

The development of a 20-locus fluorescent multiplex system as valuable tools for national DNA database

Supplementary data

Table S1-S9

Table S1

The uniform upstream primer and a series of downstream primers sequences used for internal size standard.

Primer	Sequence (5'-3')
F	GGCGAAACCCGACAGGACTA
75R	TCGGAACAGGAGAGCGCA
80R	CAGGGTCGGAACAGGAGAG
100R	GACAGGTATCCGGTAAGCGG
140R	GCTATGAGAAAGCGCCACG
160R	CTGAGATACCTACAGCGTGAGC
175R	ACGACCTACACCGAACTGAGA
180R	AGCGAACGACCTACACCGA
200R	GTGCACACAGCCCAGCTTG
225R	AGCGGTCGGGCTGAACGGGGGGTT
250R	AGACGATAGTTACCGGAT
275R	GTCGTGTCTTACCGGGT
300R	CGAGAACTGCTGCCAGTGGCG
330R	CTACATACCTCGCTCTGCTAATCC
360R	GCCACCACTTCAAGAACTCTGT
390R	ATACTGTTCTTCTAGTGTAGCCGTAG
445R	GAGCTACCAACTCTTTTCC
500R	CTGCTTGCAAACAAAAAACC

F: Forward primer; R: Reverse primer; the number before R: the amplicon size.

Supplementary data
Table S2

The PCR components and thermal cycling parameters of internal size standard

PCR components	Volume (μl)
ddH ₂ O	6
10×PCR mix	1
dNTP	0.8
Upstream primer	0.25
Downstream primers	1
pUC18	1
Tag polymerase	0.2
Total	10
Thermal cycling parameters:	
<ul style="list-style-type: none"> • denaturation for 2 min at 94°C • amplification for 30 cycles of 20 s at 94°C, 40 s at 58°C, 40 s at 72°C • extension for 10 min at 70°C 	

