Journal of Alzheimer's Disease 23 (2011) 1–3
IOS Press

Supplementary Data

Associations of Gene Sequence Variation and Serum Levels of C-Reactive Protein and Interleukin-6 with Alzheimer's Disease and Dementia

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Accepted 6 October 2010

Supplementary Table S1
Association between *CRP* and IL6 SNPs and Alzheimer's disease based on 2370 controls and 1265 AD cases

Gene/Marker	Genotype	Controls *n* (%)	AD cases *n* (%)	OR		95% CI		P_{trend}
CRP/rs2794520	GG	999 (42.2)	534 (42.5)	1		ref		
	AG	1088 (46.0)	573 (45.6)	1.02	0.88	–	1.18	
	AA	279 (11.8)	150 (11.9)	1.02	0.82	–	1.28	0.80
CRP/rs1205	GG	1005 (42.6)	536 (42.6)	1		ref		
	AG	1090 (46.2)	573 (45.6)	1.02	0.88	–	1.17	
	AA	263 (11.2)	148 (11.8)	1.06	0.85	–	1.33	0.62
CRP/rs1800947	GG	2019 (85.2)	1043 (82.7)	1		ref		
	GC	333 (14.1)	203 (16.1)	1.09	0.90	–	1.31	
	CC	17 (0.7)	15 (1.2)	1.57	0.79	–	3.74	0.22
CRP/rs1417938	AA	1097 (46.3)	620 (49.3)	1		ref		
	AT	1063 (44.9)	541 (43.0)	0.90	0.79	–	1.04	
	TT	209 (8.8)	97 (7.7)	0.80	0.62	–	1.03	0.04
CRP/rs3116650	AA	1146 (48.4)	595 (47.5)	1		ref		
	AG	1030 (43.5)	547 (43.7)	1.03	0.90	–	1.18	
	GG	191 (8.1)	111 (8.9)	1.09	0.86	–	1.38	0.51
CRP/rs11265260	AA	2151 (90.9)	1135 (89.9)	1		ref		
	AG	211 (8.9)	122 (9.7)	1.09	0.86	–	1.39	
	GG	5 (0.2)	5 (0.4)	1.87	0.53	–	6.64	0.33

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ISSN 1387-2877/11/$27.50

Supplementary Table S1
(*Continued*)

