ImmunoChip Study Implicates Antigen Presentation to T Cells in Narcolepsy

Juliette Faraco1,11, Ling Lin13, Birgitte Rahbek Kornum1,2, Eimear E. Kenny3, Gosia Trynka4, Mali Einen1, Tom J. Rico1, Peter Lichtner5, Yves Dauvilliers6,7, Isabelle Arnulf6,8, Michel Lecendreux6,9, Sirous Javidi10,11, Peter Geisler12, Geert Mayer10,11, Fabio Pizza13, Francesca Poli13, Giuseppe Plazzi1,13, Sebastiaan Overeem14, Gert Jan Lammers15, David Keimlink16, Karel Sonka16, Sona Nevsimalova16, Guy Rouleau17, Alex Desautels18,19, Jacques Montplaisir19, Birgit Frauscher20, Laura Ehrmann20, Birgit Högl20, Poul Jennum2, Patrice Bourgin21, Rosa Peraita-Adrados22, Alex Iranzo23, Claudio Bassetti24, Wei-Min Chen25, Patrick Concannon25, Susan D. Thompson26, Vincent Damotte27,28, Bertrand Fontaine27,28,29, Maxime Breban30,31,32, Christian Gieger33, Norman Klopp33, Panos Deloukas34, Cisca Wijmenga4, Joachim Hallmayer1,35, Suna Onengut-Gumuscu25, Stephen S. Rich25, Juliane Winkelmann5,36,37,38, Emmanuel Mignot11

1 Center for Sleep Sciences and Medicine, Stanford University, Palo Alto, California, United States of America, 2 Center for Sleep Medicine, Department of Clinical Neurophysiology, Faculty of Health Sciences, University of Copenhagen, Glostrup Hospital, Copenhagen, Denmark, 3 Department of Genetics, Stanford University, Palo Alto, California, United States of America, 4 University of Groningen, University Medical Center Groningen, Department of Genetics, Groningen, The Netherlands, 5 Institute of Human Genetics, Helmholtz Zentrum München–German Research Center for Environmental Health, Munich, Germany, 6 National Reference Network for Orphan Diseases (Narcolepsy and Idiopathic Hypersomnia), Paris, France, 7 Sleep Unit, Gui-de-Chauliac Hospital, INSERM-1061, Montpellier, France, 8 Sleep Disorders Unit, Hospital Pitié-Salpêtrière, Pierre and Marie Curie University, Paris, France, 9 Centre Pédiatricque des Pathologies du Sommeil, Hôpital Robert Debré, Paris, France, 10 Hephata-Klinik, Schwalmstadt-Treysa, Germany, 11 Department of Neurology, Philips University of Marburg, Marburg, Germany, 12 Department of Psychiatry and Psychotherapy, University of Regensburg, Regensburg, Germany, 13 Department of Neurological Sciences, University of Bologna/IRCCS Istituto delle Scienze Neurologiche, Bologna, Italy, 14 Kempenhaeghe Centre for Sleep Medicine, Heeze, The Netherlands, 15 Leiden University Medical Center, Department of Neurology, Leiden University Medical Center, Leiden, The Netherlands, 16 Department of Neurology, Charles University, 1st Faculty of Medicine and General Teaching Hospital, Prague, Czech Republic, 17 CHU Ste-Justine Research Centre, Centre of Excellence in Neuroimmunology, Université de Montréal (CENUM), Montreal, Quebec, Canada, 18 Neurology Service, Hôpital du Sacré-Cœur, Université de Montréal, Montréal, Quebec, Canada, 19 Center for Advanced Research in Sleep Medicine, Hôpital du Sacré-Cœur, Université de Montréal, Montréal, Quebec, Canada, 20 Department of Neurology, Innsbruck Medical University, Innsbruck, Austria, 21 University Sleep Clinic and CNRS UPR3212, Strasbourg University Hospital, Strasbourg University, Strasbourg, France, 22 Sleep and Epilepsy Unit-Clinical Neurophysiology Service, University Hospital Gregorio Marañón, Madrid, Spain, 23 Neurology Service and Multidisciplinary Sleep Unit, Hospital Clinic, CIBERNED, IDIIBAPS, Barcelona, Spain, 24 Department of Neurology, Inselspital Universitätsklinik, Bern, Switzerland, 25 Center for Public Health Genomics, University of Virginia, Charlottesville, Virginia, United States of America, 26 Division of Rheumatology, Cincinnati Children's Hospital Medical Center, Cincinnati, Ohio, United States of America, 27 Inserrm, U975, CRICM, Paris, France, 28 Pierre Marie Curie University, UMR-S975, Paris, France, 29 Assistance Publique-Hôpitaux de Paris, Department of Neurology, Hospital Pitié-Salpêtrière, Paris, France, 30 Cochin Institute, INSERM U1016/CNRS UMR 8104/Paris Descartes University, Paris, France, 31 Department of Rheumatology, Ambroise Paré Hospital AP-HP, Boulogne-Billancourt, France, 32 Université Versailles Saint Quentin en Yvelines (UVSQ), Boulogne-Billancourt, France, 33 Institute of Genetic Epidemiology, Helmholtz Zentrum München, Munich, Germany, 34 Welcome Trust Sanger Institute, Hinxton, United Kingdom, 35 Department of Psychiatry, Stanford University School of Medicine, Palo Alto, California, United States of America, 36 Institute for Human Genetics, Klinikum rechts der Isar, Technische Universität München, Munich, Germany, 37 Neurology Clinic, Klinikum rechts der Isar, Technische Universität München, Munich, Germany, 38 Munich Cluster for Systems Neuroscience (SyNergy), Munich, Germany

