Distinct HLA associations of LGI1 and CASPR2-antibody diseases

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The recent biochemical distinction between antibodies against leucine-rich, glioma-inactivated-1 (LGI1), contactin-associated protein-2 (CASPR2) and intracellular epitopes of voltage-gated potassium-channels (VGKCs) demands aetiological explanations. Given established associations between human leucocyte antigen (HLA) alleles and adverse drug reactions, and our clinical observation of frequent adverse drugs reactions in patients with LGI1 antibodies, we compared HLA alleles between healthy controls (n = 5553) and 111 Caucasian patients with VGKC-complex autoantibodies. In patients with LGI1 antibodies (n = 68), HLA-DRB1*07:01 was strongly represented [odds ratio = 27.6 (95% confidence interval 12.9–72.2), \( P = 4.1 \times 10^{-26} \)]. In contrast, patients with CASPR2 antibodies (n = 31) showed over-representation of HLA-DRB1*11:01 [odds ratio = 9.4 (95% confidence interval 4.6–19.3), \( P = 5.7 \times 10^{-6} \)]. Other allelic associations for patients with LGI1 antibodies reflected linkage, and significant haplotypic associations included HLA-DRB1*07:01-DQA1*02:01-DQB1*02:02, by comparison to DRB1*11:01-DQA1*05:01-DQB1*03:01 in CASPR2-antibody patients. Conditional analysis in LGI1-antibody patients resolved further independent class I and II associations. By comparison, patients with both LGI1 and CASPR2 antibodies (n = 3) carried yet another complement of HLA variants, and patients with intracellular VGKC antibodies (n = 9) lacked significant HLA associations. Within LGI1- or CASPR2-antibody patients, HLA associations did not correlate with clinical features. In silico predictions identified unique CASPR2- and LGI1-derived peptides potentially presented by the respective over-represented HLA molecules. These highly significant HLA associations dichotomize the underlying immunology in patients with LGI1 or CASPR2 antibodies, and inform T cell specificities and cellular interactions at disease initiation.

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Introduction

The discovery of autoantibodies against leucine-rich, glioma-inactivated 1 (LGI1), contactin-associated protein 2 (CASPR2) (Irani et al., 2010; Lai et al., 2010) and, more recently, intracellular epitopes of voltage-gated potassium channels (VGKCs) (Lang et al., 2017), have redefined the immunology of the VGKC-complex (Thieben et al., 2004; Vincent et al., 2004). Patient stratification by these antigenic targets has shown that the ‘double-negative’ VGKC-complex antibodies, those without LGI1 or CASPR2 reactivities, are observed across all ages, in healthy controls and in a variety of syndromes, many of which are not immune-mediated (Graus and Gorman, 2016; van Sonderen et al., 2016; Lang et al., 2017). In contrast, patients with LGI1 or CASPR2 antibodies often have clinically-indistinguishable late-onset forms of limbic encephalitis and neuromyotonia with associated dysautonomia, sleep disturbances, pain and seizures (Irani et al., 2010; Lai et al., 2010; Klein et al., 2013; Gadoth et al., 2017). While these features occur at different rates in LGI1- versus CASPR2-antibody cohorts, only faciobrachial dystonic seizures (FBDS) robustly predict LGI1 reactivity (Irani et al., 2011; Gadoth et al., 2017; Thompson et al., 2018). Furthermore, these two autoantibodies are both often of the IgG4 subclass and frequently co-exist in patients with the ultra-rare Morvan’s syndrome (Irani et al., 2012; Ariño et al., 2016). The striking overlaps of these rare neurological features and autoantibodies, and the frequent co-expression of their antigenic targets within mammalian CNS-membrane complexes (Irani et al., 2010; Binks et al., 2018), suggest they are involved in autoimmunization. Indeed, this has been reported in abattoir workers with autoantibodies against VGKC-complexes and, less so, CASPR2 (Meuesen et al., 2012). The nature of the available complexes, antigen presentation mechanisms and the available T cell repertoires are likely to determine which antigen dominates the ensuing T-B cell response. If so, human leucocyte antigen (HLA) variants, intimately related to antigen presentation, may play critical roles in distinguishing the aetiology of these syndromes.