Gene/Marker	Genotype	Controls n (%)	AD cases n (%)	OR	95% CI			P_{trend}
rs11766273	GG	1964 (0.83)	1041 (0.82)	1		ref		
	GA	390 (0.16)	213 (0.17)	1.06	0.88	–	1.27	
	AA	15 (0.006)	9 (0.007)	1.49	0.53	–	4.25	0.38
rs10242595	GG	1308 (0.55)	678 (0.54)	1		ref		
	GA	910 (0.38)	498 (0.39)	1.07	0.93	–	1.22	
	AA	151 (0.06)	85 (0.07)	1.03	0.78	–	1.37	0.47
rs2069861	GG	1954 (0.84)	1076 (0.87)	1		ref		
	GA	367 (0.16)	141 (0.11)	0.74	0.60	–	0.90	
	AA	15 (0.006)	13 (0.01)	1.50	0.76	–	2.99	0.04
rs1554606	AA	617 (0.26)	337 (0.27)	1		ref		
	AC	1179 (0.50)	607 (0.48)	1.00	0.85	–	1.18	
	CC	570 (0.24)	317 (0.25)	1.11	0.91	–	1.35	0.30
rs2069840	CC	1157 (0.49)	594 (0.48)	1		ref		
	CG	973 (0.41)	519 (0.42)	1.01	0.87	–	1.16	
	GG	233 (0.10)	130 (0.10)	1.10	0.87	–	1.39	0.52
rs1474347	AA	654 (0.28)	379 (0.30)	1		ref		
	AC	1159 (0.49)	590 (0.47)	0.90	0.77	–	1.06	
	CC	555 (0.23)	281 (0.22)	0.91	0.75	–	1.11	0.32
rs1800796	GG	2157 (0.91)	1162 (0.93)	1		ref		
	CG	196 (0.08)	90 (0.07)	0.84	0.66	–	1.09	
	CC	10 (0.004)	3 (0.002)	0.82	0.15	–	4.61	0.20
rs2069827	CC	1856 (0.78)	968 (0.77)	1		ref		
	AC	474 (0.20)	277 (0.22)	1.10	0.93	–	1.30	
	AA	37 (0.02)	15 (0.01)	0.95	0.50	–	1.81	0.38
rs12700386	CC	1641 (0.69)	834 (0.67)	1		ref		
	CG	661 (0.28)	374 (0.30)	1.09	0.94	–	1.27	
	GG	65 (0.03)	46 (0.04)	1.39	0.96	–	2.01	0.08
rs2056576	GG	1280 (0.54)	643 (0.52)	1		ref		
	GA	913 (0.39)	490 (0.39)	1.09	0.94	–	1.25	
	AA	173 (0.07)	113 (0.09)	1.25	0.97	–	1.61	0.07
rs10499563	AA	1498 (0.64)	774 (0.62)	1		ref		
	AG	761 (0.32)	410 (0.33)	1.02	0.88	–	1.18	
	GG	98 (0.04)	55 (0.04)	1.01	0.71	–	1.42	0.86
rs1880241	AG	1151 (0.49)	588 (0.48)	1		ref		
	AA	722 (0.31)	372 (0.30)	1.00	0.86	–	1.17	
	GG	469 (0.20)	274 (0.22)	1.12	0.92	–	1.37	0.29
rs7801617	GG	1951 (0.82)	1039 (0.82)	1		ref		
	GA	400 (0.17)	217 (0.17)	1.00	0.84	–	1.20	
	AA	19 (0.008)	9 (0.007)	0.88	0.44	–	1.77	0.93
rs1546762	GG	689 (0.29)	343 (0.27)	1		ref		
	AG	1161 (0.49)	594 (0.47)	1.02	0.88	–	1.20	
	AA	518 (0.22)	319 (0.25)	1.17	0.97	–	1.43	0.12

Odds Ratios (OR) with 95% Confidence Intervals (CI) from Alternating Logistic Regression with the most common homozygote genotype as the reference level. Adjusted for age and gender.

Supplementary Table S2
Haplotypes in CRP and IL6 and their association with AD

Haplotypes in CRP

	rs1205	rs1800947	rs1417938	rs3116650	rs11265260	Frequency (%)	Association with AD	
							Uncorrected *p*-value	Corrected *p*-value (1000 perm)
C1	G	G	T	A	A	30.6	0.11	0.34
C2	G	G	A	G	A	29.9	0.33	0.77
C3	A	G	A	A	A	26.2	0.23	0.64
C4	A	C	A	A	A	8.3	0.03	0.10

Haplotypes in IL6

	LD block 1		LD block 2						Frequency (%)	Association with AD	
	rs1546762	rs7801617	rs1800796	rs1800795	rs2069837	rs1474347	rs2069840	rs1554606		Uncorrected *p*-value	Corrected *p*-value (1000 perm)
I1	G	G							52.7	0.12	0.50
I2	A	G							30.8	0.46	0.95
I3	A	A							9.3	14.1	0.55
I4			G	C	A	C	C	A	47.1	59.3	0.99
I5			G	G	A	A	G	C	30.8	54.4	0.98
I6			G	G	G	A	C	C	8.0	15.1	0.57
I7			G	G	A	A	C	C	6.2	15.2	0.57

Block structure defined by Confidence Intervals [22] in HapMap CEU down load data between 15640 & 15660 kb (Chr. 1) for CRP and 22530 & 22550 kb (Chr. 7) for IL6. The association modeled (*p*-value) is the case-control association between control group and AD cases. Only haplotypes with frequency >5% were included. The corrected p-value is based on 1000 permutations, i.e., the test statistic is also influenced by "chance" and can vary from each time the permutation is done.