cDNA encoding protoilludene synthase, which catalyzes the first committed step in the synthesis of antimicrobial melleolides. J Biol Chem. 2011;286(9):6871–6878. doi: 10.1074/jbc.M110.165845.
- [12] Kim SB, Shin HC, Lee TS, et al. Inhibitive effect of mouse sarcoma 180 by crude polysaccharide extracted from fruiting body of *Armillaria mellea*. Korean J Mycol. 2006;34(2):98–104.
- [13] Yao L, Lv J, Duan C, et al. Armillaria mellea fermentation liquor ameliorates p-chlorophenylalanine-induced insomnia associated with the modulation of serotonergic system and gut microbiota in rats. J Food Biochem. 2022;46(2):e14075. doi: 10.1111/jfbc.14075.
- [14] Lee HY, Moon S, Shim D, et al. Development of 44 novel polymorphic SSR markers for determination of shiitake mushroom (*Lentinula edodes*) cultivars. Genes. 2017;8(4):109. doi: 10.3390/genes8040109.
- [15] Wang LN, Gao W, Chen Y, et al. Identification of commercial cultivars of *Agaricus bisporus* in China using genome-wide microsatellite markers. J Integr Agric. 2019;18(3):580–589. doi: 10.1016/S2095-3119(18)62126-4.
- [16] Boiko SM. Identification of novel SSR markers for predicting the geographic origin of fungus *Schizophyllum commune* Fr. Fungal Biol. 2022;126(11-12):764–774. doi: 10.1016/j.funbio.2022.09.005.
- [17] Franco J, Crossa J, Ribaut JM, et al. A method for combining molecular markers and phenotypic attributes for classifying plant genotypes. Theor Appl Genet. 2001;103(6-7):944–952. doi: 10.1007/ s001220100641.
- [18] Wu B, Hussain M, Zhang W, et al. Current insights into fungal species diversity and perspective on naming the environmental DNA sequences of fungi. Mycology. 2019;10(3):127–140. doi: 10.1080/21501203.2019.1614106.
- [19] Zane L, Bargelloni L, Patarnello T. Strategies for microsatellite isolation: a review. Mol Ecol. 2002;11(1):1–16. doi: 10.1046/j.0962-1083.2001.01418.x.
- [20] Yun YE, Yu JN, Lee BY, et al. An introduction to microsatellite development and analysis. Korean J Plant Taxon. 2011;41(4):299–314. doi: 10.11110/ kjpt.2011.41.4.299.
- [21] Van Deynze A, Sorrells ME, Park WD, et al. Anchor probes for comparative mapping of grass genera. Theor Appl Genet. 1998;97(3):356–369. doi: 10.1007/ s001220050906.
- [22] Tikhonov AP, SanMiguel PJ, Nakajima Y, et al. Colinearity and its exceptions in orthologous *adh* regions of maize and sorghum. Proc Natl Acad Sci U S A. 1999;96(13):7409–7414. doi: 10.1073/pnas.96.13.7409.
- [23] Kuleung C, Baenziger PS, Dweikat I. Transferability of SSR markers among wheat, rye, and triticale.

Theor Appl Genet. 2004;108(6):1147-1150. doi: 10.1007/s00122-003-1532-5.