Previously, high rates of adverse drug reactions were observed in patients with LGI1 antibodies, typically secondary to antiepileptic drugs (AEDs) and, less so, corticosteroids (Irani et al., 2011, 2013; Thompson et al., 2018). As HLA variants have been implicated in several adverse drug reactions, including those associated with AEDs and immunosuppressants (McCormack et al., 2011; Yip et al., 2015), and have essential antigen-presenting functions (Trowsdale and Knight, 2013), we hypothesized that HLA associations existed in patients with LGI1 antibodies. Indeed, recently, HLA-DRB1*07:01, HLA-DQB1*02:02 and HLA-DRB4 were found to be present in varying proportions of patients with LGI1 antibodies in two cohorts totalling 40 patients, from Korea and the Netherlands (Kim et al., 2017; van Sonderen et al., 2017).

To extend these early observations, and given the hypothesis that the VGKC complex may be the initiating immunizing agent, we sought to compare and contrast HLA-associations in a sizeable cohort of clinically well-characterized patients with antibodies against LGI1, CASPR2, both LGI1 and CASPR2, and VGKCs, and in silico to identify peptides that may be presented by these HLA molecules.

Materials and methods

Patients

One hundred and eleven Caucasian patients were identified from previous studies (n = 51) (Irani et al., 2011, 2013; Lang et al., 2017), referrals to the Oxford Autoimmune Neurology Group (n = 46) or from the Autoimmune Encephalopathy Clinic, University of California San Francisco (n = 14). These patients had serum antibodies against LGI1 only (n = 68), CASPR2 only (n = 31), both LGI1 and CASPR2 (n = 3) or intracellular aspects of VGKCs (n = 9), as determined by previously described antigen-specific cell-based assays (Irani et al., 2010; Lang et al., 2017). Clinical phenotypes, including information relating to past medical history and adverse drug reactions (Table 1), were evaluated via direct patient and relative interviews and case-note reviews. All patients provided written informed consent (REC16/YH/0013 or the IRB 10-04905 approvals).

Genotyping, HLA imputation, verification and multi-locus haplotype-block construction

The Infinium Global Screening Array-24 + v1.0 BeadChip with Illumina Infinium HTS custom markers were used for genotyping. We proceeded to impute HLA alleles using SNP2HLA at eight classical loci (HLA-A, HLA-B, HLA-C, HLA-DPA, HLA-DPB, HLA-DQA1, HLA-DQB1 and HLA-DRB1) at two-field resolution (Jia et al., 2013; Neville et al., 2017).
Table 1  Clinical features of patients with antibodies to VGKC complex proteins: LGI1, CASPR2, both LGI1 and CASPR2 or intracellular aspects of VGKCs

|                     | LGI1        | CASPR2      | LGI1 and CASPR2 | VGKC       | LGI1 versus CASPR2 (P-value)* |
|---------------------|-------------|-------------|-----------------|------------|------------------------------|
| Number of patients  | 68 (41–85)  | 31 (19–82)  | 3 (52–65)       | 9 (33–71)  | ND                           |
| Median age at onset | 63 (1–5)    | 68 (1–5)    | 56 (1–5)        | 43 (1–5)   | ND                           |
| Female (%)          | 20 (29)     | 2 (6)       | 1 (33)          | 4 (44)     | ND                           |
| **Clinical syndrome** |            |             |                 |            |                              |
| Epilepsy            | 8 (12)      | 2 (6)       | 0 (0)           | 4 (44)     | ND                           |
| Encephalitis        | 58 (85)     | 18 (58)     | 1 (33)          | 2 (22)     | ND                           |
| Morvan’s            | 1 (2)       | 3 (10)      | 2 (67)          | 0 (0)      | ND                           |
| Isolated neuromyotonia | 0 (0)     | 2 (6)       | 0 (0)           | 0 (0)      | ND                           |
| Other               | 1 (2)       | 6 (19)      | 0 (0)           | 3 (33)     | ND                           |
| **Clinical features** |            |             |                 |            |                              |
| Any seizure         | 66 (97)     | 25 (81)     | 2 (67)          | 7 (78)     | 0.01                         |
| Faciobrachial dystonic seizures | 47 (69) | 0 (0)       | 1 (33)          | 0 (0)      | <0.0001                     |
| Generalized seizure | 26 (38)     | 10 (32)     | 2 (67)          | 6 (67)     | NS                           |
| Amnesia             | 58 (85)     | 23 (74)     | 3 (100)         | 5 (56)     | NS                           |
| Neuromyotonia       | 1 (2)       | 8 (26)      | 2 (67)          | 0 (0)      | 0.0003                       |
| Neuropathic pain    | 5 (7)       | 14 (45)     | 2 (67)          | 0 (0)      | <0.0001                     |
| **Autoimmune features** |           |             |                 |            |                              |
| Other autoimmune disease | 19 (28) | 7 (23)      | 0 (0)           | 0 (0)      | NS                           |
| Atopy               | 8 (12)      | 2 (6)       | 2 (67)          | 1 (11)     | NS                           |
| Adverse effects of corticosteroids | 32 (47) | 5 (16)      | 0 (0)           | 1 (11)     | 0.004                        |
| Drug rash           | 24 (35)     | 1 (3)       | 0 (0)           | 0 (0)      | 0.0004                       |
| **Other features**  |             |             |                 |            |                              |
| Mean change in mRS (range) | 1.6 (–3 to 4) | 1.5 (0 to 4) | 1.7 (0 to 3) | 1 (0 to 2) | ND                           |
| Tumour (%)          | 9 (13)      | 4 (13)      | 2 (67)          | 1 (11)     | ND                           |