Supplementary data

Table S3

The plasmid genomic DNA sequence

Positions of various elements					
Vector size (bp)			2686		
Multiple cloning site			399-455		
LacZ α -peptide			146-469		
Ampicillin resistance gene			1626-2486		
pUC origin			867-1455		
1	TCGCGCGTTT	CGGTGATGAC	GGTGAAAACC	TCTGACACAT	GCAGCTCCCG
51	GAGACGGTCA	CAGCTTGTCT	GTAAGCGGAT	GCCGGGAGCA	GACAAGCCCCG
101	TCAGGGCGCG	TCAGCGGGTG	TTGGCGGGTG	TCGGGGCTGG	CTTAACATATG
151	CGGCATCAGA	GCAGATTGTA	CTGAGAGTGC	ACCATATGCG	GTGTGAAATA
201	CCGCACAGAT	GCGTAAGGAG	AAAATACCGC	ATCAGGCGCC	ATTCGCCATT
251	CAGGCTGCGC	AACTGTTGGG	AAGGGCGATC	GGTGCGGGCC	TCTTCGCTAT
301	TACGCCAGCT	GGCGAAAGGG	GGATGTGCTG	CAAGGCGATT	AAGTTGGGTA
351	ACGCCAGGGT	TTTCCCAGTC	ACGACGTTGT	AAAACGACGG	CCAGTGCCAA
401	GCTTGCATGC	CTGCAGGTCG	ACTCTAGAGG	ATCCCCGGGT	ACCGAGCTCG
451	AATTCGTAAT	CATGGTCATA	GCTGTTTCCT	GTGTGAAATT	GTATATCCGT
501	CACAATTCCA	CACAACATAC	GAGCCGGAAG	CATAAAGTGT	AAAGCCTGGG
551	GTGCCTAATG	AGTGAGCTAA	CTCACATTAA	TTGCGTTGCG	CTCACTGCCC
601	GCTTCCAGT	CGGGAACCT	GTCGTGCCAG	CTGCATTAAT	GAATCGGCCA
651	ACGCGCGGGG	AGAGGCGGTT	TGCGTATTGG	GCGCTCTTCC	GCTTCCTCGC
701	TCACTGACTC	GCTGCGCTCG	GTCGTTCCGC	TGCGGCGAGC	GGTATCAGCT
751	CACCTCAAAG	CGGTAATACG	GTTATCCACA	GAATCAGGGG	ATAACGCAGG
801	AAAGAACATG	TGAGCAAAAAG	GCCAGCAAAA	GGCCAGGAAC	CGTAAAAAGG
851	CCGCGTTGCT	GGCGTTTTTC	CATAGGCTCC	GCCCCCTGA	CGAGCATCAC
901	AAAAATCGAC	GCTCAAGTCA	GAGGTGGCGA	AACCCGACAG	GACTATAAAG
951	ATACCAGGCG	TTTCCCCCTG	GAAGCTCCCT	CGTGCGCTCT	CCTGTTCCGA
1001	CCCTGCCGCT	TACCGGATAC	CTGTCCGCCT	TTCTCCCTTC	GGGAAGCGTG
1051	GCGCTTTCTC	ATAGCTCACG	CTGTAGGTAT	CTCAGTTCGG	TGTAGGTCGT
1101	TCGCTCCAAG	CTGGGCTGTG	TGCACGAACC	CCCCGTTTCC	CCCGACCGCT
1151	GCGCCTTATC	CGGTAAGTAT	CGTCTTGAGT	CCAACCCGGT	AAGACACGAC
1201	TTATCGCCAC	TGGCAGCAGC	CACTGGTAAC	AGGATTAGCA	GAGCGAGGTA
1251	TGTAGGCGGT	GCTACAGAGT	TCTTGAAGTG	GTGGCCTAAC	TACGGCTACA
1301	CTAGAAGAAC	AGTATTGGT	ATCTGCGCTC	TGCTGAAGCC	AGTTACCTTC
1351	GGAAAAAGAG	TTGGTAGCTC	TTGATCCGGC	AAACAAAACA	CCGCTGGTAG
1401	CGGTGGTTTT	TTTGTGTGCA	AGCAGCAGAT	TACGCGCAGA	AAAAAAGGAT
1451	CTCAAGAAGA	TCCTTTGATC	TTTTCTACGG	GGTCTGACGC	TCAGTGGAAC
1501	GAAAACTCAC	GTAAAGGGAT	TTTGGTCATG	AGATTATCAA	AAAGGATCTT
1551	CACCTAAGATC	CTTTTAAATT	AAAAATGAAG	TTTTAAATCA	ATCTAAAGTA
1601	TATATGAGTA	AACTTGGTCT	GACAGTTACC	AATGCTTAAT	CAGTGAGGCA
1651	CCTATCTCAG	CGATCTGTCT	ATTTTCGTTCA	TCCATAGTTG	CCTGACTCCC
1701	CGTCGTGTAG	ATAACTACGA	TACGGGAGGG	CTTACCATCT	GGCCCCAGTG
1751	CTGCAATGAT	ACCGCGAGAC	CCACGCTCAC	CGGCTCCAGA	TTTATCAGCA
1801	ATAAACCAGC	CAGCCGGAAG	GGCCGAGCGC	AGAAGTGGTC	CTGCAACTTT
1851	ATCCGCCTCC	ATCCAGTCTA	TTAATTGTTG	CCGGGAAGCT	AGAGTAAGTA
1901	GTTTCGCCAGT	TAATAGTTTG	CGCAACGTTG	TTGCCATTGC	TACAGGCATC
1951	GTGGTGTCAC	GCTCGTCGTT	TGGTATGGCT	TCATTCAGCT	CCGGTTCCCA
2001	ACGATCAAGG	CGAGTTACAT	GATCCCCCAT	GTTGTGCAAA	AAAGCGGTTA
2051	GCTCCTTCGG	TCCTCCGATC	GTTGTCAGAA	GTAAGTTGGC	CGCAGTGTTA
2101	TCATCTATGG	TTATGGCAGC	ACTGCATAAT	TCTCTTACTG	TCATGCCATC
2151	CGTAAGATGC	TTTTCTGTGA	CTGGTGAGTA	CTCAACCAAG	TCATTCTGAG
2201	AATAGTGTAT	GCGGCGACCG	AGTTGCTCTT	GCCCGGCGTC	AATACGGGAT
2251	AATACGCGCG	CACATAGCAG	AACTTTAAAA	GTGCTCATCA	TTGGAAAACG
2301	TTCTTCGGGG	CGAAAACCTCT	CAAGGATCTT	ACCGCTGTTG	AGATCCAGTT
2351	CGATGTAACC	CACTCGTGCA	CCCAACTGAT	CTTCAGCATC	TTTTACTTTT
2401	ACCAGCGTTT	CTGGGTGAGC	AAAAACAGGA	AGGCAAAATG	CCGCAAAAAA
2451	GGAATAAAGG	GCGACACGGA	AATGTTGAAT	ACTCATACTC	TTCTTTTTTC
2501	AATATTATTG	AAGCATTAT	CAGGGTTATT	GTCTCATGAG	CGGATACATA
2551	TTTGAAATGTA	TTTAGAAAAA	TAAACAAATA	GGGGTTCCGC	GCACATTTCC
2601	CCGAAAAGTG	CCACCTGACG	TCTAAGAAAC	CATTATTATC	ATGACATTAA
2651	CCTATAAAAA	TAGGCGTATC	ACGAGGCCCT	TTCTGTC	

