Sequence matching analyses show that *Clostridium tetani* neurotoxin shares numerous pentapeptides (68, including multiple occurrences) with 42 human proteins that, when altered, have been associated with epilepsy. Such a peptide sharing is higher than expected, nonstochastic, and involves tetanus toxin-derived epitopes that have been validated as immunopositive in the human host. Of note, an unexpected high level of peptide matching is found in mitogen-activated protein kinase 10 (MK10), a protein selectively expressed in hippocampal areas. On the whole, the data indicate a potential for cross-reactivity between the neurotoxin and specific epilepsy-associated proteins and may help evaluate the potential risk for epilepsy following immune responses induced by tetanus infection. Moreover, this study may contribute to clarifying the etiopathogenesis of the different types of epilepsy.

1. Introduction

The term epilepsy defines a group of disturbances whose only recognized commonality is the paroxysmal synchronous discharging of groups of neurons. Localization and physiological function of the neuronal populations involved determine the clinical picture, so that (1) clinical manifestations can be extremely subtle and the diagnosis can be challenging also in terms of differential definition; (2) epilepsies can produce extremely multiform clinical pictures with a large degree of overlap [1–3]. Indeed, epileptic syndromes can also be embedded in larger syndromic clinical pictures, that is, West and Lennox-Gastaut syndromes in tuberous sclerosis complex [4, 5]. This clinical diversity has noteworthy nosological implications. Syndromic or disease status of various forms of epilepsy and the terminology used to define them are indeed still matter of debate [7–9]. Likewise, the molecular etiopathogenesis of epilepsies has to be better defined at the molecular level. Although genetic alterations [10–12], inflammation [13], and viral infections [14–16] have been considered and thoroughly studied, nonetheless, the molecular basis and the causal mechanisms of epilepsies are still unclear.

Recently, research on epilepsy has also outlined a neurodevelopmental context [17–21]. Spontaneous recurrent seizures have been observed after induction of *status epilepticus* during the second and third postnatal weeks in rodents, by use of chemoconvulsants such as pilocarpine, kainate, and tetanus toxin (TT) [22]. TT seizures as well as experimental febrile seizures and developmental lithium pilocarpine appear to share a common mechanism for enhancing hippocampal network excitability and promoting epilepsy, possibly through alterations in neurotransmitter receptors or voltage-gated ion channels ([23] and further references therein).

Moreover, numerous reports suggest that immune mechanisms might play a role in processes leading to epileptogenesis [15, 24–32]. In fact, antibodies against neural antigens involved in neurotransmission have been detected in epileptic subjects [33–39], and, remarkably, epilepsy was shown to respond to immunotherapeutic approaches [38, 40, 41]. Finally, population-based cohort studies have documented
that microbial infections during pregnancy may be a risk factor for epilepsy in offspring [42–45].

In such a multifaceted scientific-clinical context, here we analyze the peptide commonality between TT, a powerful neurotoxin used in animal models of experimental epilepsy [46–50], and human antigens that have been related to epilepsy, searching for possible immunological link(s) that might contribute to epileptogenesis. Indeed, a massive peptide overlap characterizes microbial and human proteomes [51–54] and gives grounds for questioning whether immune response(s) to microbial infections might potentially result in cross-reactions against neuronal antigens [55–58]. Pathogen versus human immune cross-reactivity might contribute to the association between microbial infections and neurological syndromes [59] and assumes a special significance during pregnancy in light of the consequent possible neurodevelopmental alterations in the fetus and offspring [26, 58].

We report that the tetanus neurotoxin and human epilepsy antigens share an ample pentapeptide platform. The bacterial versus human peptide overlap is not random and, importantly, a search through the Immune Epitope Database (IEDB; http://www.immuneepitope.org/) reveals that the shared pentapeptides are part of TT-derived epitopes. The latter datum is relevant also in light of the role of pentapeptides as minimal functional units in cell biology and immunology [60, 61]. On the whole, the results support the possibility that immune cross-reactions may occur between TT and epilepsy-related proteins.

2. Methods

TT protein sequence, UniProtKB/Swiss-Prot accession number: P04958, 1315aa long, from Clostridium tetani (NCBI Taxonomic identifier: 212717; further details at http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi) was analyzed for pentapeptide sharing with epilepsy-associated proteins as follows. First, a pentapeptide library was constructed by dissecting the TT primary sequence into pentapeptides offset by one residue, that is, MPITI, PITIN, ITINN, TINNF, INNF, and so forth. Then, each of the final 1311 pentamers was analyzed for instances of the same match within a library consisting of primary sequences of human proteins that, when altered, have been associated with epilepsy. The number of matches and the human proteins sharing matches were recorded.

Epilepsy-associated proteins were randomly retrieved from UniProtKB Database (http://www.uniprot.org/). An unbiased set of proteins that on whatever basis (i.e., differential regulation, protein modification, or mutation) had been involved in or related to epilepsy was obtained utilizing “epilepsy” and “Homo sapiens” as keywords. Only canonical protein sequences were considered. At the time of this study, the keyword-guided search produced a library of 133 human UniProt entries, for a total of 106,022aa. Epilepsy-associated proteins are reported as UniProtKB/Swiss-Prot entry names throughout the paper, unless when discussed in detail. Any pentapeptide occurrence in the set of epilepsy-associated proteins was termed a match.

