Transferability of Soybean SSR Markers in Peanut (*Arachis hypogaea* L.)

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ABSTRACT

Simple sequence repeats (SSRs) are useful DNA markers in plant genetic research. However, they are not fully exploited in peanut because of the high cost and labor intensity involved in their development. Many studies have showed that DNA markers could be transferable among related species due to the conserved regions in their genomes. The objective of this study was to investigate the transferability of soybean SSR markers to peanut because of the availability of a large number of soybean SSRs. Four hundred thirty-two soybean SSR primer pairs were used to amplify peanut genomic DNAs extracted from four cultivated peanut lines. The result showed that 25% of soybean SSR primer pairs tested in this study could amplify peanut genomic DNA. Among these transferable SSR markers, 28% have detected polymorphism among these peanut lines. These transferable markers will benefit peanut genome research by not only providing additional DNA markers in peanut, but also allowing comparative mapping to be possible between peanut and soybean.

Key Words: Transferable marker, soybean SSR, peanut.

Simple sequence repeat (SSR) markers are a valuable tool in genetic mapping, genotyping, and marker-assisted selection in breeding due to their characterization of co-dominant loci, high allelic variation, even distribution, and be easily used by PCR. In peanut, SSR markers have been developed by several groups (Hopkins *et al*., 1999; He *et al*., 2003; Ferguson *et al*., 2004; Luo *et al*., 2005a), however, they are still not fully exploited and developed compared to other crops. Peanut genome research has made less progress than other legumes because of insufficient genomic tools available (Luo *et al*., 2005a, 2005b). Thus, one of the pressing needs in peanut genomic research is to take advantage of progress made in the well-characterized legumes. Searching for transferable SSR marker developed from model legumes, such as soybean, *Medicago truncatula*, and *Lotus japonicus* is a cost-effective way to increase DNA markers for peanut genomic studies and genetic linkage map development.

Many studies have shown that RFLP and SSR markers were transferable among cereal crops (Saghai Maroof *et al*., 1996; Devos *et al*., 1998; Zhang *et al*., 1998; Hernandez *et al*., 2001; Babula *et al*., 2003; Kuleung *et al*., 2004; La Rota and Sorrells 2004; Spielmeyer *et al*., 2004), and legume crops (Boutin *et al*., 1995; Humphry *et al*., 2002; Isobe *et al*., 2003). The transferable markers are developed from the conserved genomic regions among related species. Transferability of DNA markers between the genomes of different species not only provides researchers with large pools of available markers, but also allows us to better understand the evolution and speciation of crops through comparative mapping. However, the transferability of DNA markers from other crops to peanut is unknown. Therefore, the objective of this study is to examine the transferability of soybean SSR markers to cultivated peanut.

Materials and Methods

Plant Material. Two peanut cultivars (GK7 and COAN) and two breeding lines (C11-2-39 and 448A) were used in this study to test the transferability of soybean SSR markers in peanut. These four peanut lines were selected because they are used as parental lines in current peanut breeding programs and mapping population development. The cultivar, COAN, was developed by introgression from *A. cardenasii, A. duranensis* and *A. batizocoi* to cultivated peanut (Simpson and Starr, 2001).

DNA Extraction. DNA was extracted from young leaf tissue using the CTAB method of Murray and Thompson (1980) with some modifications. Leaves (3–5 g) were ground in liquid nitrogen and suspended in a buffer containing 2% CTAB, 30 mM Tris-HCl (pH 8.0), 10 mM EDTA, and 0.1 M NaCl. One-third volume of 5 M potassium acetate was added, and the supernatant was extracted twice with phenol and once with chloroform. Nucleic acid was precipitated with two volumes of ethanol and suspended in 0.5 ml TE (10 mM Tris-HCl, pH 8.0, and 1 mM EDTA) containing 5 μg/ml RNaseA (Sigma). This mixture was then extracted twice with phenol:chloroform

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Table 1. List of transferable soybean SSR markers in peanut.

