Table 1. Oligonucleotide Primers for Amplification of the CCK-AR Gene

Name	Sequence	Position	Region	Annealing Temperature
CCKAR-PF	5-CGCTGAGAATGGTTAACGGGT	153 - 173	Promoter	56℃
CCKAR-PR	5-CATTCCTAAAGGCGACTTCAG	319 - 339		
CCKAR-E1F	5-ATTCACCAGCTCTCCAGCAC	444 - 463	Exon 1	55℃
CCKAR-E1R	5-CTCCCACAACTCAATAGTTTC	629 - 650		
CCKAR-E2F	5-TTAGCATTCTGCTGTCATCAC	1213 - 1233	Exon 2	56℃
CCKAR-E2R1	5-TGAAATCCTTGAGCAGATTGG	1460 - 1470	(upstream)	
CCKAR-E2F2	5-ATGCTCTGTCTCTTCTGCATG	1423 - 1443	Exon 2	56℃
CCKAR-E2R	5-CAAGCTCCAGAAAGAGTCAC	1537 - 1556	(downstream)	
CCKAR-E3F	5-CTTTGTTCCTTTCCCAGGCAC	2081 - 2101	Exon 3	60℃
CCKAR-E3R	5-ATGCAACCTTACCAGGACTGC	2351 - 2371		
CCKAR-E4F	5-GTTGCTGGTTATTGGATTTCT	2946 - 2966	Exon 4	56℃
CCKAR-E4R	5-CTTTTGTGCTCATTTGGCATA	3133 - 3153		
CCKAR-E5AF	5-CCAGAAAGGAAACCTAGCACC	3712 - 3732	Exon 5	60℃
CCKAR-E5AR	5-GGATGAAGGAAATGGGGGTTC	4007 - 4027	(upstream)	
CCKAR-E5BF	5-GTGCTGGATGCCCATCTTCAG	3933 - 3953	Exon 5	60℃
CCKAR-E5BR	5-TGGCACCGAGGCACTCATATG	4219 - 4239	(downstream)	

Table 2 . Oligonucleotide Primers for Amplification of the CCK-BR Gene

Name	Sequence	Position	Region	Annealing Temperature
CCKBR-PF	5-GCAGGAGAGAAATCTCTAAGAG	-333 - -311	Promoter	60℃
CCKBR-PR	5-ACCTGCTCACGCTGCGATTC	-80 - -60		
CCKBR-E1F	5-CCGGGTCGAGCTGAGTAAG	-41 - -22	Exon 1	60℃
CCKBR-E1R	5-GTACAGTGAGAAATAGCTTGTG	176 -198		
CCKBR-E2F	5-GATTTGACTGAATGAAGGCTG	1273 - 1294	Exon 2	56℃
CCKBR-E2R	5-ACATCCACAAGAGCTTTAGGC	1622 - 1643		
CCKBR-E3F	5-TGATGCTTGTGTAGTGCAAG	1687 - 1707	Exon 3	56℃
CCKBR-E3R	5-GGAATTCCTAGGATAGTTTATG	2007 - 2028		
CCKBR-E4F	5-TCTGTGATTACAGCTGGACAG	2249 - 2270	Exon 4	56℃
CCKBR-E4R	5-CATTTCCAGCTTCCTTCTCAC	2555 - 2576		
CCKBR-E5F1	5-GACTCGCCTTTTTCTCTGACC	2627 - 2648	Exon 5	58℃
CCKBR-E5R1	5-GAGAGTGCTCGGTGTGCACC	2939 - 2959	(upstream)	
CCKBR-E5F2	5-CAGTTTATAGTGCCAACACGTG	2898 - 2920	Exon 5	58℃
CCKBR-E5R2	5-GTCAGTGCATGTCATTTGCCC	3228 - 3249	(downstream)	

Table 3 . Oligonucleotide Primers for Amplification of the CCK Gene

Name	Sequence	Position	Region	Annealing Temperature
CCK-PAF	5-GAGAGTACTGCTCTGGAATGC	-294 - -274	Promoter (upstream)	64℃
CCK-PAR	5-GCCAGTCATGTATTTACCCAAC	-77 - -55		
CCK-PBF	5-GATTAACTCCACCCCACTAGAC	-192 - -171	Promoter (downstream)	64℃
CCK-PBR	5-TTGGCGTTTCCAACCGGAGCA	17-38		
CCK-E1F	5-AGCCACTTCAACCTGGTTGTC	-141- -128	Exon 1	60℃
CCK-E1R	5-CCTTTCAAAGACACACGACAC	91 - 112		
CCK-E2F	5-CTCTGTTGCCCAGCCTTTCAG	1224 - 1245	Exon 2	64℃
CCK-E2R	5-CTGGGAACAAGGGCAGAAGTG	1517 - 1538		
CCK-E3F	5-GATGCTTTTAGATGCAATGTC	6626 - 6648	Exon 3	54℃
CCK-E3R	5-ACAGACAATGAGTTATGAGTG	6882 - 6904		