A set of proteins associated with Down syndrome, a genetic disease in which infectious agents have no role, was retrieved from UniProtKB Database and used as a comparison sample. This set was formed by the following proteins listed according to the aa length, with UniProtKB/SwissProt entries in parentheses: (1) Down syndrome critical region protein 10 (P59022, DSC10), 87aa; (2) Down syndrome critical region protein 8 (Q96775, DSCR8), 97aa; (3) Down syndrome critical region protein 4 (P56555, DSCR4), 118aa; (4) Down syndrome critical region protein 9 (P59020, DSCR9), 149aa; (5) Down syndrome critical region protein 5 or phosphatidylinositol N-acetylglucosaminyltransferase subunit P (P57054, PIGP), 158aa; (6) Down syndrome critical region protein 6 or protein riplly3 (P57055, DSCR6), 190aa; (7) Down syndrome candidate region 1-like 1 or regulator of calcineurin 2 (Q14206, RCAN2), 197aa; (8) Down syndrome candidate region 1-like protein 2 or regulator of calcineurin 3 (Q9UKA8, RCAN3), 241aa; (9) Down syndrome critical region protein 1 or regulator of calcineurin 1 (P53805, RCAN1), 252aa; (10) Down syndrome critical region protein 2 or proteasome assembly chaperone 1 (O95456, PSMG1), 288aa; and (11) Down syndrome critical region protein 3 (O14972, DSCR3), 297aa.

The Immune Epitope Database (IEDB; http://www.immuneepitope.org/) was used to search for TT-derived B- and/or T-cell epitopes that had been experimentally validated as positive in the human host.

Expected occurrences for pentapeptide sharing between C. tetani neurotoxin and human proteins associated with epilepsy were calculated as follows. First, we considered the number of all possible pentapeptides, \( N \). Since each residue can be any of 20aa, the number of all possible pentapeptides \( n \) is given by \( N = 20^5 = 3.2 \times 10^5 \). Next, we considered the TT and epilepsy-associated proteins as two sets of pentapeptide size \( m \) and \( n \). That is, \( m \) is the number of pentapeptides present in the TT protein and \( n \) is the number of pentapeptides present in the epilepsy-associated protein set. If \( X \) is the number of times a pentapeptide is selected in the TT protein of size \( m \) and \( Y \) is the number of times the same pentapeptide is selected in the epilepsy-associated protein set, then \( X = m/N \) and \( Y = n/N \). Assuming that \( X \) and \( Y \) are independent, \( XY = mn/N^2 \). In other words, the expected number of times that one pentapeptide will be selected simultaneously in both TT and epilepsy-related protein set is given by \( mn/N^2 \). Neglecting the relative abundance of aa and assuming \( m \ll N \) and \( n \ll N \), we obtain a formula derived by approximation where the total number of occurrences in a second sample \( n \) (the epilepsy-related protein set) of pentapeptides occurring in the first sample \( m \) (TT) is given by \( mn/N + m/2 \).

3. Results and Discussion

3.1. Description of the Pentapeptide Sharing between TT and Epilepsy-Associated Proteins. Peptide sharing between TT and human epilepsy-associated proteins was analyzed using (1) the pentapeptide module as a matching probe and (2) a library consisting of 133 epilepsy-related protein sequences retrieved from UniProt (see under Methods).
We used pentapeptides as scanning probes in sequence similarity analyses since a grouping of five aa residues may represent a minimal unit of immune recognition in cellular and humoral responses. Indeed, scientific literature indicates that an optimal peptide length for T-cell epitopes ranges between 9 and 15 residues, with the central 5–7 aa representing the specific immune recognition contacts and the flanking residues determining the binding potential to the MHC molecules [62–66]. De facto, the HFMPT pentapeptide was reported to be a minimal antigenic determinant for MHC class I-restricted T lymphocytes [65], while the KYVKQ pentapeptide was demonstrated to be a minimal antigenic determinant for CD4(+) T-cell clones [66]; in addition, the IEDB describes numerous pentapeptide epitopes capable of binding MHC molecules (e.g., epitope IEDB IDs: 5740, 7948, 11514, 25472, and 33701) and inducing T-cell proliferation (e.g., MHC molecules (e.g., epitope IEDB IDs: 5740, 7948, 11514, 25472, and 33701) and inducing T-cell proliferation (e.g., MHC molecules (e.g., epitope IEDB IDs: 5740, 7948, 11514, 25472, and 33701) and inducing T-cell proliferation (e.g., MHC molecules (e.g., epitope IEDB IDs: 5740, 7948, 11514, 25472, and 33701)).

Likewise, humoral immune recognition/reactivity unfolds around short aa motifs ([67–70]; reviewed in [71]). A representative example is a report by Zeng and colleagues [70], according to which the C-terminal pentapeptide (aa sequence: GLRPG) of luteinizing hormone-releasing hormone is a dominant B-cell epitope able to elicit a strong anti-LHRH antibody response and to discriminate between anti-LHRH antibodies present in fertile and nonfertile mice. That is, the pentapeptide GLRPG has immunogenic and antigenic properties and also discriminates antibody specificities associated with reproductive competence.

The analyzed set of 133 human proteins related to epilepsy is listed in Box 1 according to the aa size (i.e., from IR3IP or immediate early response 3-interacting protein 1, 82aa, to GPR98 or monogenic audiogenic seizure susceptibility protein 1 homolog, 6306aa).

Following matching analyses, we found that 42 out of the 133 epilepsy-associated proteins retrieved at random from UniProt database share 58 pentapeptides (68 including multiple occurrences) with the bacterial toxin. Box 2 lists the epilepsy-related proteins that share pentapeptides with TT and the shared pentapeptides. No TT pentapeptide match was found in the comparison set of proteins associated with Down syndrome.

3.2. Nonstochasticity of the Pentapeptide Sharing between TT and Epilepsy-Associated Proteins. The comparative analysis of Boxes 1 and 2 highlights three main points. Firstly, the 68 TT pentapeptide overlap described in Box 2 exceeds the expected value. As detailed under Methods, the expected number of TT pentapeptides that may occur in the epilepsy-related protein set is given by \( mn/N + m/2 \), where \( m \) is the number of pentapeptides contained in TT (1311), \( n \) is the number of pentapeptides contained in the epilepsy-related protein set (105,490), and \( N \) is the number of all possible pentapeptides (\( 20^5 \)). Developing the equation gives 43 as expected number of pentapeptide matches, whereas the observed value is 68 (see Box 2). That is, the pentapeptide overlap between TT and epilepsy-related proteins is 1.58 times higher when compared to the expected one.