SSR locus	Repeat motif	Upper primer sequence (5′–>3′)	Lower primer sequence (5–>3′)	Allele size in Williams (soybean)
Sat_119	(AT)25	TAGGCTTTCAATTTGCAGAACT	GTTAGGTGTCCCAAGCAACTTA	152
Sat_143*	(AT)13	GAAGATTGGGTAGATACTTCAACAC	GGATGGATGGTCCATTGATTCTTT	177
Sat_146	(AT)20	GGGATCAAGTTACTTCAAAATCAT	GGCGATGGAAATAGGGCAAATAAT	257
Sat_147*	(AT)12	GTGCGACGTCATGCCTTACTCAAT	GCGCTCCGTACACTTAAAAAAGAA	265
Sat_149	(AT)21	GCGGAGCAACCACTTGTGTCTTCCTGT	GCGCGTAGTTGAATTAATTAAATTACT	208
Sat_150*	(AT)24	GCGCACATGCTCACCAAGCAAAGTAT	GCGGTAGAGCGGATTAAACTTGTC	212
Sat_151*	(AT)13	GCTGCATCAGATCACCCATCCTTC	CATGCCATGTTGTATGTATGT	230
Sat_155	(AT)19	GGGACAGCACCGTCAAGGAGGAGA	TGGGAAAGAAATTGTAGC	171
Sat_156	(AT)17	GCGGTGTGGATCCAAAAACTCAAACTT	GCGTGCTAGTTCGATCAGCTTAGTTTC	214
Sat_159	(AT)22	GCGCCTAGAAGTAATTAACTCTCT	GCATTCCCGTGCCCCACATATGCT	173
Sat_160	(AT)25	GCGCATGATAACCTATAATGAGAT	CCAGCAAGCAATGCTCGGTCTACT	204
Sat_162	(AT)36	GCGTGGTTTTTCGCTGGATATA	GCGCATTTCGTAACATATTTTTCAC	175
Sat_169	(AT)17	ATTCGTTAAATACTCCACATCAATA	TTATGCTTTGTTGTTTTTCAGTT	162
Sat_172*	(AT)18	GCGTTCTAATTTCCTGACACTGTT	GCGGGACGTAAACGGATAATAAGGT	208
Sat_180	(AT)23	GATCTAGGGCAAACAAGGTT	CTCGCTCTTCGCAACATA	235
Sat_184	(AT)23	GCGGAATTTGAGTCCTCTAAAGTG	GCGTGGCACCTCAAGATGGAAGT	264
Sat_187	(AT)29	GCGTAACGGTGATACAAACAGATT	GCGGCGACTCTGATAACAACA	239
Sat_189	(AT)10	GCGCACCTAGTTGACTCTTG	ACTACCCCACATACTTCCTTTTAT	117
Sat_192*	(AT)13	GCGGAATGGCAATAGTTGATGAGTA	GCGGGATGGGATATGAGAGTAAG	173
Sat_197	(AT)33	GCGATTTTGGTTTTGTTTTATTAG	GCGGTTAACAGCCAAGTTCTTTC	194
Sat_205	(AT)26	GCGCCTTTTCGTCTGTTCTGTTC	GCGAGCTTTTAAAAATTTAGAAATCAAT	219
