곰취속 식물 유전적 다양성 분석을 위한 EST-SSR 프라이머 세트

▢ 배경 및 필요성

- ㅇ 곰취의 급속한 재배면적 증가에 다른 근연종 및 유사종의 혼합재배로 품질 특성이 다양하여 품종 및 계통의 판별 기준 확립 필요
- ㅇ EST-SSR 분자마커를 통한 발현 유전자간 유연관계 분석으로 육종 효율화

▢ 연구 내용

- ㅇ SSR 모티프를 포함하고 있는 곰취 전사체 정보

Motif types	No. of transcripts
2bp-repeats	42
3bp-repeats	279
4bp-repeats	32
Total	353

- ㅇ SSR 프라이머 선발 : PCR 증폭을 위한 EST-SSR 프라이머세트 154개 개발

	Sequence	SSR_Type	SSR	SSR_No	Primer_Begin	Primer_End	Product_Size	Left_Primer	Right_Primer
2	cluster_13	GAT	GATGATGATGATGATGATGATGATGATGATGATGAT	14	676	919	244	TAATAGCCAAGATGTGCTTCCT	ATATTCCCCTCTTGTGACCTTT
3	cluster_47	GAT	GATGATGATGATGATGATGATGATGATGAT	11	1552	1921	370	ATGACACGTCACCTAAAGAACC	CATCATCAACACTTCCACAGTC
4	cluster_19	GAT	GATGATGATGATGATGATGATGATGAT	10	453	794	342	GGCAGATAATTTGGAGAATCAG	GCATAGATGGTGGTAAAGAAGC
5	cluster_48	GAT	GATGATGATGATGATGATGATGATGAT	10	250	646	397	ATTCCGATGAAGAAGAAGACAA	CACAGAAATGTGTTCAATCACC
6	cluster_28	GAT	GATGATGATGATGATGATGAT	8	477	620	144	GTTGACCTCCACTGAAGATGAT	AATCGTAAATCGTAAATCGGTG
7	cluster_36	ATC	ATCATCATCATCATCATCATC	7	717	937	221	AGTGAAATCACATAATCCCCAA	ACGGGGTCCAGAAGTTAATAAT
8	cluster_32	GAT	GATGATGATGATGATGATGAT	7	270	627	358	AGAAAGATAGGGCACAACAAGA	AAATTTCATAATCCCATGTTCG
9	cluster_47	ATC	ATCATCATCATCATCATCATC	7	341	726	386	AATCGTCATCAATGTCTTCACA	CAACTCTGTAAAACGAATGCAA
10	cluster_60	GAT	GATGATGATGATGATGAT	6	802	1011	210	AAGAAAATATGAAATGGCATCG	TCCATTGGTGATTAGTTGATGA

▢ 특허청구의 범위

- ㅇ 다형성 분석을 위한 EST-SSR 프라이머세트

▢ 파급효과

- ㅇ 곰취 속 식물 육종의 고도화 및 효율화

<세부 연구결과>

○ SSR motif를 포함하고 있는 곰취 전사체 정보

Motif types	No. of transcripts
2bp-repeats	42
3bp-repeats	279
4bp-repeats	32
Total	353