A second point of note is that the distribution of the pentapeptide overlap through the epilepsy-related proteins is unexpected. According to equation described above, pentapeptide sharing between two samples is as a quantity directly proportional to the number of pentapeptides in the analyzed samples; that is, it is proportional to the protein aa size. Actually, 91 epilepsy-related proteins are excluded from the pentapeptide matching with TT, independently of their length. For example, SPTNI, 2472aa (see Box 1), has no bacterial matches, while LRRC1, 524aa, shares 3 pentapeptides with TT (Box 2).

In summary, a comparative analysis of Boxes 1 and 2 highlights that 68 TT pentapeptide matches are allocated in 42 out 133 human proteins that have been related, when altered, to epilepsy, and no relationship appears to exist between pentapeptide sharing and the human protein size. Applying the equation described above to the set of 42 epilepsy-related proteins sharing 68 pentapeptides with TT and amounting to 50,254aa, the expected pentapeptide overlap is equal to 20, so that the observed occurrence value is 3.4 times higher.

Finally, a third punctum saliens is that nonrandomness characterizes also the distribution of the TT pentapeptides among the 42 epilepsy-associated proteins. Box 2 shows that a few TT pentapeptides are repeated in the 42 epilepsy-associated protein set. Indeed, TT pentapeptides EILPS, SLSIG, and FCKAL recur twice, and TT pentapeptides FGGQD, KIEIK, and TFLRD occur three times (Box 2; see pentapeptides underlined). Box 2 also shows that MK10 (mitogen-activated protein kinase 10; 464aa); CDKL5 (cyclin-dependent kinase-like 5; 1030aa); and KCM1A1 (calcium-activated potassium channel subunit alpha-1; 1236aa) share two sequentially overlapping pentapeptides with TT, that is, share the hexapeptides SVDDAL, KNSFSE, and PKEIEK, respectively. The nonrandom TT pentapeptide sharing clearly emerges from Figure 1, where expected and observed occurrence values are graphically compared.

It can be seen that, in conflict with the theoretical trend of the TT pentapeptide matching as a function of epilepsy-related protein length (Figure 1, columns in gray), the observed to expected ratio of pentapeptide matching shows no relationship with the human protein length (Figure 1, columns in black). For example, contrary to mathematical expectations, MK10 (464aa long) has three pentapeptide matches, whereas VP13A (3174aa long) has one match (see Box 2 and Figure 1).

3.3. Immunologic Potential of the Pentapeptide Sharing between TT and Epilepsy-Associated Proteins. Having defined the TT versus epilepsy-associated proteins pentapeptide overlap, it was next tested whether such a sharing has an immunologic potential. To this aim we used IEDB, a database that describes B- and T-cell epitopes for humans, nonhuman primates, rodents, and other animal species, and searched for TT-derived epitopes that had been validated as immunopositive in humans. At the time of the search, we obtained a list of 517 TT-derived epitopes. The pentapeptides common to epilepsy-associated proteins and TT (see Box 2, sequences in italic) were used as probes to scan the 517 TT-derived epitope set in order to define potential cross-reactive peptide sequences. Results are reported in Table 1.
Box 1: List of the 133 epilepsy-associated proteins analyzed for TT pentapeptide sharing. Proteins were randomly retrieved from UniProtKB (http://www.uniprot.org/) as described under Methods. Proteins are indicated by UniProtKB/Swiss-Prot entry names, and listed according to increasing aa length reported in parentheses.

Box 2: Peptide sharing between TT and epilepsy-associated proteins. Proteins reported by UniProtKB/Swiss-Prot entry names and listed according to the aa length. Pentapeptides shared with TT are italic in parentheses. Pentapeptides present more than once in the epilepsy antigen set are underlined. Sharing of two consecutively overlapped pentapeptides (i.e., a hexapeptide) is indicated by an asterisk.

Figure 1: Observed versus expected pentapeptide matching between TT and epilepsy-related proteins. The 42 proteins sharing pentapeptides with TT are allocated along the x-axis according to increasing aa length. Gray columns: expected matches calculated according to the formula \( mN + m/2 \), where \( m \) is the number of pentapeptides present in the neurotoxin (1,311) and \( n \) is the number of pentapeptides present in the epilepsy-associated protein (see Methods). For example, in the case of IR3IP protein, 82aa, the possible pentapeptide overlap is equal to 1,311 \( \times 78 / 3,200,000 + 1,311 / 2 \). Black columns: observed to expected ratio of the pentapeptide matching. Observed matching values from Box 2.
In essence, Table 1 shows that all of the 58 pentapeptides common to the 42 epilepsy-associated proteins and TT (Box 2, peptide sequences in parentheses and in italic) are present in 116 TT-derived epitopes that had been established to be immunopositive in humans. This datum indicates a potential vulnerability of the 42 epilepsy-associated proteins to cross-reactions following anti-TT immune responses. Moreover, many TT-derived epitopes share fragments with distinct epilepsy-related proteins and are of particular significance to a multiple cross-reactivity risk, since, for example, an immune response targeting the TT epitope FmnnVF-WLRVPKVsahle (see Table 1, IEDB ID 17207, with shared fragments in capital letter) has the potential to cross-react with the following three crucial proteins related to different forms of epilepsy:

(i) GBRA1 or gamma-aminobutyric acid receptor subunit alpha-1, the major inhibitory neurotransmitter in the vertebrate brain that mediates neuronal inhibition by binding to the GABA/benzodiazepine receptor and opening an integral chloride channel [72],

(ii) SCN8A or voltage-gated sodium channel subunit alpha 1 (GABR1), a protein that mediates the voltage-dependent sodium ion permeability of excitable membranes [73],

(iii) EFHC1 or myocilin-1, a protein that may enhance calcium influx through CACNA1E and stimulate programmed cell death [74].

Such a multiple cross-reactivity potential is shown also by other TT-derived epitopes, eg, epitopes IEDB IDs 30436, 48049, 113407, and so forth.