Sat_217	(AT)21	GCGAAAAATTGTCAATGATATGATCAGTAAG	GCGGTCCTAGATGAAAAATGCTTTGTAA	293
Sat_218	(AT)26	GCGCACGTTAAATGAACTGGTATGATA	GCGGGCCAAAGAGGAAGATTGTAAT	290
Sat_219*	(AT)26	GCGTCATGCCACGTGATATTTTAT	GCGTGTGTCCCAAATGTGATTCA	262
Sat_222	(AT)21	GCGGTCATGTGTCCCATTTAATTTAATCAA	GCGATGTGCCTCAAAAACTAACATCAATAA	168
Sat_228	(AT)24	GCGTGACTACGGGAAGTTGGAAC	GCGTTGGCGGTAAGAGCACTATA	252
Sat_229*	(AT)21	GCGTGTGCTACTTCACATCTTGAGAGAAAGA	GCGAGGGTTTAGAAAAAGATTCACCAAATAT	257
Sat_230	(AT)26	GCGGTGGGACATTGGTTTAAGTTATTTT	GCGGGATATCTTCAGCGATGGATTTTA	283
Sat_234*	(AT)22	GCGATGCGTTTAATAAGTTTTGAAAAATGCC	GCGGAAACCATCCTTATATGTCAATTGCTCA	332
Sat_235*	(AT)26	GCGTTGGGATGGGTGTAAAACATT	GCGGAAGGCAAGTCAAGTTGATGAG	281
Sat_237*	(AT)25	GCGTTCCTGAATTTTCTTCTTTGTTGTA	GCGTTTTGGTTTTACTTGCTATTTATCCT	223
Sat_240	(AT)15	GCGGGCAGAAGTCTAATGAATGTGAAATGA	GCGGTTGTGACCGAAATAGATGTTATTTAAT	232
Sat_241	(AT)21	GCGTATTTTCTAATTCCACTATAACTTCAAT	GCGGGTATAAGTATCCATCAAATGTCAG	301
Sat_242*	(AT)18	GCGGATCCACCACTTGTTCTAAGAATCTC	GCGTAGGGTCGGGTTTTAGTATGTCATT	265
Sat_244	(AT)27	GCGTCAACCGGTGAAAAAACCTA	GCGTGGCTGGCAGTAGTCTATATCA	224
Sat_247	(AT)21	GCGGGGCAGGATATGATATTGTT	GCGTATTCGCCAAGCACTACTTTTT	260
Sat_250*	(AT)19	GCGGTTTTTGCTTTAGGACATTTTGATA	GCGTTGGGTACAACATATAATATTTTGGA	296
Sat_252	(AT)25	GCGTTTTTCTGTCATGTCTTTGAATTTT	GCGGCAGGTCTCATACAAGTCATCATCT	192
Sat_253	(AT)22	GCGATTGGTTGGGTGTTTAATTTTAAGAT	GCGTGTTGATGGTATAAAGATCGCTACTCT	275
Sat_260	(AT)25	GCGCCGTTAGTTGTCGAGGTGTCAACC	GCGTCGGTGATTAAAAATAAGTATCAAAG	300
Sat_279	(AT)28	GCGTTGCGTTGTTACGTGAAAGCACAGAAAC	GCGACTGGTTAATCTAGTCAGACTTAACAGA	276