Abstract

Recent advances in the identification of susceptibility genes and environmental exposures provide broad support for a post-infectious autoimmune basis for narcolepsy/hypocretin (orexin) deficiency. We genotyped loci associated with other autoimmune and inflammatory diseases in 1,886 individuals with hypocretin-deficient narcolepsy and 10,421 controls, all of European ancestry, using a custom genotyping array (ImmunoChip). Three loci located outside the Human Leukocyte Antigen (HLA) region on chromosome 6 were significantly associated with disease risk. In addition to a strong signal in the T cell receptor alpha (TRAα), variants in two additional narcolepsy loci, Cathepsin H (CTSH) and Tumor necrosis factor (ligand) superfamily member 4 (TNFSF4, also called OX40L), attained genome-wide significance. These findings underline the importance of antigen presentation by HLA Class II to T cells in the pathophysiology of this autoimmune disease.


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Introduction

Narcolepsy is a life-long sleep disorder caused by the autoimmune-mediated loss of 70,000–90,000 hypocretin (orexin)-producing neurons in the hypothalamus. Prevalence is approximately 0.02–0.03% in Caucasian populations, and somewhat higher in Japanese (0.16%). Family and twin studies support the importance of genetic (10–40 fold increased risk in first degree relatives) as well as environmental factors (25% concordance in identical twins) [1]. Onset is typically around puberty and displays a seasonal pattern of incidence, with highest rates in spring and summer. Likely triggering factors are influenza A, notably the pandemic H1N1 2009 variant, and Streptococcus Pyogenes infections [2–5]. Unique among autoimmune diseases, the condition is almost completely associated with Human HLA DQ0602, a heterodimeric protein encoded by the DQA1*01:02-DQB1*06:02 haplotype (90% versus 25% frequency in European ancestry cases and controls, respectively). The overwhelming effect of this haplotype on risk suggests the importance of antigen presentation by DQ0602. As seen in other autoimmune diseases, additional HLA alleles carried in trans of this haplotype also confer modulatory effects [6,7]. Most notably, DQA1*01:02-DQB1*06:02 homozygosity increases predisposition by 2–4 fold. Further, DQA1 and DQB1 alleles known to heterodimerize with DQ0602, the natural receptor of DQB0602. The TRA@ locus was sparsely covered on the ImmunoChip (15 SNPs within a 1 Mb window of chromosome 19p13.2, as additional suscep-

Results/Discussion

One previously reported, and two novel non-HLA loci surpassed genome-wide significance (gws) P<5×10−8 in this study (Figure 1 and Table 2). The strongest association was with rs1154155 (MAF = 0.15, P = 8.87×10−30 OR = 1.72) in the T cell receptor (TCR) alpha (TRA@) locus, on chromosome 14, replicating signal previously reported using smaller samples [7,12,13]. The TCR protein is comprised of alpha and beta chains. As for immunoglobulin loci, TCR loci undergo somatic DNA recombination during T cell development, generating a large number of possible proteins specific to individual T-cell clones. T cells bearing specific recombinants are then negatively or positively selected, allowing adaptation of the immune system to past environmental history.