○ PCR 증폭을 위해 개발된 곰취 EST-SSR 분자마커 primer 염기서열

1	Sequence_	SSR_Type	SSR	SSR_No	Primer_Begin	Primer_End	Product_Size	Left_Primer	Right_Primer	Sequence
2	cluster_13	GAT	GATGATGATGATGATGATGATGATGATGATGATGATGATGAT	14	676	919	244	TAATAGCCAAGATGTGCTTCCT	ATATTCCCCTCTTGTGACCTTT	AACCTAGAAAAGTCTAAGCGAGTTAAACCCTTTCGTTGTGGTGAGTTTGATGACTGCATTCAGA
3	cluster_47	GAT	GATGATGATGATGATGATGATGATGATGATGAT	11	1552	1921	370	ATGACACGTCACCTAAAGAACC	CATCATCAACACTTCCACAGTC	ACTACTTCTCACTGGTATTGAAAAGGAACTGGATAGTGGATTTGTATCTCATATCAACAAAAAC
4	cluster_19	GAT	GATGATGATGATGATGATGATGATGATGAT	10	453	794	342	GGCAGATAATTTGGAGAATCAG	GCATAGATGGTGGTAAAGAAGC	ATGGTACAGTTCATGAAAGCAATGCGAGACGAACGCGGTGAAATGGTCAGGAACGCTCATATA
5	cluster_48	GAT	GATGATGATGATGATGATGATGATGATGAT	10	250	646	397	ATTCCGATGAAGAAGAAGACAA	CACAGAAATGTGTTCAATCACC	AAGGAAGCCATGGCAGAGATTAACTGCAACGAAGAACCAAACGTACTCCCTTCTAAGCGCAAA
6	cluster_28	GAT	GATGATGATGATGATGATGATGAT	8	477	620	144	GTTGACCTCCACTGAAGATGAT	AATCGTAAATCGTAAATCGGTG	CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCAATATCAAAACCCTTGAGAGAAAA
7	cluster_36	ATC	ATCATCATCATCATCATCATC	7	717	937	221	AGTGAAATCACATAATCCCCAA	ACGGGGTCCAGAAGTTAATAAT	GATAGTGAACCATTTCCCAAACCCACACCCGCAGTGTACATAACACAAATAAGGTTATGACCAT
8	cluster_32	GAT	GATGATGATGATGATGATGAT	7	270	627	358	AGAAAGATAGGGCACAACAAGA	AAATTTCATAATCCCATGTTCG	AACAGTGTAGTCTACCTCAAGTCTCAATTCTCATCGTGAATTTCTCAGGACCTTAATTCTTCCATT
9	cluster_47	ATC	ATCATCATCATCATCATCATC	7	341	726	386	AATCGTCATCAATGTCTTCACA	CAACTCTGTAAAACGAATGCAA	ccGATTTCAGGACCCAATCGGGCTAAACCCGTCAGGGGTTGGTTGGGCATGAATCCATCCACCT
10	cluster_60	GAT	GATGATGATGATGATGAT	6	802	1011	210	AAGAAAATATGAAATGGCATCG	TCCATTGGTGATTAGTTGATGA	TGATAATGTTAATAATGATGATCTGGAAGAGGAAGACCCTATTGCTCTTGTTGCTGCTGCTGCT
11	cluster_63	GAT	GATGATGATGATGATGAT	6	1867	2248	382	CTTGATGAAGAATTCTGGGAAG	AATATAAAATTTCGCGAGGGAT	TGTGGAGTTGAGATTACAAGGAGCCGAGAAAAGCAGCAAAAGATGATGAGTTTTTTAGCAAA
12	cluster_12	GAT	GATGATGATGATGATGAT	6	1455	1767	313	CCAATCAGTTCTAACGAAAAGG	TCTTTATTGAGGGCTGACACTT	TATTTGCATTTCCAAATGGATATCATAGTGGATCACATAAGGAGAACACTGGATTTGACTTCAG
13	cluster_12	GAT	GATGATGATGATGATGAT	6	1481	1779	299	TGATGACATGCCAACTAAAGAG	GCTACGTTCGTCTCTAGCTGTT	AAGTCCCATTAGAGAAAGAAGACATGAAAAAGAGAAACTTGTTGAAAAGGTGGGAAGAAGGA
14	cluster_15	ATC	ATCATCATCATCATCATC	6	450	741	292	CACACATTCATTAGGGTTCCTT	CTAGTTGGAGACGAAGGAATTG	GTGATGTGAATTGAAATTGAGAAGAAAAAAATGGCTAGTTTGGTCCCTGGTGTTTTGTTGAAAT
15	cluster_15	GAT	GATGATGATGATGATGAT	6	574	903	330	TTTGAGAGGAAGTATTAGGGCA	TAATTTCCGCATTTCAGCTAAT	ACACCAAACGCGCCCACCGTCTCTGCCCTACTCTCGACGGCGTCTCCGATATGCTAACCGTCATT
16	cluster_35	GAT	GATGATGATGATGATGAT	6	563	848	286	AATCAGGAATTATCCACCATTG	TTTTCTAAACGTTTCCAAGCAT	AATCTCTTTCAATCGGTAAAAACTAAAAACAAACAATTTTCGGAACCCTAGTTATGGAGCTTTTT
17	cluster_42	ATC	ATCATCATCATCATCATC	6	275	513	239	AATCACCAAACACATCCTCTTC	AGCGAATTTCACTTTATCCAAA	ATTTCTCTCCGCCGTATCGCCACCGTATCTCTATCTTTCTGCCGTGAAGTGATGGTTACTGACGT
18	cluster_43	GAT	GATGATGATGATGATGAT	6	354	669	316	GATTGTTCTGTCATCCTTCCAT	CTACCAGATTCACCTCCATTGT	GATCTCCCACTACATACAAATACAATTATCTCCTTTATTTTTCATTTCAATTTGTTAAAAATGGGT