Table 4. Polymorphisms of the CCK-AR Gene in Schizophrenic Patients and Controls

	Controls	Schizophrenics	Fisher's exact probability test for alleles
Promoter region			
201 A / A	43(53%)	60(73%)	P=0.0181* OR=1.972 (1.12-3.46)
201 A / G	34(43%)	22(26%)	
201 G / G	3(4%)	1(1%)	
246 G / G	79(98.7%)	81(97.4%)	P=0.4970 OR=1.519
246 G / A	0(0%)	1(1.3%)	
246 A / A	1(1.3%)	1(1.3%)	
Intron 1			
608 G / G	68(85%)	74(89.9%)	P=0.6622 OR=1.2649 (0.53-3.02)
608 G / A	12(15%)	8(8.8%)	
608 A / A	0(0%)	1(1.3%)	
1260 T / T	8(10%)	17(21.3%)	P=0.0907 OR=1.4893 (0.95-2.32)
1260 T / A	41(51.3%)	41(51.3%)	
1260 A / A	31(39.3%)	25(27.4%)	
1266 T / T	23(28.8%)	32(40%)	P=0.8210 OR=1.0625 (0.68-1.66)
1266 T / C	50(62.4%)	38(43.7%)	
1266 C / C	7(8.8%)	13(16.3%)	
Exon 5			
3849 C / C (296Ile/Ile)	69(87.2%)	77(92.5%)	P=0.2184 OR=1.9687 (0.71-5.45)
3849 C / T (296Ile/Ile)	11(13.8%)	6(7.5%)	
3876 G / G (306Leu/Leu)	79(98.7%)	82(98.7%)	P=0.75 OR=1.000
3876 G / A (306Leu/Leu)	1(1.3%)	1(1.3%)	

*P value after Bonferroni correction: 0.0905. OR, odds ratio; 95% confidence intervals are given in round brackets.

Table 5. Distributions of Genetic Variants of the CCK-BR Gene in Schizophrenic Patients and Controls

	Controls	Schizophrenics	*P* value	Odd's ratio [95% confidence intervals]
Promoter region				
-215 C / C	168(98.8%)	75(93.75%)		
-215 C / A	2(1.2%)	5(6.25%)	0.0359*	5.600 [1.062-29.531]
Exon 1				
109 C / C (37Leu/Leu)	96(96%)	77(96.25%)		
109 C / T (37Leu/Phe)	4(4%)	3(3.75%)	0.6220	0.935 [0.203-4.306]
Exon 2				
1550 G / G (125Val/Val)	87(87%)	73(91.25%)		
1550 G / A (125Val/Ile)	13(13%)	7(8.75%)	0.2554	0.642 [0.243-1.693]
Exon 3				
1962 T / T (207His/His)	85(85%)	67(83.75%)		
1962 T / C (207His/His)	15(15%)	13(16.25%)	0.4887	1.100 [0.490-2.469]
1985 G / G (215Arg/Arg)	98(98%)	77(96.25%)		
1985 G / A (215Arg/His)	2(2%)	3(3.75%)	0.3955	1.909 [0.311-11.716]
Intron between exon4 and 5				
2491 C / C	95(95%)	74(92.5%)		
2491 C / A	5(5%)	6(7.5%)	0.3485	1.541 [0.452-5.246]
Exon 5				
2811 G/G (319Arg/Arg)	99(99%)	80(100%)		
2811 G/A (319Arg/Gln)	1(1%)	0(0%)	0.5556	0.000

P values were calculated by Fisher's exact test. * Significant difference. *P* =0.25 after Bonferroni correction.

Table 6. Distributions of Genetic Variants of the CCK Gene in Schizophrenic Patients and Controls

	Controls	Schizophrenics	χ^2	*P* value
Promoter region				
-196 A / A	31(31.0%)	24(30.0%)		
-196 A / G	49(49.0%)	41(51.25%)		
-196 G / G	20(20.0%)	15(18.75%)	0.0953	0.9535
-45 C / C	52(52.0%)	46(57.5%)		
-45 C / T	40(40.0%)	29(36.25%)		
-45 T / T	8(8.0%)	5(6.25%)	0.5984	0.7414
Intron 1				
1270 C / C	52(52.0%)	46(57.5%)		
1270 C / G	40(40.0%)	29(36.25%)		
1270 G / G	8(8.0%)	5(6.25%)	0.5984	0.7414
Intron 2				
6662 C / C	76(76.0%)	68(85.0%)		
6662 C / T	23(23.0%)	12(15.0%)		
6662 T / T	1(1.0%)	0(0.0%)	2.7129	0.2576

P values were calculated by χ 2 test (two-tailed, d.f.=2).