Table S4

Allele frequencies and genetic parameters for 19 STR loci in Northern Chinese Han population (n=3000).

Allele	TPOX	D16S539	TH01	CFS1PO	D13S317	D3S1358	D21S11	D18S51	D6S1043	Penta E	FGA	D2S1338	D5S818	D8S1179	Penta D	D7S820	vWA	D12S391	D19S433
4			0.0002																
5			0.0003							0.0465					0.0002				
6	0.0002		0.0979							0.0002			0.0005		0.0040				
7	0.0007		0.2644	0.0005	0.0015			0.0003		0.0027			0.0153		0.0053	0.0017			
8	0.5072	0.0085	0.0562	0.0022	0.2699			0.0002	0.0002	0.0060			0.0038	0.0008	0.0457	0.1366			
9	0.1238	0.2813	0.5220	0.0524	0.1440			0.0002	0.0015	0.0082			0.0687	0.0007	0.3121	0.0626			
10	0.0265	0.1231	0.0172	0.2361	0.1440			0.0005	0.0327	0.0417			0.1970	0.0944	0.1178	0.1668	0.0002		0.0007
11	0.3103	0.2456	0.0003	0.2404	0.2289			0.0037	0.0976	0.1225			0.3407	0.0744	0.1660	0.3365			0.0027
12	0.0302	0.2135		0.3844	0.1640	0.0007		0.0324	0.1336	0.1103			0.2171	0.1378	0.1834	0.2514			0.0409
13	0.0012	0.1121		0.0722	0.0375	0.0003		0.2067	0.1396	0.0501	0.0002	0.0002	0.1461	0.2284	0.1256	0.0392	0.0025		0.2956
14		0.0145		0.0103	0.0097	0.0432		0.2112	0.1366	0.0891			0.0088	0.1937	0.0307	0.0027	0.2549	0.0007	0.2484
15		0.0013		0.0015	0.0005	0.3629		0.1775	0.0158	0.1044	0.0002		0.0017	0.1760	0.0083	0.0002	0.0309	0.0145	0.0659
16						0.3247		0.1260	0.0037	0.0871	0.0002	0.0032	0.0002	0.0756	0.0007		0.1747	0.0055	0.0127
17						0.1902		0.0742	0.0397	0.0839	0.0018	0.0427		0.0148			0.2477	0.0894	0.0007
18						0.0722		0.0387	0.1752	0.0756	0.0227	0.0812		0.0030			0.1867	0.2319	0.0003
19						0.0052		0.0415	0.1545	0.0612	0.0475	0.1104		0.0003			0.0804	0.2241	
20						0.0005		0.0320	0.0559	0.0484	0.0487	0.0782					0.0202	0.1732	
21								0.0204	0.0073	0.0277	0.0971	0.0167					0.0013	0.1069	
22								0.0200	0.0005	0.0157	0.1647	0.0350						0.0836	
23								0.0087	0.0007	0.0100	0.2376	0.1560					0.0002	0.0429	
24								0.0038		0.0047	0.1872	0.1084						0.0179	
25								0.0013		0.0018	0.1049	0.0444						0.0070	
26							0.0002	0.0003		0.0015	0.0494	0.0062						0.0013	
27							0.0032			0.0003	0.0070	0.0028						0.0005	
28							0.0472				0.0013	0.0153							
29							0.2553				0.0005	0.0858							
30							0.3010				0.0002	0.0886							
31							0.0976					0.0302							
32							0.0279					0.0098							
33							0.0042					0.0008							
34							0.0007					0.0002							
9.1																0.0018			
9.2																			0.0003
9.3			0.0414																
10.1																0.0002			
10.3																0.0002			
11.2															0.0002				0.0005
12.1																0.0002			
12.2																			0.0038
13.2																			0.0397
14.1										0.0002									
14.2																			0.1089
15.2						0.0002											0.0002		0.1408
16.2								0.0002			0.0002								0.0337