The T cell receptor binds foreign or self-peptides presented by Class II MHC proteins (such as the DQ alpha/beta heterodimer), allowing initiation and regulation of immune responses. It is thus the natural receptor of DQB0602. The TRA@ locus was sparsely covered on the ImmunoChip (15 SNPs within a 1 Mb window of rs1154155, none with r2 above 0.5) precluding fine mapping or haplotype analysis, although providing robust replication of the previously reported findings. SNP rs1154155 is located close to the J10 segment region of the locus, with linkage disequilibrium (LD) data suggesting the involvement of a specific J segment in the narcolepsy pathophysiology. The association with TRA@ is unique to narcolepsy, as no other autoimmune diseases have been associated with this locus.

Two SNPs rs34599349, and rs34843303, located in intron 1 of Cathepsin H (CTSH), a papain-like cysteine protease, reached gws MAF = 0.11, P = 1.78×10−8 OR = 1.34 and MAF = 0.11, P = 2.79×10−8 OR = 1.35, respectively). Another SNP located in intron 1, rs3825932T has been previously reported to be associated with type 1 diabetes [14,15]. Although in close proximity,
this marker is in weak LD with rs34593439 and rs34843303 ($r^2 = 0.23$ and 0.23 respectively) and shows no significant association in the present sample ($P = 0.01$). The local region of LD surrounding these markers encompasses exon 1, where 4 potentially functional polymorphisms have been identified. One of which, SNP rs2289702T (p.Gly1Arg, MAF = 0.11), is in tight LD with our markers (pairwise $r^2 = 0.96$ and 0.98 respectively, 1000genomes data, phase 1 release V3) and could be the culprit behind this association. Following imputation in a 1 Mb window surrounding CTSH, SNPs rs2289702 and rs34593439 were the two most highly associated variants (respectively) (Figure 2). The Arg allele of rs2289702 also underlies a minor histocompatability antigen restricted by HLA-A*3101 and HLA-A*3303, causing selective resistance to SLE, whereas our most significantly associated SNP markers in narcolepsy are downstream of the gene in a separate haplotype block. The SNPs associated with SLE and narcolepsy are composed of SNPs upstream of the gene confer susceptibility or resistance to SLE, whereas our most significantly associated SNP markers in narcolepsy are downstream of the gene in a separate haplotype block. The SNPs associated with SLE and narcolepsy are weak LD, and rs444648, an established marker of SLE, is not strongly associated with narcolepsy ($p = 0.016$). Interestingly, rs7553711 maps to a potential enhancer site (H3K4Me1 site, UCSC browser, Layered H3K27 Track). rs7553711 is known to be strongly associated with systemic lupus erythematosus (SLE) [21] and systemic sclerosis [22,23] and SNPs in this region were densely represented on the ImmunoChip. Two distinct haplotypes of SNPs upstream of the gene confer susceptibility or resistance to SLE, whereas our most significantly associated SNP markers in narcolepsy are downstream of the gene in a separate haplotype block. The SNPs associated with SLE and narcolepsy are weak LD, and rs444648, an established marker of SLE, is not strongly associated with narcolepsy ($p = 0.016$). Interestingly, rs7553711 maps to a potential enhancer site (H3K4Me1 site, UCSC browser, Layered H3K27 Track). The association of narcolepsy with SNPs in TNFSF4 is consistent with a primary role of antigen presentation to T cells in narcolepsy. Like CTSH, OX40L is primarily expressed in MHC Class II-positive antigen presenting cells (e.g. dendritic and B cells). Optimal activation of T cells following the binding of T cell receptor- MHC class II/antigen complex requires the action of additional costimulatory factors, notably involving receptor/ligand pairs from the tumor necrosis superfamily. The interaction of two of these, OX40 receptor (encoded by TNFRSF4) and OX40L ligand (encoded by TNFSF4), provides an important costimulatory signal supporting Th1 and Th2 responses, promoting expansion and survival of effector T cells and the generation of T memory cells. Although less understood, OX40/OX40L interactions also play a role in the activity and homeostasis of T regulatory cells. Signaling of this pair is tightly controlled, as OX40 is not

Table 1. Sample collections.