- [24] Prodorutti D, Pertot I, Gessler C, et al. Genetic diversity of Armillaria spp. infecting highbush blueberry in northern Italy (Trentino region). Phytopathology. 2009;99(6):651–658. doi: 10.1094/PHYTO-99-6-0651.
- [25] Xing R, Gao QB, Zhang FQ, et al. Genetic diversity and population structure of *Armillaria luteo-virens* (Physalacriaceae) in Qinghai-Tibet Plateau revealed by SSR markers. Biochem Syst Ecol. 2014;56:1–7. doi: 10.1016/j.bse.2014.04.006.
- [26] Elías-Román RD, Medel-Ortiz R, Alvarado-Rosales D, et al. Armillaria mexicana, a newly described species from Mexico. Mycologia. 2018;110(2):347–360. doi: 10.1080/00275514.2017.1419031.
- [27] Coetzee MPA, Wingfield BD, Wingfield MJ. Armillaria root-rot pathogens: species boundaries and global distribution. Pathogens. 2018;7(4):83. doi: 10.3390/pathogens7040083.
- [28] Chillali M, Wipf D, Guillaumin JJ, et al. Delineation of the European Armillaria species based on the sequences of the internal transcribed spacer (ITS) of ribosomal DNA. New Phytol. 1998;138(3):553-561. doi: 10.1046/j.1469-8137.1998.00124.x.
- [29] Park KH, Oh SY, Park MS, et al. Re-evaluation of Armillaria and Desarmillaria in South Korea based on ITS/tef1 sequences and morphological characteristics. For Pathol. 2018;48(6):e12447. doi: 10.1111/efp.12447.
- [30] Ferguson BA, Dreisbach TA, Parks CG, et al. Coarse-scale population structure of pathogenic Armillaria species in a mixed-conifer forest in the Blue Mountains of northeast Oregon. Can J For Res. 2003;33(4):612–623. doi: 10.1139/x03-065.
- [31] Smith ML, Bruhn JN, Anderson JB. The fungus Armillaria bulbosa is among the largest and oldest living organisms. Nature. 1992;356(6368):428-431. doi: 10.1038/356428a0.
- [32] Zhang T, Cai G, Rong X, et al. A combination of genome mining with an OSMAC approach facilitates the discovery of and contributions to the biosynthesis of melleolides from the Basidiomycete *Armillaria tabescens*. J Agric Food Chem. 2022;70(39):12430– 12441. doi: 10.1021/acs.jafc.2c04079.
- [33] Walterová L, Botella L, Hejna O, et al. Characterization of mycoviruses in *Armillaria ostoyae* and *A. cepistipes* in the Czech Republic. Viruses. 2024;16(4):610. doi: 10.3390/v16040610.
- [34] Caballero JRI, Lalande BM, Hanna JW, et al. Genomic comparisons of two *Armillaria* species with different ecological behaviors and their associated soil microbial communities. Microb Ecol. 2023;85(2): 708–729. doi: 10.1007/s00248-022-01989-8.
- [35] Nagy S, Poczai P, Cernák I, et al. PICcalc: an online program to calculate polymorphic information content for molecular genetic studies. Biochem Genet. 2012;50 (9–10):670–672. doi: 10.1007/s10528-012-9509-1.
- [36] Prospero S, Jung E, Tsykun T, et al. Eight microsatellite markers for *Armillaria cepistipes* and their transferability to other *Armillaria* species. Eur J Plant Pathol. 2010;127(2):165–170. doi: 10.1007/s10658-010-9594-0.
- [37] Ohm RA, de Jong JF, Lugones LG, et al. Genome sequence of the model mushroom *Schizophyllum commune*. Nat Biotechnol. 2010;28(9):957–963. doi: 10.1038/nbt.1643.

- [38] Stajich JE, Wilke SK, Ahrén D, et al. Insights into evolution of multicellular fungi from the assembled chromosomes of the mushroom *Coprinopsis cinerea* (*Coprinus cinereus*). Proc Natl Acad Sci U S A. 2010;107(26):11889– 11894. doi: 10.1073/pnas.1003391107.
- [39] Martin F, Aerts A, Ahrén D, et al. The genome of *Laccaria bicolor* provides insights into mycorrhizal symbiosis. Nature. 2008;452(7183):88–92. doi: 10.1038/ nature06556.
- [40] Qu J, Huang C, Zhang J. Genome-wide functional analysis of SSR for an edible mushroom *Pleurotus* ostreatus. Gene. 2016;575(2 Pt 2):524–530. doi: 10.1016/j.gene.2015.09.027.
- [41] Karaoglu H, Lee CMY, Meyer W. Survey of simple sequence repeats in completed fungal genomes. Mol Biol Evol. 2005;22(3):639–649. doi: 10.1093/molbev/ msi057.
- [42] Zamanmirabadi A, Hemmati R, Dolatabadian A, et al. Status of SSR, cSSR, iSSR and VNTR motifs in *Leptosphaeria maculans* based on high throughput sequencing data. Mycol Iran. 2021;8(2):95–107.
- [43] Lee HY, Raveendar S, An H, et al. Development of polymorphic simple sequence repeat markers using high-throughput sequencing in button mushroom (*Agaricus bisporus*). Mycobiology. 2018;46(4):421– 428. doi: 10.1080/12298093.2018.1538072.

- [44] Lee JW, Lee Mw An JY, et al. Microsatellite DNA fingerprinting analysis of natural monument Gingko trees using microsatellite markers. J Korean For Soc. 2017;106(4):408–416.
- [45] Cho KS, Won HS, Jeong HJ, et al. Development of multiplex microsatellite marker set for identification of Korean potato cultivars. Korean J Hortic Sci Technol. 2011;29(4):366–373.
- [46] Li X, Liu X, Wei J, et al. Development and transferability of EST-SSR markers for *Pinus koraiensis* from cold-stressed transcriptome through Illumina sequencing. Genes. 2020;11(5):500. doi: 10.3390/genes11050500.
- [47] Jiao Y, Jia HM, Li XW, et al. Development of simple sequence repeat (SSR) markers from a genome survey of Chinese bayberry (*Myrica rubra*). BMC Genom. 2012;13(1):201. doi: 10.1186/1471-2164-13-201.
- [48] Mengistu FG, Motoike SY, Caixeta ET, et al. Cross-species amplification and characterization of new microsatellite markers for the macaw palm, *Acrocomia aculeata* (Arecaceae). Plant Genet Resour. 2016;14(3):163–172.
- [49] Hur M, Lee J, Kim Y, et al. Development of whole genome sequence-based novel SSR markers in *Astragalus membranaceus* (Fisch.). Korean J Med Crop Sci. 2021;29(6):418–424. doi: 10.7783/KJMCS. 2021.29.6.418.