Also, it seems important to highlight that MK10 (mitogen-activated protein kinase 10, also known as stress-activated protein kinase JNK3 or p493F12 kinase), a protein that shows the highest unexpected level of pentapeptide overlap to ‘TT’ (Figure 1) and also has a high immunologic potential as illustrated in Table 1 (i.e., MK10 pentapeptide(s) are present in 7 TT-derived epitopes), is selectively expressed in a subpopulation of pyramidal neurons in the CA1, CA4, and subiculum regions of the hippocampus, and layers 3 and 5 of the neocortex [75]. That is, there is a potential cross-reactivity risk specifically allocated in brain areas directly linked to epileptogenesis [76,77].

4. Conclusions

This study describes a vast pentapeptide commonality between TT-derived epitopes and epilepsy-associated proteins. This peptide sharing acquires a relevant pathologic potential in light of the fact that pentapeptide modules have the capacity of inducing immune response(s) and are main players in immune recognition [61–71]. Immunologically, two sequences that share a pentapeptide are potentially subject to a cross-reaction [60].

In the disease model examined here, that is, tetanus infection and epilepsy, the ample cross-reactivity platform between TT-derived epitopes and human epilepsy-associated antigens supports the hypothesis of an immune involvement in epilepsy. As a matter of fact, all the 42 epilepsy-related proteins listed in Box 2 are potential targets of cross-reactions (see Table 1). Qualitatively, the peptide overlap occurs in human proteins canonically associated with epilepsy such as gamma-aminobutyric acid receptor subunit alpha-1 (GBRA1), gamma-aminobutyric acid type B receptor subunit 1 (GABRI), sodium channel protein subunits (SCN1A, SCN2A, SCN8A, and SCN9A), and calcium-activated potassium channel subunit alpha-1 (KCMA1) (Table 1). Obviously, an immune attack against such epilepsy-associated proteins may cause alterations to neural structures and functions, especially when the neurodevelopmental intrauterine phase is considered. Being of nonsecondary importance, the non-stochastic character of the peptide overlap between TT and epilepsy-associated proteins (Figure 1) indicates that the potential cross-reactivity extent (and the associated risk of developing epilepsy and neurodevelopmental disorders) will increase with the number of anti-TT immune stimulations.

An additional relevant point is the “antigenic patchwork” shown in Table 1. Indeed, the potential peptide crossreactome involved in different extent and in different combinations of 42 epilepsy-associated proteins might help understand the complex neurobiological network that, on once hit and perturbed, may underlie different epileptic forms [1–9]. Also, it has to be noted that Table 1 includes proteins such as CNTP2 or contactin-associated protein-like 2, RELN or reelin, and TSCI or tuberous sclerosis 1 protein, which are also landmark antigens for autism and the associated impairment in communication/language skills and behaviors [78–81]. Hence, Table 1 may provide a mechanistic framework to allocate the occurrence of epilepsy, intellectual disability, and autism spectrum disorder in patients with tuberous sclerosis complex. Likewise, data from Table 1 might contribute to answering a critical question in neuropsychopathology, that is, the coexistence of patients with combined schizophrenia and epilepsy [82–85]. Indeed, Table 1 substantiates the hypothesis according to which the thread joining epilepsy and schizophrenia may reside in neurodevelopmental molecules such as leucine-rich glioma inactivated (LGI) proteins and GPR98, a G protein-coupled receptor, originally known as VLGRI or very large G protein-coupled receptor [86]. De facto, Table 1 shows that fragments from LGI1, LGI2, and GPR98 are present in 1, 7, and 18 TT-derived epitopes, respectively. In other words, the potential cross-reactivity targeting LGI1, LGI2, and GPR98 following an anti-TT response is high.