<table>
<thead>
<tr>
<th>Case Cohort</th>
<th>Number</th>
<th>Region of Origin</th>
</tr>
</thead>
<tbody>
<tr>
<td>Virginia</td>
<td>1,030</td>
<td>North America, Europe*</td>
</tr>
<tr>
<td>Germany</td>
<td>801</td>
<td>North America, Europe*</td>
</tr>
<tr>
<td>Stanford VA</td>
<td>55</td>
<td>North America, Europe*</td>
</tr>
<tr>
<td>Total</td>
<td>1,886</td>
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</tbody>
</table>

<table>
<thead>
<tr>
<th>Control Cohort</th>
<th>Number</th>
<th>Region of Origin</th>
</tr>
</thead>
<tbody>
<tr>
<td>1958 UK Birth Cohort</td>
<td>4,289</td>
<td>UK</td>
</tr>
<tr>
<td>FT.NL.PLSP</td>
<td>3,609</td>
<td>Italy, Netherlands, Poland, Spain</td>
</tr>
<tr>
<td>KORA</td>
<td>980</td>
<td>Germany</td>
</tr>
<tr>
<td>CCHMC</td>
<td>794</td>
<td>North America</td>
</tr>
<tr>
<td>Fr1</td>
<td>347</td>
<td>France</td>
</tr>
<tr>
<td>Fr2</td>
<td>402</td>
<td>France</td>
</tr>
<tr>
<td>Total</td>
<td>10,421</td>
<td></td>
</tr>
</tbody>
</table>

*Numbers of samples by country of origin are listed in the Methods section. Case cohort names represent location of genotyping, and do not reflect country of origin of samples.
expressed in resting T cells, only appearing approximately one day following initial activation. Similarly, OX40L is found only at sites of inflammation, first on the surface of antigen presenting cells, but later on diverse cell types including mast cells, suggesting a role distinct from T cell priming or memory cell generation. OX40-OX40L interactions are known to be involved in autoimmune disease, (e.g. SLE) likely acting through a disruption of tolerance. OX40 signaling within responding T cells renders them resistant to Treg-mediated suppression, and acts within the Treg cells to inhibit suppressive functions. In addition, sustained inflammatory response may result from excessive OX40-OX40L signaling and consequent increased survival of effector T-cells (see [24,25]).

Two other regions showed suggestive associations, including SNPs between MIR-552 and GJB5 on Chromosome 1p34.3 (rs10915020 MAF = 0.84, P = 5.40^-10, OR = 1.32), and near ZNF365 on chromosome 10q21.2 (rs10995245 MAF = 0.35, P = 3.24^-10, OR = 1.20). ZNF365 is highly expressed in the brain and has been implicated in susceptibility to breast cancer, Crohn's Disease, and more recently, atopic dermatitis [26–28]. None of these reached genome-wide significance levels after correcting with the EMMAX [29] procedure in the current study, although nearly reaching or surpassing Bonferroni significance (P = 4.5x10^-8) (Table S1). Increased sample size and replication will be needed to confirm these loci.

Our study, analyzing 1886 narcolepsy-cataplexy cases of European ancestry, is the largest collaborative cohort study of narcolepsy to date, including samples from across the United States, Canada and Europe, and representing the majority of available case samples of European ancestry. To preserve the statistical power afforded by this sample size, we elected not to split our cases into discovery and replication cohorts, and thus our study is limited by the lack of replication in an ethnically similar population. We identified two novel narcolepsy susceptibility genes, CTSH and TNFSF4 (OX40L), and confirmed strong associations with HLA and TRAQ. The two new loci identified outline with striking clarity that the key pathology underlying narcolepsy likely resides in the interaction between T cells and antigen presenting cells.

Although a role of antigen presentation to CD4 T cells is likely the primary susceptibility pathway for the disorder, narcolepsy was not associated with all components of this pathway as represented on the array. For example, we found no association at the P<10^-4 threshold with the class II invariant chain, AEP and cathepsin B (CTSB) genes or, more surprisingly, with genes encoding other co-stimulatory molecules such as CD28, cytotoxic T-lymphocyte antigen-4 (CTLA4) and their cognate ligands, CD80 and CD86 (these have been involved in many other autoimmune disorders) (see Table S1). The present results also show limited overlap in susceptibility loci between narcolepsy and loci associated with classical autoimmune disorders, a fact that may be unsurprising based on the lack of readily identifiable autoantibodies, or other clear signs of inflammatory damage in the disease. To date, the TCR locus has only been observed in narcolepsy. Notably, we