19	cluster_44	ATC	ATCATCATCATCATCATC	6	71	206	136	AAGCCCCAACTAGAATTCTTTC	TTAATTTCTGGTGGTTTCCTTG	GAGTTTCAAGAAACCCCAAACCAAAAATGGAATCCCCCTTCCTTCTTGCCTAGGTTTCGACTCCA
20	cluster_45	ATC	ATCATCATCATCATCATC	6	66	443	378	AATTACAACCTCTCTCAGCCAA	ATTCAAACCTGCTGGAGAACTA	AAAAGCCACAAGCTTTGAATTGTCCAAGATGTAATTCTTCACACACAAAGTTTTGTTATTACAAC
21	cluster_40	GAT	GATGATGATGATGAT	5	1958	2233	276	AGTTCAAACGAAGATGAAGGAA	GGGACTGCATTCATAGTCTCAT	CGTCATTTAAATTTGCTATCGGAATGGATATTGGGCTAGGTCAAGAGTTTCAAATATTACCGTTC
22	cluster_57	GAT	GATGATGATGATGAT	5	2423	2767	345	GGCGAAGAAAGAGTTGTAATTG	AAGAAAGTGTATGTTGCTGCCT	AGTGTGCCTTTTTTGAATCGTATATAACGCATTAGTTATATATAAAAAGTCAAAAAACATGAAAA
23	cluster_12	ATC	ATCATCATCATCATC	5	711	1019	309	AAGAAATCATCAAAAGACCGAA	TCATTCTCGCTTACATCATCAG	TATGGGGAGAGCATATTCGGTGCGAAGTTTCCAGATGAATCATCCAAGCTGAAACATGATGAA
24	cluster_13	GAT	GATGATGATGATGAT	5	1394	1756	363	GAGGACCCAATCAAGAATGATA	CAGGCAGTACTGATTCACCTTT	GGTTTTATTCCCATTGATAGTTCTTCATTTTACCCTAGTCCCGAGAAGATTTCTACTTTACTGCCCA
25	cluster_14	ATC	ATCATCATCATCATC	5	1689	2012	324	ATTCTAAAGGCTTGTGCAATGT	ATGACCCAATCTATCCAAAGTG	ATGCTTTGAAAGAGAAAGAGTCTCCTTTGTGTGTTATTGCAGATGATAGTGTTTTCTTAACAACT
26	cluster_19	GAT	GATGATGATGATGAT	5	914	1247	334	GGTCGATGAGGTAGTTGAAGAG	TTTCCACCATTATCAACATCAA	GGATTTGTGACTGTGATGGATTTTGTTTGGGCGGATGAGTATGATGCGATAAATGGACCGAAT
27	cluster_20	ATC	ATCATCATCATCATC	5	1074	1405	332	GGGAAACTTCTTTATGTCCCTT	CAATGCTTGCTCAAAATGTAAA	GCATAGTATTCTTTGATGAGGTAGATGCTCTGACAACACAGCGTGGAAAGGAAGGGGGATGG
28	cluster_28	GAT	GATGATGATGATGAT	5	307	620	314	AACCCCGTTTATTCTTTCTCTC	AATCGTAAATCGTAAATCGGTG	AAACATCAAACGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCAATATC
29	cluster_28	GAT	GATGATGATGATGAT	5	955	1295	341	TTTGAAAGTTAGTGAATCGCCT	CTCAAGCTCTCGATCTTTCCTA	ACCGCAATGGCACCGAATGAAATGGTTGGATAACAGAGTTAGGCTTTTGATTCAAGTTGTAGCT
30	cluster_31	GAT	GATGATGATGATGAT	5	487	825	339	AATTTCTAAAGATGACGAGCCA	TTTCATATTCCACTTCGTTTCC	GGAATCAACTTGTTGCTAAGCTTTCAATCCGTGTCTCAACTATTTGATCAAATAGTCTACTCATC
31	cluster_34	GAT	GATGATGATGATGAT	5	581	917	337	GTGCTAGTTTGTTTATGGGCTC	CATCACGATCAGAAACATCATC	TTATATTGAACTCATGGGGAAAAAGAAGCCCGGAGCTCGTGAGGAGGATAGTGTTGTAGGTG
32	cluster_44	GAT	GATGATGATGATGAT	5	659	829	171	CTCTTGCGTATTTCAACAATGA	ACTGTTGAATCCCTAAAGCTGA	AGGGTTTTTAAAATGGTGGCTGATAAAGGTAAGAAACCCAAGATCGCAGAAGAAAAAGCCGA
33	cluster_45	GAT	GATGATGATGATGAT	5	96	442	347	TAGTACCCGAGTTGTGGAAGTT	TTACTACCAGGCTTTTATCGGA	AATCTCATTTAACCAGCTAGCTAGTTAGCAATGGTGGCCACGTCACTTCAACTAGATCTCAATCT
34	cluster_47	GAT	GATGATGATGATGAT	5	185	564	380	TTTCTAAGTCCCCAATGAAGAA	ACTCTTGGCTTCACAAAATGAT	AGGTTGAAATCATTCATACAAGTCACAACACATTTGCTGAAGAAAGTTTTTTTTGACACACGAAT
35	cluster_47	ATC	ATCATCATCATCATC	5	39	416	378	ACTTCATCTTCTCAGTTGCGTT	CTTTAGACCCTGAGAAAGGGTT	ATCTTCATTCAATGGCTTCCTTTACTCTCTCTCCTGCTACTTCATCTTCTCAGTTGCGTTCTGGTAA
36	cluster_26	GAT	GATGATGATGAT	4	903	1276	374	TTTTATCGAACTGCTGATGATG	CCGTAAATTGATGCTGGTTAAT	TGTTGACCCCGATTCTGTCAACTCAGCTGTAGAAGACTCAGAAAAAGGTAAACTTGTAATCAAC
37	cluster_27	GAT	GATGATGATGAT	4	2117	2330	214	TGACAGACAATTAAAAACTGCG	CACCCACAACCTTAACTTCAAT	ACCAAACGGGGACCACATCGTTAAGGTTAGTTGTGTCCAAACACAAGCTATTCAACAATATGCC

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