Given the caveat that peptide immunoreactivity is influenced by numerous factors, for example, binding affinity [87], cripticity (i.e., determinants embedded in membrane structures do not induce immune responses under physiological conditions) [88], and posttranslational modifications (i.e., citrullination) [89], the present data might contribute to further our understanding of epilepsies. In particular, data from Table 1 might represent a peptide platform to be tested in antibody binding assays using sera from epileptic subjects. Accompanied by parallel immunoassays based on the utilization of epilepsy-related proteins as antigens, such an approach might not only validate the TT-epilepsy link proposed in this study, but also lead to a definition at
| IEDB ID | TT-derived epitope | Immune context | Epilepsy-associated proteins |
|---------|-------------------|----------------|-----------------------------|
| 1270    | afcpeyptfdnieVITSL| HLA-Class II, allele undetermined | ACHA2                      |
| 1389    | afrnVDGSGLV5kilg  | HLA-Class II, allele undetermined | GPR98 D2HDH EPMIP           |
| 1501    | agevqrlFRDlpdkfnayl| HLA-Class II, allele undetermined | CLCN2                      |
| 1929    | ahiyvnnesseVIVHKamdi | HLA-DRB1* 04:01 | CLN5                        |
| 2219    | akkkleleDTSKnilmqyi | HLA-Class II, allele undetermined | SCN8A                      |
| 3156    | amlnlilifpgPVLNKNEV | HLA-Class II, allele undetermined | ASAH1 LRRCI                |
| 3418    | anskfigiteLKKLEskink | HLA-DRB1* 11:01 | TSC1                        |
| 3832    | apsyTNGKLniyyrlyngl | HLA-DRB5* 01:01, HLA-DRB1* 13:01 | WDR62                      |
| 7603    | danLISidkndlyektl | HLA-DRB1* 03:01 | GPR98                      |
| 8734    | dinndisidSGFNSvity | HLA-DRB1* 01:01 | GPR98                      |
| 8778    | disGFSsvitypdaqvpq | HLA-DRB1* 15:01 | GPR98                      |
| /8903   | dksdsvtivpyigPALNv | HLA-DPB1* 04:01, HLA-DRB1* 15:01 | NMDE1                      |
| 9297    | dltfaeKNSFSSeepfqdei | HLA-DRB1* 01:01, HLA-DRB1* 04:01 | CDKL5                      |
| 9595    | DPALLLmheLIHVHglyy | HLA-DR2; HLA-Class II, allele undetermined | AFG32 CLN6 WDR62              |
| 9595    | drLSSANlyingvlmsgasai | HLA-DR2; HLA-Class II, allele undetermined | GPR98                      |
| 10472   | DTQSKnilmqykanfsfigitelLKKLEski | HLA-Class II, allele undetermined | SCN8A TSC1                |
| 11980   | efDTQSKnilmqykanfsfigitel | B-cell | SCN8A                      |
| 13095   | eLIHVLHglygmqvss | HLA-DR2; HLA-Class I, allele undetermined | WDR62                      |
| 13125   | eLKKLEskinkvstkipfes | HLA-Class II, allele undetermined | TSC1                        |
| 13813   | eqdpsaggatscamnlnlifpgpPVLNKNEV | HLA-Class II, allele undetermined | ASAH1 LRRCI                |
| 15087   | eysissmkHSLSIGSgwsvsl | B-cell | PWP2 GP6 CDKL5 RELN           |
| 15411   | fdkdsnGQYIVnedfqiy | HLA-Class II, allele undetermined | PWP2                       |
| 16555   | fiaeKNSFSSeepfqdeivsyn | B-cell | CDKL5                      |
| 17134   | fnaylankwvrITTNDrls | HLA-Class II, allele undetermined | NHLC1                      |
| 17205   | fnnftVSFWLVRPK | HLA-Class II, allele undetermined | GBRA1 SCN8A                |
| 17206   | fnnftVSFWLVRPKvahle | HLA-DR3 | GBRA1 SCN8A EFHC1           |
| 17207   | fnnftVSFWLVRPKvahle | HLA-DRB1* 11:01, HLA-DR, HLA-DR1, HLA-DR5, HLA-DR7, HLA-DR11, HLA-DPw4, HLA-Class II, allele undetermined | GBRA1 SCN8A EFHC1           |
| 17208   | fnnftVSFWLVRPKvahleqy | HLA-DRB1* 01:01, HLA-DRB1* 04:01, HLA-DRB1* 07:01, HLA-DRB1* 11:01 | GBRA1 SCN8A EFHC1           |
| 17487   | fqlynSIMYGFTElglkk | HLA-Class II, allele undetermined | SL9A6 SL9A9 LGII            |
| 18217   | fveysGDFKLlvsynnnheivgy | B-cell | EFHC2 CNTP2                |
| 18356   | fwlRVPKvahleqytne | HLA-DRB1* 11:01 | SCN8A EFHC1                |
| 19469   | gevqiTRFDlpdkfnaylkw | B-cell | CLCN2                      |
| 21599   | gpdkqiadeinnlknKLEEkan | B-cell | ARHG9                      |
| 22769   | gtneysissmkHSLSIGS | DQB1* 06:02, DRB5* 01:01 | PWP2 GP6 CDKL5             |
| 24238   | hLKDKIlgcdwylvpdtogwtn | HLA-Class II, allele undetermined | ROGD1                      |
| 25597   | idkisvdstivpyiPALNI | HLA-Class II, allele undetermined | NMDE1                      |
| 25666   | idsflsGDFIKlyvsyn | HLA-DRB1* 15:01 | EFHC2 CNTP2                |
| 26808   | iriknedltaeelKNSFSSe | HLA-Class II, allele undetermined | CDKL5                      |
| 27639   | ingkaihvnnesseVIVHK | HLA-Class II, allele undetermined | CLN5                        |
| IEDB ID | TT-derived epitope | Immune context       | Epilepsy-associated proteins |
|---------|--------------------|----------------------|-----------------------------|
| 29241   | ivdylnqskTLPNDrttpv | HLA-Class II, allele undetermined | GPR98 |
| 29331   | ivkQGYEGnfg        | HLA-Class II, allele undetermined | TSEAR |
| 29407   | ivpyigPALNlv       | HLA-Class II, allele undetermined | NMDE1 |
| 29408   | ivpyigPALNv        | HLA-DRB1*15:01        | NMDE1 TSEAR |
| 29843   | KAKWgtvntqKRSYQ    | HLA-Class II, allele undetermined | LGI2 WDR62 |
| 29891   | kamdiyenNDMEFnftVSFWLRvp | B-cell       | SCNA9 GBA1 |
| 30269   | kdVQLKNitdymntnapsy| HLA-DRB1* 01:01, HLA-DRB1* 04:01 | GPR98 |
| 30436   | KEIEKyltySLSITFLRDPwgnp | B-cell       | CSMD3 KCMA1 GCP6 GTR1 SCNA1A SCNA2A SCNA8A CLCN2 |
| 30572   | keqiadeinlnkKLEEkan| HLA-Class II, allele undetermined | ARHG9 |
| 32521   | knidymntnapsyTNGKL | HLA-Class II, allele undetermined | WDR62 |
| 32546   | knldcwvdneEDIValkstil | B-cell       | GABR1 |
| 33527   | kstilNinndiidiSGFNs | B-cell       | GPR98 |
| 34301   | kwierKLVKAKWgtvntq | HLA-DRB1* 01:01 | ARHGA LGI2 |
| 34887   | lambdaVfTTNDrLSSANlyin | B-cell       | NHLC1 GPR98 |
| 35058   | lcikINnedfiaeKNFNS | HLA-DRB1* 04:01 | CDKL5 |
| 35566   | lekryekwierKLVKAKWL | HLA-Class II, allele undetermined | ARHGA LGI2 |
| 35993   | lhfFGQDAnLISDkndl  | HLA-Class II, allele undetermined | SCNA1A SCNA2A SCNA8A GPR98 |
| 36667   | lipvasskdVQLKNitdym | HLA-DRB1* 11:01 | GPR98 |
| 38977   | krrMTNVSDDAlnstkiki | HLA-Class II, allele undetermined | VP13A MK10 |
| 40770   | lygmqssshEIIPSkieym | HLA-Class II, allele undetermined | ACHA2 ACHA4 |
| 41527   | mfnfRVSFWRVPKVvsash | HLA-DRB1* 11:01 | GBA1 SCNA8A EFHC1 |
| 42847   | mtnSVDDAlnstkkiyysyp | HLA-DRB1* 11:01 | MK10 |
| 43280   | napsyTNGKlniyrrylnglf | B-cell       | WDR62 |
| 43519   | nndrvLSSANvingvlnmsae | HLA-Class II, allele undetermined | GPR98 |
| 43591   | neEDIValkstilndin | HLA-Class II, allele undetermined | GABR1 |
| 43939   | nftVSFWRVPKV | HLA-Class II, allele undetermined | GBA1 SCNA8A |
| 43940   | nftVSFWRVPKVvsashle | HLA-DRB1* 11:01 | GBA1 SCNA8A EFHC1 |
| 44007   | ngkaihvlnnesseVIVHKamdi | B-cell       | CLN5 |
| 44396   | nivkQGYEGnfi      | HLA-Class II, allele undetermined | TSEAR |
| 44200   | niddntiyqyqaSkPSTTL | HLA-DRB1* 01:01 | SL9A6 |
| 44383   | NTSLtigkskqyqDAPALL | HLA-Class II, allele undetermined | ACHA2 AFG32 CLN6 |
| 44557   | NKEVrgivrvndknfypc | HLA-Class II, allele undetermined | LRRC1 |
| 44667   | nlidmiiidisSGFNssvi | HLA-Class II, allele undetermined | GPR98 |
| 45102   | nnnfVSFWRVPKVvsahle | HLA-Class II, allele undetermined | GBA1 SCNA8A EFHC1 |
| 46136   | ntiyqyqaSkPSTTLqrit | HLA-Class II, allele undetermined | SL9A6 |
| 46853   | PALLLmheLHVLHlglygmq | HLA-Class II, allele undetermined | CLN6 WDR62 |
| 46855   | PALNivkQGYEGnfgalet | HLA-Class II, allele undetermined | NMDE1 TSEAR |
| 48049   | PKEIEKyltySLSITFLRDF | HLA-Class II, allele undetermined | GCP6 CSMD3 KCMA1 GTR1 SCNA1A SCNA2A SCNA8A CLCN2 |
| 48697   | pnrnliasnyfnhlKDKIIgc | B-cell       | ROGDI |
| 49984   | pvrkGIPyApeyksaastteih | B-cell       | CBPA6 |
| 51254   | qkSPPTTLrITMTNVSDDAlnsp | B-cell       | SL9A6 VP13A MK10 |
| 56528   | ryekwierKLVKAKWLgtvntq | B-cell       | ARHGA LGI2 |
| 57935   | sfvksGDFKlyvssnymneh | HLA-Class II, allele undetermined | EFHC2 CNTP2 |
| 57947   | sfwLRVPKVvsahle | HLA-DR5, HLA-DRB1* 11:01 | SCNA8A EFHC1 |
| 58527   | SIGSGwsvslgmnliwtlk | HLA-DRB1* 03:01 | RELN |
| 59500   | SLTLlelgelcikikn | HLA-Class II, allele undetermined | LRRC1 |
the molecular level of the repeatedly advanced association between antibodies and epilepsy [33–41]. Moreover, of not less importance, immunoassay validation could also represent a prelude to specific therapies based on peptide modules able to block epileptogenic anti-TT autoantibodies [38–41, 90]. Immunological research in this direction has been programmed in our lab.