Live cell-based assays were used for LGI1 and CASPR2 antibody determination (Irani et al., 2010), and fixed assays to detect antibodies against the intracellular aspects of VGKCs (Lang et al., 2017). Statistical comparisons with Fisher’s exact test throughout.

To complement this, DRB1, DRB4 and DQ alleles underwent intermediate-resolution HLA-typing using PCR-sequence-specific primers (SSP), updated from Bunce et al. (1995). PCR-SSP defined the first-field plus a string of second-field possibilities: the highest frequency allele in Caucasians was considered most likely. For all discordant data, the PCR-SSP first-field was accepted as the final result. HLA alleles from 5553 Caucasian healthy controls (from Oxford Biobank) were available from imputation using the same platforms, and confirmed in 70 individuals within the same laboratory by PCR-SSP (Neville et al., 2017). Probable haplotype blocks were calculated on the basis of a Bayesian algorithm using PHASE V2 software with 10 000 iterations for three haplotype blocks: HLA-C-B, HLA-DRB1-DQA1-DQB1, and HLA-DPA1-DPB1 (Stephens et al., 2001; Stephens and Donnelly, 2003). Further details on genotyping and imputation are provided in the Supplementary material.

**Statistical analyses**

For each antibody group, Fisher’s exact test (two-tailed) was used to compare the HLA allele and haplotype carrier frequencies between patients and the healthy control dataset. Hochberg’s method was used to correct for multiple comparisons. Corrected P-values < 0.05 were considered significant, and are presented. Odds ratios (ORs) were calculated using the median-unbiased estimation method.
HLA binding predictions
The NetMHCIIpan 3.1 server model based on artificial neural networks (Andreotta et al., 2015) evaluated HLA haplotype binding affinities for 15-amino acid-long consecutive overlapping peptides from full-length LGI1 and CASPR2 sequences (UniProt accession numbers O95970 and Q9UHC6, respectively). Predicted peptide affinities (nM) were compared to 200 000 random peptides of the same length to generate rank values: this measure is less susceptible to the intrinsic capacity of some HLA alleles to generate high-affinity predictions, and rank values (%) <3 were considered strong binders. As expected, consecutive 15-mer peptides with high rank values often shared a common sequence.

Results
Clinical differences between patients stratified by VGKC-complex autoantibody targets
Table 1 summarizes the clinical features of the 111 patients, subgrouped by their autoantibody specificities. In agreement with previous studies, onset ages were typically around 60 years, and patients with LGI1 or CASPR2 antibodies most frequently had encephalitis or epilepsy. Around 60% of the patients were female. Table 1 shows the clinical features of the 111 patients. In line with previous reports, LGI1 antibodies had more severe clinical presentation, with 54% of patients suffering from drug-induced rashes (35% versus 3% in CASPR2, P = 0.004). The reported rashes were secondary to AEDs (n = 13: including carbamazepine (n = 6), phenytoin (n = 4), lamotrigine (n = 2) and valproate (n = 1)), antibiotics (n = 6: penicillins (n = 5) and metronidazole (n = 1)) and immunosuppressants (n = 5: azathioprine (n = 2), corticosteroids (n = 2) and methotrexate (n = 1)). Thus, the LGI1- and CASPR2-auto- body groups displayed differing clinical autoimmune features suggesting divergent immunogenetic pathways.