Table 1. continued.

SSR locus	Repeat motif	Upper primer sequence (5′–>3′)	Lower primer sequence (5–>3′)	Allele size in Williams (soybean)
Sat_283	(AT)26	GCGTGGTGCACGATCATATAGAG	GCGTCTCCTTCGCTATCTCAAAC	195
Sat_285	(AT)34	GCGATCCCACAATATTTCTATTTCTTT	GCGGGCAAAATGCAGATGTATAAAC	289
Sat_286	(AT)32	GCGTTGCTTGCTAAGTAGTGTTTTTAATCCT	GCGTCTCCCATCATGCAACTTCAATA	161
Sat_290	(AT)34	GCGATGCCAAACTAGCTGAAGAGAAAT	GCGTAGCCTGCTTGGATGGTAGATTC	265
Sat_293	(AT)26	GCGTTAGGCAAATGAGATGTCAA	GCGCAGGGCAGTCATCGGAGGTAT	278
Sat_296*	(AT)32	GCGAGACCCATTTAATTCTCAATATCAGACA	GCGCCCGTGAATGAGTCAAACAAGTA	233
Sat_298	(AT)28	GCGCGTCGAAGCAAAAATTAAA	GCGGCGAAACCCACAAAGCATA	282
Sat_299*	(AT)23	GCGACAAGGCACTCACATCTCTTCTC	GCGCTACCCATAACAAAAAGTTCAAATC	292
Sat_351	(AT)21	GCGCCACCCAAGGGCATCTTTCG	GCGGGCCGCAACTATGAAAAGAC	277
Sat_355	(AT)27	GCGATAACACTAAATGACCAGCAGGATT	GCGGAGCCAAGTATCAAACCAAAACAAC	213
Sat_357*	(AT)17	GCGAGGGTTTAAGGTGTAGGTTGT	GCGCACCGCTTTTGTTTCTTTTTG	260
Sat_361	(AT)19	GCGTTAGATTTCCTTAGAATACATTGCTTCC	GCGTTGACACTCATGATGTTATCTTACACC	275
Sat_362	(AT)23	GCGCAAACAAGTTATACCTTTATATTGGTGA	GCGAAGGGAACCTAACGTATGTCTTTTA	196
Satt503	(ATT)18	GGGTGGCCATGGAATAAT	TTTCGGGTAGATGAGTGTAGG	256
Satt504	(ATT)21(ATTT)9	GCGCATGTGCAACTTGAAAAACA	TCGTTGGTTGACCCAATGTCATC	210
Satt507	(ATT)22	GCGCTCAGCCTTGTTAAATCACTT	GCGCTACTCTCGTGTCGTTAGTTA	217
Satt509	(ATT)30	GCGCTACCGTGTGGTGGTGTGCTACCT	GCGCAAGTGGCCAGCTCATCTATT	238
Satt520	(ATT)12	GCGGTGTGCAAGAGTGACA	GCGCATTTGGACTTTCTA	271
Satt522*	(ATT)16	GCGAAACTGCCTAGGTTAAAA	TTAGGCGAAATCAACAAT	262
Satt523	(ATT)15	GCGATTTCTTCCTTGAAGAATTTTCTG	GCGCTTTTTCGGCTGTTATTTTTAACT	168
Satt524	(ATT)14	GCGAATTATCCAAAGATACACTTAGTC	GCGGGTCTTACGAACGTGTCACATTAT	168
Satt530	(ATT)12	CATGCATATTGACTTCATTATT	CCAAGCGGGTGAAGAGGTTTTT	220
Satt531*	(ATT)14	GCATGCAACTGAGGGAGCAGAT	GCCACAAATTATGCAGAATATA	240
Satt535	(ATT)10	GCGCCCAACAACTTATAGTTATATA	GCGCTAGATTTTAGGCAGAGATTAA	253
Satt550*	(ATT)16	CGTCAATTAAGCAAAAATGTGA	GCGCGGATGAGCGTGCGTTTTTA	210
Satt552	(ATT)14	CGAACCGGCAAAACCAAGAT	GATCCGCATTGGTTTCTTACTT	154
Satt556	(ATT)14	GCGATAAAACCCGATAAATAA	GCGTTGTGCACCTTGTTTTCT	167
Satt570	(ATT)11	CTCATGTGGTCCTACCCAGACTCA	CGCTATCCCTTTGTATTTTCTTTTGC	105
Satt573	(ATT)10	GCGGATTTCGATTTGAATATACTTAC	CCTGTGGCTGTTATACTATGCATATA	167
Satt576*	(ATT)19	GCGGGACACACACAAACACCTACA	GCGGGTTTGCGTTCTTATATTATC	297
Satt593	(ATT)15(TTG)10(TTC)4	GCGGGGTTGTTGATCTATAATGTAA	GCGGGTTTGGATTTTATAATGTGAT	190
Satt596	(ATT)17	TCCCTTCGTCCACCAAAT	CCGTCGATTCCGTACAA	252
Satt597*	(ATT)13	GCTGCAGCGTGTCTGTAGTAT	CGAGGCACAACCATCACCAC	155
Satt622	(ATT)27	GCGGTGTAGGTAATAATTTTAATTCTCAT	GCGGTGTAGGTTTCACACTTCATTCAC	236
Satt623	(ATT)15	GCGGTGCAATGATTTTAATGATATGAT	GCGCGTGTAAAAGGTTATAACGTGTAA	238
Satt624	(ATT)23	GCGATGGCTTGTGGGAACACTAAT	GCGGACGTGGGACCAACACACTAA	151
Satt631*	(ATT)21	GGTAGATCCAGGAGCTTGAGTCAG	GCGCATCTCACTGCACTTGATTTT	175
Satt633	(ATT)12	GGGACACTATCGGCCTAGAAAGTT	GGGTGATAAAGTTCCCCCTCTAAG	131
Satt641	(ATT)10	GCGGAACATCACGGTTATA	GCGGGAGGCTCTGTCTCTTAGA	318
Satt650*	(ATT)10	CAGTTGGCTGGTCAAATC	TCTGGGTTACTTTTATTGTCA	247

Table 1. continued.

