*HLA-DRB1*1501* and Spinal Cord Magnetic Resonance Imaging Lesions in Multiple Sclerosis

Madeleine H. Sombekke, MD; Carsten Lukas, MD; J. Bart A. Crusius, PhD; Diego Tejedor, PhD; Joep Killestein, MD, PhD; David Arteta, PhD; Antonio Martínez, PhD; Bernard M. J. Uitdehaag, MD, PhD; Dirk L. Knol, PhD; A. Salvador Peña, MD, PhD; Jeroen J. G. Geurts, PhD; Philip L. De Jager, MD, PhD; Frederik Barkhof, MD, PhD; Hugo Vrenken, PhD; Chris H. Polman, MD, PhD

Arch Neurol. 2009;66(12):1531-1536

eTable. Single-Nucleotide Polymorphisms Included on DNA Chip

Gene	rs-nr	Chromosome	Polymorphism	HWE[a]	MAF
ADAMTS14	rs4747075	10q22	A/G	$P<.01$	0.30
ADAMTS14	rs7081273	10q22	C/G	NS	0.34
ADAMTS14	rs4746060	10q22	C/T	NS	0.08
Apo I/Fas	rs1800682	10q23	C/T	NS	0.47
Apo I/Fas	rs3781202	10q23	C/T	$P<.01$	0.40
Apo I/Fas	rs2234978	10q23	C/T	NS	0.31
BTNL2	rs2076530	6p21.3	A/G	$P<.01$	0.26
CIITA	rs3087456	16p13	A/G	NS	0.26
CACNG4	rs4790896	17q24	A/G	NS	0.41
CCR5	rs333	3p21	-/+	NS	0.11
CD24	rs8734	6q21	C	NA	0.00[b]
CNTF	rs1800169	11q12	A/G	NS	0.12
CRYAB	rs14133	11q21-q23	C/G	NS	0.27
CRYAB	rs762550	11q21-q23	A/G	NS	0.42
CRYAB	rs2234702	11q21-q23	C	NA	0.00[b]
CTLA4	rs231775	2q33	A/G	NS	0.37
CTLA4	rs5742909	2q33	C/T	NS	0.09
EBF1	rs1368297	5q34	A/T	NS	0.38
GABBRA1	rs1805057	6p22	C	NA	0.00[b]
HELZ	rs2363846	17q24	C/T	NS	0.48
HLA	rs2395166	6p21.3	C/T	NS	0.47
HLA	rs2213584	6p21.3	A/G	NS	0.40
HLA	rs2227139	6p21.3	C/T	NS	0.40
HLA	rs3135388	6p21.3	A/G	NS	0.33
HLA	rs9268458	6p21.3	A/C	NS	0.20
HLA	rs6457594	6p21.3	A/G	$P<.01$	0.40
HLA-DRA	rs2395182	6p21.3	G/T	NS	0.38
HLA-DRA	rs2239802	6p21.3	C/G	NS	0.38
IFNAR1	rs2257167	21q22	C/G	NS	0.08
IFNGR2	rs9808753	21q22	A/G	NS	0.14
IKBL	rs3130062	6p21.3	C/T	NS	0.18
IL-10	rs1800896	1q32	A/G	NS	0.46
*IL-1*β	rs1799916	2q14	A	NA	0.00[b]
*IL-1*β	rs1143627	2q14	A/G	NS	0.34
*IL-1*β	rs1143634	2q14	C/T	NS	0.23
IL-1RN	rs419598	2q12-q14	C/T	NS	0.31
IL-1RN	2073 C/T Intron2	2q12-q14	C/T	NS	0.30
IL-2	rs2069763	4q26	G/T	NS	0.36
IL-2	rs2069762	4q26	G/T	NS	0.27
IL-4R	rs1801275	16p12	A/G	NS	0.20
IL-7R	rs11567685	5p13	C/T	NS	0.25
IL-7R	rs7718919	5p13	G/T	NS	0.13
IL-7R	rs11567686	5p13	A/G	NS	0.34
MC1R	rs1805009	16q24	C/G	NA	0.01[b]
MC1R	rs1805006	16q24	A/C	NA	0.00[b]
MEFV	rs28940577	16p13.3	A	NA	0.00[b]
MGC33887	rs987931	17q24	G/T	NS	0.32
MOG	rs3130250	6p22	A/G	NS	0.19
MOG	rs3130253	6p22	A/G	NS	0.12
NDUFA7	rs2288414	19p13.2	C/G	NA	0.03[b]
NDUFA7	rs561	19p13.2	A/G	NS	0.21
NDUFS5	rs2889683	1p34.2	C/T	NS	0.31
NDUFS5	rs6981	1p34.2	A/G	NA	0.04[b]
NDUFS7	rs2074897	19p13.3	A/G	$P<.01$	0.47
NOS2A	rs1137933	17q11.2	A/G	NS	0.25
NOS2A	rs2779248	17q11.2	C/T	NS	0.39
NOTCH4	rs367398	6p21.3	A/G	NS	0.16
PD-1	rs11568821	2q37	G/A	NS	0.11
PITPNC1	rs1318	17q24	A/G	NS	0.21
PITPNC1	rs2365403	17q24	C/G	NS	0.18
PNMT	rs876493	17q11-q23	A/G	NS	0.39
PRKCA	rs7220007	17q24	A/G	NS	0.49
PRKCA	rs887797	17q24	C/T	NS	0.30
PRKCA	rs2078153	17q24	C/G	NS	0.23
PRKCA	rs3890137	17q24	A/G	NS	0.37
PTPN22	rs2476601	1p13	A/G	NS	0.11