Patients with LGI1 or CASPR2 antibodies have strong and distinct HLA allelic profiles
We proceeded to analyse HLA associations, as summarized in Fig. 1 and Table 2. Consistent with previous smaller reports (Kim et al., 2017; van Sonderen et al., 2017), almost all LGI1-antibody-positive patients carried HLA-DRB1*07:01 (91%, compared to 26% in healthy controls) [OR 27.6 (95% confidence interval, CI 12.9–72.2), P = 4.1 × 10^-26]. Further, 13% (9/68) were homozygous for DRB1*07:01, compared to 2% (115/5553) healthy controls [OR 7.3 (95% CI 3.3–14.4), P = 3 × 10^-4]. Alleles recognized to be part of haplotypes involving HLA-DRB1*07:01 (González-Galarza et al., 2015) were over-represented, namely HLA-DQA1*02:01, HLA-DQB1*02:02, HLA-DQB1*03:03 and HLA-DPB1*11:01. Additionally, associations were found with two HLA class I alleles, HLA-B*57:01 [OR = 3.7 (95% CI 2.0–6.5); P = 0.014] and HLA-C*06:02 [OR = 3.9 (95% CI 2.4–6.3); P = 4.6 × 10^-5]. After conditioning on the commonest allele, HLA-DRB1*07:01, two other DQ alleles reached statistical significance consistent with evidence of an independent association, HLA-DQA1*01:03 [OR = 4.4 (95% CI 2.2–8.1); P = 4 × 10^-3] and HLA-DRB1*01:03 [OR = 14.7 (95% CI 3.6–51.5), P = 0.04].

In striking contrast, analysis of the CASPR2-antibody group identified a single risk allele; HLA-DRB1*11:01, which was present in 48% of CASPR2-antibody patients compared to 4% of patients with LGI1 antibodies and 9% of healthy controls [OR = 7.3 (95% CI 4.6–19.3); P = 5.7 × 10^-4]. One CASPR2-antibody patient was homozygous for HLA-DRB1*11:01. Interestingly, the four patients with non-immune conditions and CASPR2 antibodies (Table 1) did not carry HLA-DRB1*11:01, giving it a 56% (15/27) frequency in the remainder. No additional alleles were observed after conditioning on HLA-DRB1*11:01.

Intriguingly, of the three patients with co-existent CASPR2 and LGI1 antibodies, only one carried HLA-DRB1*07:01 and none carried HLA-DRB1*11:01. However, all three carried HLA-B*44:02, HLA-C*05:01, HLA-DQA1*03:01 and HLA-DQB1*03:01, a different complement of alleles to the patients with antibodies to either LGI1 or CASPR2 (Supplementary Fig. 1). There were no significant findings within the group with intracellular VGKC antibodies (Supplementary Fig. 1).

Haplotype-specific distinctions between patients with LGI1 and CASPR2 antibodies
Next, to understand the en bloc allelic inheritance and in vivo relevance of HLA combinations that may present LGI1 and CASPR2 antigens, we explored associations involving HLA haplotypes (Fig. 1B and full analysis in Supplementary Figs 2–4). We noted that HLA-DQA1*02:01, HLA-DQB1*02:02,
HLA-DQB1*03:03 and HLA-DPB1*11:01 show evidence of linkage disequilibrium with HLA-DRB1*07:01 (r² values 0.64, 0.49, 0.13, 0.10 and D’, 1, 0.95, 0.8 and 1, respectively) (Supplementary material). This was reflected in the most frequent HLA class II haplotypes found in patients with LGI1 antibodies, namely HLA-DRB1*07:01-DQA1*02:01-DQB1*03:03 [OR = 5.2 (95% CI 3.2–8.6); P = 2.3 × 10⁻⁹], DRB1*07:01-DQA1*02:01-DQB1*03:03 [OR = 3.1 (95% CI 1.7–5.5); P = 0.02] and DPA1*02:01-DPB1*11:01 [OR = 4.8 (95% CI 2.5–8.5); P = 3.8 × 10⁻⁴]. In addition, LGI1-antibody status was associated with a HLA class I haplotype, HLA-C*06:02-B*57:01 [OR = 3.6 (95% CI 1.9–6.2); P = 8.8 × 10⁻³]. By contrast, only one HLA class II haplotype was associated with CASPR2 antibodies: DRB1*11:01-DQA1*05:01-DQB1*03:01 [OR = 7.4 (95% CI 3.5–15.2); P = 5.7 × 10⁻⁵].