SSR locus	Repeat motif	Upper primer sequence (5′–>3′)	Lower primer sequence (5–>3′)	Allele size in Williams (soybean)
Satt652	(ATT)18	GCGAACATTCCAAAATTAATGATAAAAA	GCGGGGTAATATGCACTCTCCAGTAT	217
Satt658	(ATT)11	GCGTTGAGTGGTAAAATTTATAATTAAA	ACTTGGCCCGCGAAGTGCTCAATTG	227
Satt569	(ATT)14	GCGCAAATTGCTTCACGCATCCAAAT	GCGGCCTACTATAGTGAAGGGTATA	177
Satt678	(ATT)10	CTAAGCGTGACAAACAGACCATTA	CGGCCATATCTACCAATCAGA	158
Satt679*	(ATT)15	GCGAACAAAGGAAGAATAGAG	CAATTACCCCCAACAACTAAGT	262
Satt681	(ATT)20	GCGGTGCACTTGTCAATCTGTT	GCGGTGAGGCATATGTCAGTC	241
Satt688	(ATT)11	ATGCCTCCAAAGAGAAAT	CTGCCCATTGACCCATCT	175
Satt692*	(ATT)12	GCGAAGATTGGTCTTTTATGTCAAATG	GCGGAGGAATACAAGTCTCTATTCAA	231
Satt699*	(ATT)9	GCGGATATTTTTGTCCTCAATAAT	GCGTACCGTATGTGGAGTTT	181
Satt700	(ATT)12	GCGGGGGTTAAGAGGAGGAAAAATA	GCGCACTTTGCAAATGAGAGAT	147
Satt702	(ATT)26	GCGGGGTTCTGTGGCTTCAAC	GCGCATTGGAATAACGTCAAA	
Satt709*	(ATT)20	GCGTGACGAATTCTGTTCTAACTC	GCGCATACGCCACTCCACTCA	281
Satt712	(ATT)21	GCGAATATAGCCAAATTTAGGTTGAATGACA	GCGACCACCCATCACCTCCACCTCAAACAAC	
Satt716*	(ATT)10	GCGTTTGCAGTTTGGATGATGTTGAT	GCGAACCCTTGAGTTGGACATGTTGA	
Satt718	(ATC)15(ATT)15	GCGTGCAACACCTCAAGTTTCAAATAC	GCGTAGCTCTTTCCAAAGTTTTCATC	
Satt721	(ATT)13	GCGTGGTTGGAAGGAAGAGAATGAC	GCGAAAGGCTGGCTGACACTGACT	206
AW132402	(AT)17	GCGCCTCCCTCCTCTCCTTTCTT	GCGTTTCCCACATATTCTATCATTTGTT	153
AW781285	(CGA)8	GCGTCTTTTGCACGATGAA	GCGAATGGTGGGAGAAA	138
BE021153	(GT)10	GCGAAACTGCTTGTATTTTA	GCGCTCCAATTGAAAGTG	153
*BE475343**	(GT)11	GCGTCTCCCTGTCTCTC	GCGAGCTTAAAACAATCATC	181
AW186493	(CTT)13	GCGGTGATCCGTGAGATG	GCGGAAAGTAGCACCAAGAG	219
BE806387	(CTT)14	GCGACCCCTTTTGTCTTCTT	GCGGAGGCCAGAGATGAA	205
AF162283	(CT)11	GCGAGTTCTGGATGTAGG	GCGTGGCGGCTTTGGTAG	221
*BE823543**	(CT)10	GCGAAATGCCGAAAGAG	GCGGGGATAAGAAAAACAAT	156
AZ536570	(AT)12	GCGGCATGACAAGGAAATCT	GCGAATTAAAGGCAAAAGGAAAA	175
AW620774	(CTT)9	GCGATTTCCCCTCTTACTC	GCGAAAAACCAAGTTC	152
*AZ302047**	(AT)15	GCGTGGAGCGAAAATCAACTCTT	GCGATGACCCCGTAATGGTGA	234
AW756935	(ATT)18	GCGGCTGGTGATTGTGTAAT	GCGTAATATAGTTTTGTATTGAAAT	232

*The primers detected polymorphism among four peanut lines.