Conflict of Interests

The authors declare that there is no conflict of interests regarding the publication of this paper.

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References

[1] C. D. Ferrie, "Idiopathic generalized epilepsies imitating focal epilepsies," *Epilepsia*, vol. 46, no. 9, pp. 91–95, 2005.
[2] E. C. Wirrell, B. R. Grossardt, E. L. So, and K. C. Nickels, "A population-based study of long-term outcomes of cryptogenic focal epilepsy in childhood: cryptogenic epilepsy is NOT probably symptomatic epilepsy," *Epilepsia*, vol. 52, no. 4, pp. 738–745, 2011.
[3] A. T. Berg, “Epilepsy, cognition, and behavior: the clinical picture,” *Epilepsia*, vol. 52, supplement 1, pp. 7–12, 2011.

[4] U. Stephani, “The natural history of myoclonic atonic epilepsy (Doose syndrome) and Lennox-Gastaut syndrome,” *Epilepsia*, vol. 47, supplement 2, pp. 53–55, 2006.

[5] C. J. Chu-Shore, P. Major, S. Camposano, D. Musykewicz, and E. A. Thiele, “The natural history of epilepsy in tuberous sclerosis complex,” *Epilepsia*, vol. 51, no. 7, pp. 1236–1241, 2010.

[6] N. Gaspard and L. J. Hirsch, “Pitfalls in ictal EEG interpretation: critical care and intracranial recordings,” *Neurology*, vol. 80, supplement 1, pp. S26–S42, 2013.

[7] A. T. Berg, S. F. Berkovic, M. J. Brodie et al., “Revised terminology and concepts for organization of seizures and epilepsies: report of the ILAE Commission on Classification and Terminology, 2005–2009,” *Epilepsia*, vol. 51, no. 4, pp. 676–685, 2010.

[8] C. P. Panayiotopoulos, “The new ILAE report on terminology and concepts for the organization of epilepsies: critical review and contribution,” *Epilepsia*, vol. 53, no. 3, pp. 399–404, 2012.

[9] G. Avanzini, “A sound conceptual framework for an epilepsy classification is still lacking,” *Epilepsia*, vol. 51, no. 4, pp. 720–722, 2010.

[10] R. Ottman, J. F. Annegers, N. Risch, W. A. Hauser, and M. Susser, “Relations of genetic and environmental factors in the etiology of epilepsy,” *Annals of Neurology*, vol. 39, no. 4, pp. 442–449, 1996.