Given these significant and distinct allelic and haplotypic HLA associations, for each serologically-defined group, we evaluated their value in explaining sub-phenotypes (limbic encephalitis or epilepsy; peripheral or CNS), long-term outcomes or adverse drug reactions (Supplementary Table 1), and found no significant HLA allele or haplotype associations. However, within LGI1-antibody patients, five of six patients with antibiotic-induced rashes carried HLA-B*57:01 known to associate with risk of rash to abacavir and flucloxacillin (Yip et al., 2015), and four of six patients with psoriasis harboured the psoriasis risk allele C*06:02 (Arakawa et al., 2015), suggesting the extended haplotypes may explain these specific co-morbidities. Finally, from the nine LGI1- and four CASPR2-antibody patients with a tumour, there were no significant HLA differences compared to non-tumour patients (Supplementary Table 2).

**DRB4 analysis**

To extend a previous report (van Sonderen et al., 2017), the HLA-DRB1 paralogue HLA-DRB4 was sequenced and observed to be absent or a null allele in 61% (19/31) of the CASPR2-antibody cohort and 44% (4/9) of the intracellular VGKC-antibody cohort, consistent with the healthy control frequencies. However, only 16% (11/68) of the LGI1-antibody cohort showed an absent or null HLA-DRB4 allele, and these 11 patients all carried HLA-DRB1*07:01 (Supplementary Table 3).

**Predictions of HLA-binding peptides**

These robust HLA class II associations strongly implicate CD4⁺ T cells in the pathogenesis of both LGI1- and CASPR2-antibody-associated diseases. To locate potentially high-affinity peptides that complex with HLA class II heterodimers, and may interact with patient T cells, **in silico**
modelling was used and focused on all the class II haplotypes identified above (Fig. 2).

Overall, many peptides from both LGI1 and CASPR2 ranked highly for potential binding to several HLA-DR, HLA-DP and HLA-DQ variants (Fig. 2A and C), likely consistent with the varied intrinsic properties of different HLA molecules. Furthermore, for HLA-DRB1*07:01 and HLA-DRB1*11:01, which pair with the invariant DRA chain, and for HLA-DQA1*02:01-DQB1*02:02 heterodimers, peptide ranks showed little difference between LGI1- and CASPR2-derived peptides, suggesting a lack of antigen selectivity. Also, no highly-ranked peptides were identified to bind the LGI1-antibody-associated heterodimer HLA-DQA1*02:01-DQB1*03:03, making it an unlikely candidate molecule for LGI1 peptide presentation. By contrast, the CASPR2-antibody-associated HLA-DQA1*05:01-DQB1*03:01 heterodimer was predicted to bind some high-ranking peptides from the CASPR2 sequence only, suggesting CASPR2 specificity.

As expected for the shared core sequences between consecutive 15-mers, many highly ranked peptides were from tightly clustered locations within the full-length protein (Fig. 2B, D and Supplementary Table 4). Most peptides within these clusters showed potential to bind the HLA variants observed in both the LGI1- and CASPR2-antibody cohorts (Fig. 2B and D, black circles). This included one previously identified peptide (Kim et al., 2017) and argues against its role in disease specificity. However, 9/13 LGI1-derived peptides and 7/13 from the CASPR2 sequence showed binding potential that was more restricted to the variants associated with the corresponding antibody cohort (Fig. 2B and D, pink circles). From LGI1, 4/9 core peptides were predicted to bind with high affinity (<40 nM), typically to HLA-DRB1*07:01, although interestingly the highest affinity peptide was predicted to bind HLA-DPA1*02:01-DPB1*11:01 (Supplementary Table 4). From CASPR2-derived peptides, 7/7 were predicted to bind with high affinity, distributed across the variants within the
versus CASPR2 antibodies. Furthermore, they strongly implicate HLA variants govern the generation of LGI1 and CASPR2 antibodies, and their co-expression in the frequently overlapping clinical features in patients with these patients, at both allelic and haplotypic levels. Given marked and strikingly different HLA associations for LGI1 and CASPR2-autoantibody mediated diseases, and shows this study is the first comparative HLA analysis of LGI1-CASPR2-antibody-associated haplotype (Supplementary Table 4).