<table>
<thead>
<tr>
<th>Variant</th>
<th>Chr</th>
<th>BP</th>
<th>MAF_N</th>
<th>MAF_C</th>
<th>P</th>
<th>OR</th>
<th>CI</th>
<th>Locus</th>
<th>Risk allele</th>
</tr>
</thead>
<tbody>
<tr>
<td>rs1154155</td>
<td>14</td>
<td>22072524</td>
<td>0.2292</td>
<td>0.1478</td>
<td>8.87x10^-10</td>
<td>1.715</td>
<td>1.543-1.905</td>
<td>TCRA</td>
<td>G</td>
</tr>
<tr>
<td>rs34593439</td>
<td>15</td>
<td>77022012</td>
<td>0.1359</td>
<td>0.1053</td>
<td>1.78x10^-98</td>
<td>1.337</td>
<td>1.212-1.455</td>
<td>CTSH</td>
<td>A</td>
</tr>
<tr>
<td>rs7553711</td>
<td>1</td>
<td>171398531</td>
<td>0.3462</td>
<td>0.2851</td>
<td>4.08x10^-98</td>
<td>1.328</td>
<td>1.176-1.519</td>
<td>TNFSF4</td>
<td>C</td>
</tr>
</tbody>
</table>

Chr: Chromosome; BP: position according to NCBI build 36 (Hg18) coordinates; MAF_N: minor allele frequency in narcolepsy (_N) and controls (_C); P: P value according to variance component model (EMMAX). EMMAX does not provide OR (Odds Ratio) or adjusted allele frequencies, therefore MAF, OR, and 95% confidence intervals (CI) were calculated with Plink on subset of 8,474 samples with the greatest PCA homogeneity (see Figure S2; EV 11.21, 0.004, EV 4.12, 0.01).

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found no associations with loci widely shared among other autoimmune diseases such as interleukin genes and receptors (IL2, IL21, IL12, IL2RA, IL23R) acting in differentiation; PTPN22, SH2B3 and TAGAP involved in immune-cell activation and signaling; and IRF5, TNFAIP3 involved in TNF signaling and innate immunity (Table S1). Together with findings implicating pandemic H1N1 influenza as a trigger, narcolepsy may offer a unique opportunity, furthering our understanding of how HLA class II presentation of foreign and self-antigens predispose to autoimmunity.

Methods

Ethics statement

Informed consent in accordance with governing institutions was obtained from all subjects. The research protocol at Stanford was approved by the IRB Panel on Medical Human Subjects.

Samples

Cases included in this study all met criteria for narcolepsy/hypocretin deficiency (clear-cut cataplexy and DQB1*06:02 positive, or low cerebrospinal fluid hypocretin-1). Samples included 1901 patients sourced from the Stanford Center for Narcolepsy database (North America, and worldwide collaborators), and 585 samples contributed by the European narcolepsy network (EU-NN). ImmunoChip typing was performed at centers in the US and in Germany. Informed consent in accordance with governing institutions was obtained. Countries of origin included: United States (657), France (296), Italy (157), Germany (157), the Netherlands (111), Czech Republic (104), Canada (101), Austria (83), Denmark (74), Spain (51) and Norway (32). A further 63 cases came from Argentina, Australia, Finland, Israel, Poland, Portugal, Slovakia, Switzerland and Turkey, each with fewer than 20 samples. Control genotypes were contributed through multiple immunochip consortium collaborators including 4289 samples.
from the United Kingdom 1958 Birth Cohort, 3609 samples from selected European countries including Italy (1251), Netherlands (1179), Poland (529) and Spain (656), 980 samples from the German KORA cohort; 794 Samples from Cincinnati through CCHMC [30]; and 749 French samples (2 collaborators).