Gene	rs-nr	Chromosome	Polymorphism	HWE[a]	MAF
PTPRC	rs17612648	1q31	C/G	NS	0.03[b]
PTPRC	rs4915154	1q31	A/G	NS	0.00[b]
CCL5	rs2280788	17q11.2-q12	C/G	NS	0.02[b]
CCL5	rs2107538	17q11.2-q12	C/T	NS	0.18
Spp1	rs1126616	4q21	C/T	NS	0.23
Spp1	rs1126772	4q21	A/G	NS	0.18
Spp1	rs2853744	4q21	G/T	NS	0.05
Spp1	rs9138	4q21	A/C	NS	0.24
Spp1	rs4754	4q21	C/T	NS	0.24
TNF	rs1800629	6p21.3	A/G	NS	0.17
TRAIL	rs1131568[c]	3q26	C/T	NS	0.32
UCP2	rs659366	11q13	C/T	NS	0.37
VDR	rs1544410	12q13	A/G	NS	0.48
VDR	rs731236	12q13	A/G	NS	0.48

Abbreviations: *ADAMTS14*, a disintegrin and metalloproteinase with thrombospondin motif, type 1 motif 14; *Apo I/Fas*, tumor necrosis factor (TNF) receptor superfamily, member 6; *BTNL2*, butyrophilinlike 2; *CIITA*, class II, major histocompatibility complex, transactivator; *CACNG4*, calcium channel, voltage-dependent, gamma subunit 4; *CCL5*, chemokine (C-C motif) ligand 5; *CCR5*, chemokine (C-C motif) receptor 5; *CNTF*, ciliary neurotrophic factor; *CRYAB*, α-B crystallin; *CTLA4*, cytotoxic T-lymphocyte-associated protein 4; *EBF1*, early B-cell factor 1; *GABBRA1*, gamma-aminobutyric acid (GABA) B receptor 1; *HELZ*, helicase with zinc finger; *HLA*, human leukocyte antigen; *HLA-DRA*, human leukocyte antigen DR alpha; HWE, Hardy-Weinberg Equilibrium in our sample; *IFNAR1*, interferon (alpha, beta, and omega) receptor 1; *IFNGR2*, interferon gamma receptor 2 (interferon gamma transducer 1); *IKBL*, inhibitory κ-B–like gene; *IL-10*, interleukin 10; *IL-1*β, interleukin 1β; *IL-1RN*, interleukin 1 receptor antagonist; *IL-2*, interleukin 2; *IL-4R*, interleukin 4 receptor; *IL-7R*, interleukin 7 receptor; *MAF*, minor allele frequency in our sample; *MC1R*, melanocortin 1 receptor; *MEFV*, Mediterranean fever; *MGC33887*, coiled-coil domain containing 46; *MOG*, myelin oligodendrocyte glycoprotein; NA, not applicable; *NDUFA7*, NADH dehydrogenase (ubiquinone) 1α subcomplex, 7; *NDUFS5*, NADH dehydrogenase (ubiquinone) Fe-S protein 5; *NDUFS7*, NADH dehydrogenase (ubiquinone) Fe-S protein 7; *NOS2A*, nitric oxide synthase 2; *NOTCH4*, Notch homolog 4; NS, not significant; *PD-1*, programmed cell death 1; PITPNC1, phosphatidylinositol transfer protein, cytoplasmic 1; *PNMT*, phenylethanolamine *N*-methyltransferase; *PRKCA*, protein kinase C, alpha; *PTPN22*, protein tyrosine phosphatase, nonreceptor type 22; *PTPRC*, protein tyrosine phosphatase, receptor type C; rs-nr, RefSNP accession identification; *Spp1*, secreted phosphoprotein 1 (osteopontin); *TRAIL*, TNF-related apoptosis inducing ligand; *UCP2*, uncoupling protein 2; *VDR*, vitamin D (1,25-dihydroxyvitamin D3) receptor.

[a] *P* value of HWE significant. $P < .01$ indicates deviation from HWE.

[b] Excluded due to minor allele frequency $P < .05$.

[c] Previous rs-number: rs9880164.