**Discussion**

This study is the first comparative HLA analysis of LGI1- and CASPR2-autoantibody mediated diseases, and shows marked and strikingly different HLA associations for these patients, at both allelic and haplotypic levels. Given the frequently overlapping clinical features in patients with LGI1 and CASPR2 antibodies, and their co-expression in VGKC complexes, these findings indicate that dichotomous predisposing HLA variants govern the generation of LGI1 versus CASPR2 antibodies. Furthermore, they strongly implicate T cells in disease initiation and the candidate HLA-binding peptide partners generated by our in silico data may help identify these interacting T cells.

While HLA-DRB1*07:01 and linked class II alleles, including the haplotype HLA-DRB1*07:01-DQA1*02:01-DQB1*02:02, showed very strong associations with LGI1-antibody patients, this was not observed among CASPR2-antibody patients in whom we found clear associations with HLA-DRB1*11:01 only. Among LGI1-antibody patients, DRB1*11:01 was observed at around healthy control rates, DRB4 was less frequently detected than DRB1*07:01, homozygosity for HLA-DRB1*07:01 was recognized, and other independent associations involved HLA class I alleles HLA-B*57:01 and HLA-C*06:02. Albeit limited by their intrinsic rarity, intriguingly, the three patients with both LGI1 and CASPR2 antibodies had yet another complement of HLA alleles. Perhaps this implicates further divergence in molecular mechanisms responsible for the generation of both autoantibody specificities within an individual. However, the HLA associations do not appear to distinguish between sub-phenotypes, outcomes or, in contrast to a previous observation, the presence of associated tumours (van Sondere et al., 2017). Also, the 9–27% frequencies of these HLA variants in healthy Caucasians are far higher than disease prevalence, implicating additional loci, environmental or stochastic influences in disease manifestation.

Furthermore, our data also provide several intriguing insights into the immunopathogenesis of these diseases. First, they extend the frequent HLA associations in IgG4-related diseases (Huijbers et al., 2015), but here, exceptionally, with no DQ5 association. Second, the presence of dominant HLA class II associations implicates extracellular antigen processing and CD4 T cells in disease initiation (Trowsdale and Knight, 2013), but the LGI1 antibody class I associations found here, and HLA-B*44:03 and HLA-C*07:06 reported in seven patients previously (Kim et al., 2017), are compatible with a role for intracellular antigen processing, including viruses and drugs. These class I differences between studies may be explained by ethnicity, sample size and relatively weak associations (Kim et al., 2017; van Sondere et al., 2017). Indeed, this extended haplotype and the related complex linkage disequilibrium in this region of the genome warrant further analysis. Furthermore, our original hypothesis of adverse drug reaction-related HLA variants may relate to the linked adverse drug reaction-related class I and II HLA variants (HLA-DRB1*07:01, HLA-DQA1*02:01, HLA-B*57:01) (Yip et al., 2015). These and future observations in patients with LGI1 antibodies may inform the genetic basis of more common adverse drug reactions. Third, the HLA similarities between tumour and non-tumour LGI1-antibody cases suggests the absence of a unique paraneoplastic signature, in contrast to Lambert-Eaton myasthenic syndrome (Wirtz et al., 2005). Perhaps this implies tumours in patients with LGI1 antibodies largely reflect the age-matched background rate, rather than a distinct immune