(1:1) and precipitated with two volume of ethanol, dissolved in 0.2 ml of TE, and diluted to 50 ng/µl for PCR amplification.

PCR Amplification. Soybean SSR primer pairs were provided by Drs. Cregan and Song at the USDA-ARS, Beltsville, MD. A total of 432 soybean SSR primer pairs including 200 $(AT)_n$ motifs (named as Sat #), 197 $(ATT)_n$ motifs (named as Satt #), and 35 EST-SSR (named as GenBank accession #) primer pairs were used. PCR amplification was carried out in 10 µl solution containing 0.25 units of *AmpliTaq* polymerase (Applied Biosystems, CA), 1.5 µM of each primer, 5 µl of FailSafe PCR 2X PreMix-B (Epicentre, WI), and 50 ng peanut genomic DNA. Amplification was carried out under the following conditions: 3 min at 94 C for initial denaturation; two cycles of 30 sec at 94 C, 30 sec at 65 C, and 1 min at 72 C; two cycles of 30 sec at 94 C, 30 sec at 56 C, and 1 min at 72 C; 30 cycles of 15 sec at 94 C, 30 sec at 55 C, and 1 min at 72 C; and 10 min at 72 C for final extension (Mellersh and Sampson, 1993). PCR products were analyzed on a 6% denaturing polyacrylamide gel and visualized by silver staining (He and Prakash, 1997).

Results and Discussion

Out of 432 soybean SSR primer pairs tested, 109 (25%) were amplifiable in peanut (Table 1). Among 109 soybean SSR markers, 28% detected polymorphism among 4 cultivated peanut lines (Fig. 1). The polymorphism detection rate in this study is higher than the previous report (He *et al*. 2003). This difference may be due to the fact that cultivar 'COAN' contains wild species segments of chromosomes, from which additional genetic variation could be detected. For 54 $(AT)_n$ markers, 30% detected genetic variation, while 28% of 43$(ATT)_n$ markers detected a polymorphism. The transferability of EST-SSR in peanut was higher (34%) than genomic SSR markers, but only 25% of EST-SSR markers could detect polymorphism (Table 2). The result of more transferable markers from the coding regions (EST-SSR) was consistent with the previous study (Liewlaksaneeyanawin *et al*., 2003) because coding regions are more conserved between related species.

These amplifiable markers implied that 25% of primer-binding sites were conserved between soybean and peanut. However, most banding patterns amplified by these transferable markers were similar to multiple-band patterns produced by random amplified polymorphic DNAs (RAPDs) rather than typical SSR banding patterns (Fig. 1). Choumane *et al*. (2004) reported that 54.4% of chickpea SSR primer-binding sites were conserved among the three genera, chickpea, dry pea, and lentil. They also found that SSR motifs were present in chickpea, but absent either in dry pea or lentil, after sequencing the amplicons produced by the same chickpea SSR primer. In this study, we speculate that amplicons from soybean SSR primers that produced complex patterns may not contain SSR motifs. This speculation needs to be confirmed by sequencing these amplicons. Nevertheless, these transferable SSR markers derived from soybean could be used to detect genetic variation in peanut.

Among legume crops, there is a high level of conservation between cowpea and mungbean,