[11] X. Wang and Y. Lu, “Genetic etiology of new forms of familial epilepsy,” *Frontiers in Bioscience*, vol. 13, no. 8, pp. 3159–3167, 2008.

[12] M. J. Martínez, M. A. López-Ariztegui, N. Puente, I. Rubio, and M. I. Tejada, “CDKL5 gene status in female patients with epilepsy and Rett-like features: two new mutations in the catalytic domain,” *BMC Medical Genetics*, vol. 13, article 68, 2012.

[13] A. Vezzani, J. French, T. Bartfai, and T. Z. Baram, “The role of inflammation in epilepsy,” *Nature Reviews Neurology*, vol. 7, no. 1, pp. 31–40, 2011.

[14] Y. Takahashi, K. Matsuda, Y. Kubota et al., “Vaccination virus,” *Handbook of Clinical Neurology*, vol. 111, pp. 521–531, 2013.

[15] J. E. Libbey and R. S. Fujinami, “Neurotropic viral infections leading to epilepsy: focus on Thelier’s murine encephalomyelitis virus,” *Future Virology*, vol. 6, no. 11, pp. 1339–1350, 2011.

[16] T. Bozzi, S. Casarosa, and M. Caleo, “Epilepsy as a neurodevelopmental disorder,” *Frontiers in Psychiatry*, vol. 3, article 19, 2012.

[17] P. Sgadò, M. Dunleavy, S. Genovesi, G. Provenzano, and Y. Bozzi, “The role of GABAergic system in neurodevelopmental disorders: a focus on autism and epilepsy,” *International Journal of Physiology, Pathophysiology and Pharmacology*, vol. 3, no. 3, pp. 223–235, 2011.

[18] R. Tuchman and M. Cuccaro, “Epilepsy and autism: neurodevelopmental perspective,” *Current Neurology and Neuroscience Reports*, vol. 11, no. 4, pp. 428–434, 2011.

[19] R. J. Hagerman, “Epilepsy drives autism in neurodevelopmental disorders,” *Developmental Medicine and Child Neurology*, vol. 55, no. 2, pp. 101–102, 2013.

[20] A. M. van Eeghen, M. B. Pulsifer, V. L. Merker et al., “Understanding relationships between autism, intelligence, and epilepsy: a cross-disorder approach,” *Developmental Medicine and Child Neurology*, vol. 55, no. 2, pp. 146–153, 2013.

[21] S. N. Rakhade and F. E. Jensen, “Epileptogenesis in the immature brain: emerging mechanisms,” *Nature Reviews Neurology*, vol. 5, no. 7, pp. 380–391, 2009.

[22] A. M. van Eeghen, M. B. Pulsifer, V. L. Merker et al., “Understanding relationships between autism, intelligence, and epilepsy: a cross-disorder approach,” *Developmental Medicine and Child Neurology*, vol. 55, no. 2, pp. 146–153, 2013.

[23] S. N. Rakhade and F. E. Jensen, “Epileptogenesis in the immature brain: emerging mechanisms,” *Nature Reviews Neurology*, vol. 5, no. 7, pp. 380–391, 2009.

[24] A. M. van Eeghen, M. B. Pulsifer, V. L. Merker et al., “Understanding relationships between autism, intelligence, and epilepsy: a cross-disorder approach,” *Developmental Medicine and Child Neurology*, vol. 55, no. 2, pp. 146–153, 2013.

[25] S. N. Rakhade and F. E. Jensen, “Epileptogenesis in the immature brain: emerging mechanisms,” *Nature Reviews Neurology*, vol. 5, no. 7, pp. 380–391, 2009.
[39] C. I. Akman, M. C. Patterson, A. Rubinstein, and R. Herzog, “Limbic encephalitis associated with anti-GAD antibody and common variable immune deficiency,” Developmental Medicine and Child Neurology, vol. 51, no. 7, pp. 563–567, 2009.

[40] E. Krastinova, M. Vigneron, P. Le Bras, J. Gascual, and C. Goujard, “Treatment of limbic encephalitis with anti-glioma-inactivated 1 (LGII) antibodies,” Journal of Clinical Neuroscience, vol. 19, no. 11, pp. 1580–1582, 2012.

[41] A. M. L. Quek, J. W. Britton, A. McKeon et al., “Autoimmune epilepsy: clinical characteristics and response to immunotherapy,” Archives of Neurology, vol. 69, no. 5, pp. 582–593, 2012.

[42] M. Nørgaard, V. Ehrenstein, R. B. Nielsen, L. S. Bakketeig, and G. Lucchese, A. Stufano, and D. Kanduc, “Proposing low-

[43] M. Sedigh-Sarvestani, G. I. Thuku, S. Sunderam et al., “Rapid eye movement sleep and hippocampal theta oscillations precede seizure onset in the tetanus toxin model of temporal lobe epilepsy,” The Journal of Neuroscience, vol. 25, no. 11, pp. 1865–1871, 2005.

[44] M. Otte, P. Bielefeld, R. M. Dijkhuizen, and K. P. J. Braun, “Focal neocortical epilepsy affects hippocampal volume, shape, and structural integrity: a longitudinal MRI and immunohistochemistry study in a rat model,” Epilepsia, vol. 53, no. 7, pp. 1264–1273, 2012.

[45] M. Sedigh-Sarvestani, G. I. Thuku, S. Sunderam et al., “Rapid eye movement sleep and hippocampal theta oscillations precede seizure onset in the tetanus toxin model of temporal lobe epilepsy,” The Journal of Neuroscience, vol. 34, no. 4, pp. 1105–1114, 2014.

[46] D. Kanduc, A. Stufano, G. Lucchese, and A. Kusluk, “Massive peptide sharing between viral and human proteins,” Peptides, vol. 29, no. 10, pp. 1755–1766, 2008.