17.2								0.0002											0.0035
17.3									0.0002										
18.2									0.0005				0.0002						0.0008
18.3													0.0002						
19.1													0.0002						
19.2																0.0002			
19.3																	0.0007		
20.2																			
20.3																			
21.2									0.0002										
21.3																			
22.2									0.0035										
22.3																			
23.2									0.0003										
23.3																			
24.2									0.0002										
25.2																			
26.2																			
27.2																			
28.2								0.0072											
29.2								0.0017											
30.2								0.0125											
30.3								0.0055											
31.2								0.0774											
32.2								0.1180											
33.1								0.0002											
33.2								0.0355											
34.1								0.0002											
34.2								0.0042											
35.2								0.0007											
He	0.6276	0.7931	0.6403	0.7277	0.7935	0.7117	0.8205	0.8542	0.8719	0.9193	0.8612	0.8559	0.7798	0.8385	0.8018	0.7818	0.8068	0.8509	0.8038
DP	0.8012	0.9214	0.8219	0.8829	0.9330	0.8732	0.9407	0.9618	0.9705	0.9875	0.9619	0.9774	0.9125	0.9541	0.9384	0.9132	0.9298	0.9530	0.9412
PIC	0.5680	0.7539	0.5945	0.6864	0.7764	0.6708	0.7871	0.8372	0.8605	0.9142	0.8369	0.9089	0.7371	0.8199	0.7838	0.7374	0.7708	0.8172	0.7863
PE	0.3254	0.5863	0.3421	0.4724	0.5870	0.4466	0.6376	0.7031	0.7384	0.8349	0.7170	0.7064	0.5621	0.6723	0.6024	0.5657	0.6117	0.6965	0.6061

He: Heterozygosity; DP: Discrimination power; PIC: Polymorphism information content; PE: Probability of exclusion

Supplementary data

Table S5

The genotypes of sample A and sample B were used in mixture studies

Locus	Sample A	Sample B
D19S433	13/14	14/14.2
<u>D5S818</u>	12/12	10/13
<u>D21S11</u>	29/31.2	28/31
<u>D18S51</u>	16/18	17/17
<u>D6S1043</u>	12/20	21/21
<u>D3S1358</u>	17/18	15/16
<u>D13S317</u>	9/11	13/13
<u>D7S820</u>	8/11	10/10
<u>D16S539</u>	9/13	8/11
CSF1PO	12/12	10/12
<u>Penta D</u>	12/13	3.2/9
Amel	X/Y	X/Y
vWA	16/19	16/19
D8S1179	14/15	14/15
<u>TPOX</u>	11/11	8/13
<u>Penta E</u>	7/14	5/13
TH01	6/9.3	6/7
D12S391	18/23	18/19
D2S1138	22/25	22/22
<u>FGA</u>	20/23	19/27

Underline of locus indicates that alleles between sample A and sample B are totally different.