

Supplementary data

Identification, characterization and validation of ssr markers from the gerbera est database

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Supplementary data 1. List of 50 EST-SSR markers for Gerbera: locus name, primers sequence, repeat motif, optimal annealing temperature for PCR and their length expected (bp), Blast E-value, identity (%), putative function and species.

Locus name	Primer sequence 5'-3'	Repeat Motif	Annealing temperature	Length expected (pb)	Blast E-Value	Identity (%)	Putative function	Species
GERB1	TTTCAAGACCGGGATCGAGT CACAATCTCCCATAGAGACACACA	(TGTA)5	56.6	200	4.00E-60	69	hypothetical protein	<i>Ricinus communis</i>
GERB2	TGGTGGTTTCCAGAGTGTCG ACCAGGTCATTCATCACCGA	(TTTG)5	56.4	248	6.00E-68	85	nucleolysin tia-1, putative	<i>Ricinus communis</i>
GERB3	GGTAACACCAGGTTGGGCAT TATGCCCGGCAGGAATAAAC	(ATTT)5	56.4	192	7.00E-10	80	global transcription factor group	<i>Populus trichocarpa</i>
GERB4	AAACCCTGAAGTCAAGCGGA CAACAAGCGATATAAAGCAACACA	(GT)11	54.9	238	2.00E-14	88	hypothetical protein	<i>Vitis vinifera</i>

GERB5	TGGACCTTCCACTTCCATTTTC GGGTATTGACGCACGGTCTT	(CT)12	56.5	239	2.00E-70	78	inorganic pyrophosphatase	<i>Populus trichocarpa</i>
GERB6	CTCGCTCGGTAGCAATTGTG CAAAGTCGTCGTTGAGCTGG	(GA)34	57.4	277	3,2	30	hypothetical membrane protein	<i>Gardnerella vaginalis 5-1</i>
GERB7	TCCAAATAGAGAGCGAGAGCG CGGAAAAAGGCGCGAGAG	(CT)42/(AG)59	57.4	274	6.7	35	meiotically up-regulated 152 protein	<i>Coprinopsis cinerea</i>
GERB8	GCCCAGTCCAAGTAAAACGC AAACACACTATAGAGAGAGAGGGGG	(GA)69	58.5	281	4.00E-77	90	methionine synthase	<i>Coffea arabica</i>
GERB9	CCTAAAAGGTGCATTAATTGTTCTC CGGCGTAAATTCCAACCCTA	(AAT)11	55.8	250	2.00E-36	88	mitochondrial pyruvate dehydrogenase	<i>Glycine max</i>
GERB10	AGAAGGTCCGTCCTGGATGA TTGGTAAAAGCCGTCTCCGT	(AAT)9	56.4	300	2.00E-30	50	hypothetical protein	<i>Populus trichocarpa</i>
GERB11	GCAAGTTTCAAATATGGGGG TTCTCGCTCTCTATCCACCC	(CT)24/(TA)23/(GT)20	55.4	300	2.00E-54	75	cobalamine-independent methionine synthase	<i>Solenostemon scutellarioides</i>
GERB12	CAGTGTTCAGGGCAGAGTT GGGGGCATACGATGCATAAA	(CT)12	56.4	260	0.033	90	hypothetical protein LOC100248036	<i>Vitis vinifera</i>
GERB13	GGGTGAAAAAGGAAAGGGA TCTACCCCGTCTCGTGTTT	(TC)36	56.4	238	200E-12	49	At1g77122	<i>Arabidopsis thaliana</i>

GERB14	CCTACACAGAAGCGAAGGGG ACACGAAACACGAAGCCTCA	(GAA)7	57.4	261	3.00E-10	82	hypothetical protein	<i>Populus trichocarpa</i>
GERB15	CCCAGAAACCCATCTTGGA CCTATGGATGCATTATCCCTTT	(AT)31	54.6	231	7.00E-38	72	hypothetical protein	<i>Vitis vinifera</i>
GERB16	CTCGCGCTCGTGATAGACAG CAAACAAAACATCAGTTTGCG	(TG)11	55.6	172	-	-	-	No hit
GERB17	TCGCTCTTGCAAACCAGAAA TGCCTGAAAAGTTCACCCAA	(CT)16	53.4	269	1.00E-09	94	similar to acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative	<i>Vitis vinifera</i>
GERB18	GTGGTGGTTTCCGTGGAGG CACTAGCACCACCATAGCCG	(GGC)4-(GGC)4	59.5	219	-	-	-	No hit
GERB19	TTAATTGGCCTTTGATCCGC TGCAACTACCTAAAAGTCGAATGC	(TTA)15	54.8	298	2.00E-58	82	unnamed protein product	<i>Vitis vinifera</i>
GERB20	ATCAATTGGCGAAGGTCACA CCGGCACTCTGGAGTCCTAT	(AG)26	56.4	246	5.00E-22	86	hypothetical protein ARALYDRAFT_485347	<i>Arabidopsis lyrata subsp.</i>
GERB21	GTCCGACGACAACATTGGAA CCTGTTAATTGCTACAAAACGGG	(AGC)7	55.7	260	0.28	41	Hypothetical protein HPV225_1465	<i>Helicobacter pylori</i>
GERB22	AAACACCACCAAATCAAATGC TGCCATGGATGTGTTTCCTTC	(AAT)8	53.5	370	1.00E-20	70	GAST1 protein precursor, putative	<i>Ricinus communis</i>