Data analysis and statistics

Genotyping of cases was performed following Illumina’s recommendation at U Virginia, USA, U of Munich, Germany, and Stanford University, Palo Alto, CA USA. NCBI build 36 (hg10) mapping was used as reference. Illumina manifest file ImmuNo_BeadChip_1149691_B.bpm was used in the majority of cases. In cases where file ImmuNo_BeadChip_11419691_A was used, map positions were converted to be consistent with 1149691_B, or omitted from the analysis. Genotypes were called using Illumina GeneExpress (Illumina GenomeStudio GenTrain2.0 algorithm), with extensive additional curation. Individuals with call rate under 98% (123 controls, 147 cases), and samples which were related (pi hat > 0.2) were excluded from further analysis. Data from all sources were merged in forward-strand format. We identified 142,054 high quality SNPs with call rate above 99% (in both cases and controls separately), and passing HWE filtering in controls (P > 1x10^-6) using the Plink suite of software [31]. We excluded a broad region around the HLA complex (7,893 markers at Chr 6:24,067–35,474 kb) due to the strong LD effects with DQB1*06:02. This region contained nearly 3000 SNPs associated with narcolepsy at GWA significant levels. We additionally excluded SNPs with minor allele frequency below 1% (22,921 SNPs). Finally 111,240 high quality SNPs of MAF ≥ 0.01 (including 91,804 MAF ≥ 0.05) were selected for the analysis presented here. Principal components analysis (PCA) was performed to identify 162 outliers (133 controls, 29 cases; Golden Helix SVS, v7), and those were removed. Genome wide association analysis was performed using a variance component model implemented in EMMAX [29]. The EMMAX software does not return odds ratio or adjusted allele frequency data after correction for stratification. We therefore calculated OR and MAF does not return odds ratio or adjusted allele frequency data after model implemented in EMMAX [29]. The EMMAX software

Cleavage prediction

Sequence used: MWATLPLLCAAGAWL( G/R) VPVCAGAVL(C/V)- SLEFKHCSWTSHKTY3TEEYHHRQTFAS

SignalIP: http://www.cbs.dtu.dk/services/SignalP/ Both alleles are predicted to have normal cleavage


Supporting Information

Figure S1 Principal components analysis of the study population. Eigenvectors 1 versus 2 in cases and controls are displayed (a–c). Dashed lines in panel a indicate boundaries of a subset of 8474 samples used to calculate OR and allele frequencies (see Methods).

Table S1 Top ranking non-HLA narcolepsy risk variant signals to P = 1x10^-7. All non-HLA variants (MAF > 1% passing QC measures), and with P values < 1x10^-4. are displayed. Chr.: Chromosome; BP: position according to NCBI build 36 (Hg18) coordinates; MAF_N: minor allele frequency in narcolepsy (_N) and controls (_C); P: P value according to variance component model (EMMAX). EMMAX does not provide OR (Odds Ratio) or adjusted allele frequencies, therefore MAF, OR, and 95% confidence intervals (CI) were calculated with Plink on subset of 8474 samples with the greatest homogeneity (see Figure S1 ; EV 11.21<0.004, EV 4.12<0.01). Threshold for significance using Bonferroni correction: 4.5x10^-7.

Acknowledgments

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Author Contributions

Conceived and designed the experiments: J Faraco, L Lin, P Deloukas, J Hallmayer, SS Rich, E Mignot. Performed the experiments: J Faraco, L Lin, BR Kornurn, G Trynka, TJ Rico, P Lichtner, W-M Chen, S Onenget-Gumuscu, SS Rich, J Winkelmann, E Mignot. Prepared the DNA from the British 1958 Birth Cohort collection, coordinated collection for genotyping: Mehdi Tafiri, Johannes Mathis, Raphael Heinzer, José Haba-Rubio, Aleksandra Wierzbicka, Eva Feketeova, Joan Santamaria, Christian Baumann, Ramin Khlatami, and Per Egil Helsa. Matthew Brown coordinated the use of one cohort of French controls. We acknowledge the use of DNA from the British 1958 Birth Cohort collection provided through the Wellcome Trust. We also thank Jing Zhang, Anna Voros for help in sample preparation, Valentine Olivier for participation in imputation and manuscript preparation, and Hyatti E. Moore and Steve Schoeteter for providing software scripts. We thank J. Barrett at the Sanger Institute for coordinating ImmunoChip SNP selection and J. Stone at Illumina for coordinating array production.

Imputation

Imputation and phasing of ImmunoChip genotypes were performed using Beagle v3.3 [34] against 4 European populations (286 individuals from CEU, TSI, GBR, IBS) in the 1000 genomes integrated data set [phase 1 release v3] within a 1 Mb window of the top hit at the CTSH and TNFSF4 loci. SNPs with an imputation R2 value ≥ 0.8 (representing reliability of imputation) were considered in the analysis. Pairwise LD was calculated in Plink. Association P values in Figure 2 were calculated with Plink, as EMMAX would be inappropriate in this context, and therefore P values are slightly different than those presented in Table 2.

http://faculty.washington.edu/browning/beagle/beagle.html


Antigen Presentation in Narcolepsy Susceptibility
References