**Table 2** Significant allele (top) and haplotype (bottom) associations in patients with LGI1 (n = 68) or CASPR2 (n = 31) antibodies

| Antibody group | Allele / haplotype | OR  | 95% CI lower | 95% CI upper | Fisher’s exact test | Corrected (Hochberg) P-value |
|---------------|-------------------|-----|-------------|-------------|--------------------|-----------------------------|
| LGI1          | B*57:01           | 3.7 | 2.0         | 6.5         | 5.2 × 10⁻⁵         | 1.0 × 10⁻²                   |
| LGI1          | C*06:02           | 3.9 | 2.4         | 6.3         | 1.6 × 10⁻⁷         | 4.6 × 10⁻⁵                   |
| LGI1          | DPB1*11:01        | 4.9 | 2.6         | 8.7         | 8.4 × 10⁻⁶         | 2.0 × 10⁻³                   |
| LGI1          | DQA1*02:01        | 8.9 | 5.2         | 16.1        | 3.0 × 10⁻¹⁷        | 8.7 × 10⁻¹⁵                  |
| LGI1          | DQB1*02:02        | 8.1 | 4.9         | 13.7        | 9.5 × 10⁻¹⁷        | 2.8 × 10⁻¹⁴                  |
| LGI1          | DQB1*03:03        | 4.7 | 2.8         | 7.7         | 3.6 × 10⁻⁸         | 1.0 × 10⁻⁵                   |
| LGI1          | DRB1*07:01        | 27.6| 12.9        | 72.2        | 1.4 × 10⁻²⁸        | 4.1 × 10⁻²⁶                  |
| CASPR2        | DRB1*11:01        | 9.4 | 4.6         | 19.3        | 2.0 × 10⁻⁶         | 5.7 × 10⁻⁶                   |
| LGI1          | DRB1*07:01-DQA1*02:01-DQB1*02:02 | 5.2 | 3.2         | 8.6         | 4.7 × 10⁻¹¹        | 2.3 × 10⁻⁹                   |
| LGI1          | DRB1*07:01-DQA1*02:01-DQB1*03:03 | 3.1 | 1.7         | 5.5         | 4.4 × 10⁻⁴         | 2.1 × 10⁻²                   |
| LGI1          | DPA1*02:01-DBP1*11:01 | 4.8 | 2.5         | 8.5         | 1.0 × 10⁻⁵         | 3.8 × 10⁻⁴                   |
| LGI1          | C*06:02-B*57:01   | 3.6 | 1.9         | 6.2         | 1.3 × 10⁻⁴         | 8.8 × 10⁻³                   |
| CASPR2        | DRB1*11:01-DQA1*05:01-DQB1*03:01 | 7.4 | 3.5         | 15.2        | 1.1 × 10⁻⁶         | 5.7 × 10⁻⁵                   |

Corrected P-values indicate comparison between disease and healthy controls.
mechanism, although a paucity of tumours classically associated with paraneoplastic neurological syndromes may limit our interpretation. Finally, our in silico predictions suggest that HLA-DQA1*02:01-DQB1*03:03 is unlikely to mediate presentation of LG11-derived peptides, whereas the HLA-DQA1*05:01-DQB1*03:01 heterodimer may be implicated in the CASPR2-antibody phenotype. Also, the promiscuity of both CASPR2 and LG11 peptides for some HLA variants, including HLA-DRB1*07:01 (Kim et al., 2017), may explain why immunization with the same VGKC complexes may generate two distinct disease entities, and underlie the observed co-existence of both antibodies at rates far higher than expected by chance (Irani et al., 2012). However, this in silico approach is inherently limited by the possibility that high affinity peptides are more effectively deleted through central tolerance. Nevertheless, taken together, the range of antigen-restricted peptides derived herein, and the relative HLA variant frequencies in disease versus control populations, generate hypothesis-driven approaches to expand disease-specific T cells in vitro and complement recent clinical and laboratory observations which strongly implicate T cell dependence of antibody-mediated diseases (Makuch et al., 2018; Wilson et al., 2018a, b).

In summary, the distinct HLA associations in patients with LG11 and CASPR2 autoantibodies, together with differing clinical features relating to autoimmunity, support an immunological dissociation in generation of these clinically-overlapping autoantibody-mediated syndromes. The dominant class II HLA involvement combined with in silico predictions, offers potential to better understand the likely initiating T-B cell interactions. Further work should focus on the environmental factors that influence the presentation of peptides in genetically predisposed individuals.

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Conflicts of interest

S.R.I. and P.W. are co-applicants and receive royalties on patent application WO2010/046716 entitled ‘Neurological Autoimmune Disorders’. The patent has been licensed to Euroimmun AG for the development of assays for LG11 and other VGKC-complex antibodies. Other authors report no conflicts of interest.

Supplementary material

Supplementary material is available at Brain online.

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