GERB23	TCGTGCCAGCATTTGAACTT CGGTAAACCCAAACCCAGAA	(GGT)7	54.4	130	2.00E-51	76	hypothetical protein	<i>Vitis vinifera</i>
GERB24	CAAACACCCCCTACCCTTGA GAGGGAGAGGGCAAGGAGTT	(TCT)8	58.4	200	-	-	-	No hit
GERB25	TCCATCATCACTTCCCCTCC TTTCCCGGAATTGAATTTGC	(TTC)7	53.3	142	6.00E-31	54	hypothetical protein	<i>Vitis vinifera</i>
GERB26	TTTCCACCAAGCTTCCTCGT GCGATGAGTCAAGCATCAACA	(CT)10	55.5	132	9.2	30	hypothetical protein, conserved	<i>Trypanosoma brucei gambiense DAL972</i>
GERB27	GTGAGATCGTCCTCGAGAGATAG TTTTTGGGGATCCAACCAAC	(AG)17	56.5	700	-	-	-	No hit
GERB28	TCTCTCTCTCTCGCTCGC TTCTCTCTCACACTCACACACA	(CG)12	58.7	285	-	-	-	No hit
GERB29	ATGTTGGCGAATCCGAGAAT CGGATCCATAGATAAAAACGCA	(AT)14	53.6	262	2.00E-15	40	hypothetical protein	<i>Vitis vinifera</i>
GERB30	TTGAGGAAGAAAGCGAGCCT ATTTCTTTTGTTCATCCATTTCATT	(TAA)7	52.5	320	3.00E-10	55	hypothetical protein	<i>Vitis vinifera</i>
GERB31	GGATTGGCTGCCTTTAGCTG CAAGCAACAACGTCGGAAAA	(ATT)5	55.4	114	2.4	28	hypothetical protein BRAFLDRAFT_102235	<i>Branchiostoma floridae</i>

GERB32	TTTTCGACAATGATGGTGCC CAAAAGCCTCCAAAAATGCAA	(AAT)11	52.5	145	2.00E-47	70	hypothetical protein ARALYDRAFT_895389	<i>Arabidopsis lyrata subsp.</i>
GERB33	GCGATGGCAGCAATACCTTT TTTGGCTTCATCCCCTTTTG	(CTT)7	54.4	297	1.00E-41	90	unknow	<i>Glycine max</i>
GERB34	TTCTTTCCATCGGCCTTGTT TTCCCGATTAAACCGTCGTT	(CAA)7	53.4	140	3.00E-76	64	hypothetical protein LOC100263945	<i>Vitis vinifera</i>
GERB35	GCAGGCGCTAAGTCCATTTT CGCAAAATCAGACTCACCCA	(AT)10	56.4	148	-	-	-	No Hit
GERB36	GCTCGTGACCCAAGGAGAGT TCAACTTCAAAGTTCAAACATCCA	(TG)11	56.1	156	8.00E-23	58	predicted protein	<i>Populus trichocarpa</i>
GERB37	TTGGCGTGGAGGGTTTTATC TATCTGTCCGTGCAACGCTT	(TTAT)5	55.4	199	4.00E-43	78	predicted protein	<i>Populus trichocarpa</i>
GERB38	TGAAGGGAAATGGAATGGCT TCAACCTGTGCCTGCATCTT	(GAA)9	54.4	196	1.00E-19	54	hypothetical protein LOC100266636	<i>Vitis vinifera</i>
GERB39	TTTGTCCCCATAAAGCTGGG TGCCCAGATTGCAATGAAAA	(CAA)5	53.3	239	0.095	38	conserved hypothetical protein	<i>Brevibacillus brevis NBRC 100599</i>
GERB40	GACATCAAACCGTCGTCCAA	(AAT)8	55.5	206	8.00E-22	69	predicted protein	<i>Populus trichocarpa</i>

	CCACAATAGCCCATCAAGACA								
GERB41	CGCCTCAAAAACCATATCCTG TTCCTCTTAGCTGCGGGAAG	(CT)8	56.5	103	2.00E-36	69	hypothetical protein LOC100266598	<i>Vitis vinifera</i>	
GERB42	TTCAAAATTCGGTGAGAGGGA TCGCTTTCTTGTGGCTTCA	(GA)9	53.5	310	1.00E-38	98	hypothetical protein	<i>Hypochoeris radicata</i>	
GERB43	GGTATCCGAAGAGGCTGCTG AAGGCTTGATTGTTGTTGTTGAA	(TG)8	55.9	230	1.00E-45	67	hypothetical protein	<i>Vitis vinifera</i>	
GERB44	CAATAAAACGGTGACCAAACG TCCCCAAGTGTCTTCCCAG	(AG)9	55.6	213	8.00E-130	86	predicted protein	<i>Populus trichocarpa</i>	
GERB45	GGAATTTGCGTGGATTAACGA CTTGGATTCAGCTCGGGTC	(AT)9	55.5	236	-	-	-	No hit	
GERB46	CTTTCAATCCGAAAGCGAGG GAGTCTGACACATGCGCGTT	(AG)8	56.4	204	-	-	-	No hit	
GERB47	CTGTCGACAAAACACGCACA TGAGGGAGAGTGCTGCGATA	(CT)9	54.4	127	-	-	-	No hit	
GERB48	GATTTGGGTTGGCCTTTTGA GTAGCTACCGTCACCGGACC	(TC)8	57.5	182	3.00E-20	88	sterol C-24 reductase	<i>Zinnia elegans</i>	
GERB49	GTGGAAACTCTGTCCTGGGG	(CT)8	59.5	248	1.00E-18	46	hypothetical protein LOC100266616	<i>Vitis vinifera</i>	

CCCCCTCTCTGATACCCACA

GERB50 CAAGGTTGTGTTAGCCAGGGA

(AG)8

58.5

267

2.00E-12

46

hypothetical protein

Vitis vinifera

GTGGTGGAGGTGGAGGAAAG