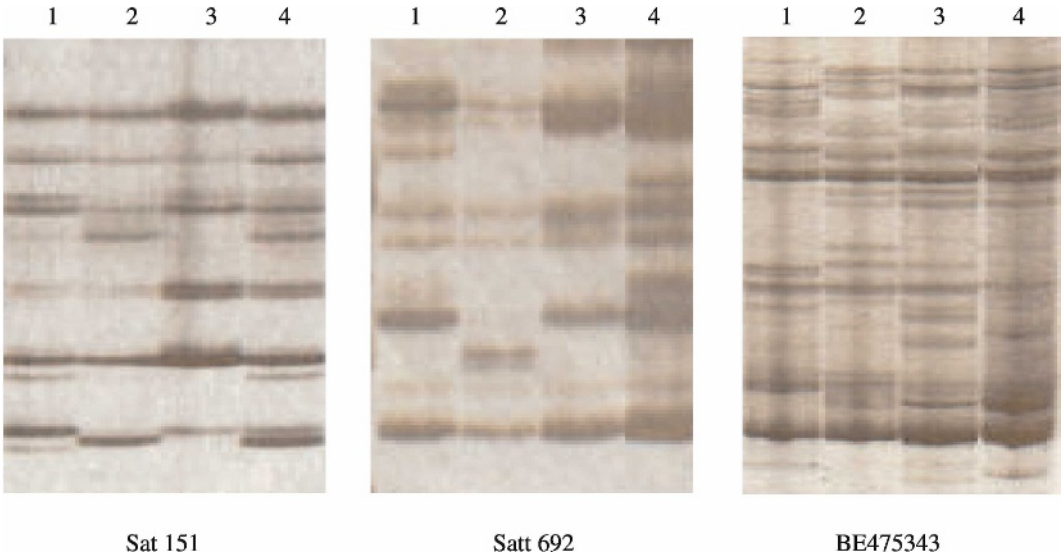

Fig. 1. Genetic variation among four peanut lines detected by soybean SSR markers Sat 151, Satt 692, and BE475343. Lane 1–4 are cultivars C11-2-39, GK7, 448A, and COAN, respectively.

Table 2. Transferability of soybean SSR markers in peanut.

Soybean marker	Total marker	Amplifiable marker	Polymorphic marker	Transferability %[a]	Poly/ampl %[b]
(AT)n	200	54	16	27	30
(ATT)n	197	43	12	22	28
EST-SSR	35	12	3	34	25
Total	432	109	31	25	28

[a]Transferability = Amplifiable markers/total markers.
[b]Poly/ampl = Polymorphic markers/amplifiable markers.

mungbean and common bean, and mungbean and lablab genomes (Menancio-Hautea *et al*., 1993; Boutin *et al*., 1995; Humphry *et al*. 2002). In contrast, the homology between soybean and common bean was retained only in dispersed blocks throughout their genomes (Boutin *et al*., 1995). Although the comparative mapping has been progressed in legume crops, the comparison of peanut genome with other legumes could not be carried out due to the lack of a set of common DNA markers. The level of transferability observed in this study would provide genome tools for comparative mapping between peanut and soybean because there are a large number of soybean SSR markers available. The comparative mapping between peanut and soybean will allow us to gain deeper insight into the degree of chromosome colinearity between them, and to elucidate the biological relationship among legume crops.

In our previous study, we have searched for SSR markers in 1350 peanut ESTs. Three hundred fifty-three ESTs were found to contain SSRs. Primers were designed for 44 EST-SSRs and 9 of them detected polymorphism, for a polymorphism rate of 20% in coding regions (Lou *et al*. 2005a). This study shows that 25% of transferable soybean EST-SSR markers detected a polymorphism in peanut genome. The results from both studies may suggest that there might be an abundance of mutations in coding regions in peanut. Using EST-SSR markers in comparative mapping between peanut and soybean will allow us to predict the location of genes of interest from soybean which has a well developed genetic map compared to peanut for which such information is scarce.

Peanut and most legume crops belong to the same subfamily Papilionoideae of the Leguminosae family. However, peanut is isolated in a different clade (dalbergioid) from most legume crops in the legume phylogenetic tree (Doyle and Luckow, 2003). There is a relatively under-developed infrastructure of genomic tools in peanut. Therefore, in peanut, there is a great need to integrate the knowledge gained from the study of model legume genomes with the important biological and agronomic questions of peanut. Identification of transferable DNA markers from model legumes in peanut would be useful for peanut improvement through comparative genome research because the information of these transferable markers from other legumes is known. The common transferable DNA markers among legumes would also provide us tools to compare legume genomes, gain insight into relationship of legumes, and elucidate legume evolution.

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