[47] G. Lucchese, A. Stufano, M. Calabro, and D. Kanduc, “Charting the peptide crosstalk between HIV-1 and the human proteome,” Frontiers in Bioscience, vol. 3, no. 4, pp. 1385–1400, 2011.

[48] B. Trost, G. Lucchese, A. Stufano, M. Bickis, A. Kusluk, and D. Kanduc, “No human protein is exempt from bacterial motifs, not even one,” Self/Nonself, vol. 1, no. 4, pp. 328–334, 2010.

[49] G. Lucchese, A. Stufano, and D. Kanduc, “Proposing low-similarity peptide vaccines against mycobacterium tuberculosis,” Journal of Biomedicine and Biotechnology, vol. 2010, Article ID 832341, 8 pages, 2010.

[50] S. L. Bavaro, M. Calabrò, and D. Kanduc, “Pentapeptide sharing between Corynebacterium diphtheria toxin and the human neural protein network,” Immunopharmacology and Immunotoxicology, vol. 33, no. 2, pp. 360–372, 2011.

[51] D. Kanduc, “Describing the hexapeptide identity platform between the influenza A H5N1 and Homo sapiens proteomes,” Biologics, vol. 4, pp. 245–261, 2010.

[52] R. Ricco and D. Kanduc, “Hepatitis B virus and homo sapiens proteomewide analysis: a profusion of viral peptide overlaps in neuron-specific human proteins,” Biologics: Targets and Therapy, vol. 4, pp. 75–81, 2010.

[53] G. Lucchese, G. Capone, and D. Kanduc, “Pentapeptide sharing between influenza A H1N1 hemagglutinin and human axon guidance proteins,” Schizophrenia Bulletin, vol. 40, no. 2, pp. 362–375, 2014.

[54] A. Hoshino, M. Sai toh, A. Oka et al., “Epidemiology of acute encephalopathy in Japan, with emphasis on the association of viruses and syndromes,” Brain & Development, vol. 34, no. 5, pp. 337–343, 2012.

[55] D. Kanduc, “Homology, similarity, and identity in peptide epitope immunodefinition,” Journal of Peptide Science, vol. 18, no. 8, pp. 487–494, 2012.

[56] D. Kanduc, “Pentapeptides as minimal functional units in cell biology and immunology,” Current Protein & Peptide Science, vol. 14, no. 2, pp. 111–120, 2013.

[57] D. B. Sant’Angelo, E. Robinson, C. A. Janeway Jr., and L. K. Denzin, “Recognition of core and flanking amino acids of MHC class II-bound peptides by the T cell receptor,” European Journal of Immunology, vol. 32, no. 9, pp. 2510–2520, 2002.

[58] J. B. Rothbard and M. L. Gefter, “Interactions between immunogenic peptides and MHC proteins,” Annual Review of Immunology, vol. 9, pp. 527–565, 1991.

[59] J. B. Rothbard, R. M. Pemberton, H. C. Bodmer, B. A. Askonas, and W. R. Taylor, “Identification of residues necessary for clonally specific recognition of a cytotoxic T cell determinant,” The EMBO Journal, vol. 8, no. 8, pp. 2321–2328, 1989.

[60] M. J. Reddehase, J. B. Rothbard, and U. H. Koszinowski, “A pentapeptide as minimal antigenic determinant for MHC class I-restricted T lymphocytes,” Nature, vol. 337, no. 6208, pp. 651–653, 1989.

[61] B. Hemmer, T. Kondo, B. Gran et al., “Minimal peptide length requirements for CD4+ T cell clones—implications for molecular mimicry and T cell survival,” International Immunology, vol. 12, no. 3, pp. 375–383, 2000.

[62] K. S. Turner and J. van der Scheer, “On the serological specificity of peptides. III,” The Journal of Experimental Medicine, vol. 69, no. 5, pp. 705–719, 1939.

[63] G. Lucchese, A. Stufano, M. Calabro, and D. Kanduc, “Computational peptide dissection of Melan-a/MART-1 oncoprotein antigenicity,” Peptides, vol. 25, no. II, pp. 1865–1871, 2004.

[64] S. Tanabe, “Epitope peptides and immunotherapy,” Current Protein & Peptide Science, vol. 8, no. 1, pp. 109–118, 2007.

[65] W. Zeng, J. Pagnon, and D. C. Jackson, “The C-terminal pentapeptide of LH/HRH is a dominant B cell epitope with antigenic and biological function,” Molecular Immunology, vol. 44, no. 15, pp. 3724–3731, 2007.

[66] G. Lucchese, A. Stufano, B. Trost, A. Kusluk, and D. Kanduc, “Peptidology: short amino acid modules in cell biology and immunology,” Amino Acids, vol. 33, no. 4, pp. 703–707, 2007.

[67] P. Cossette, L. Liu, K. Brisebois et al., “Mutation of GABRA1 in an autosomal dominant form of juvenile myoclonic epilepsy,” Nature Genetics, vol. 31, no. 2, pp. 184–189, 2002.
[73] K. R. Veeramah, J. E. O’Brien, M. H. Meisler et al., “De novo pathogenic SCN8A mutation identified by whole-genome sequencing of a family quartet affected by infantile epileptic encephalopathy and SUDEP,” *American Journal of Human Genetics*, vol. 90, no. 3, pp. 502–510, 2012.

[74] T. Suzuki, A. V. Delgado-Escueta, K. Aguan et al., “Mutations in *EFHC1* cause juvenile myoclonic epilepsy,” *Nature Genetics*, vol. 36, no. 8, pp. 842–849, 2004.

[75] A. A. Mohit, J. H. Martin, and C. A. Miller, “p493F12 kinase: a novel MAP kinase expressed in a subset of neurons in the human nervous system,” *Neuron*, vol. 14, no. 1, pp. 67–78, 1995.

[76] C. E. Stafstrom, “The role of the subiculum in epilepsy and epileptogenesis,” *Epilepsy Currents*, vol. 5, no. 4, pp. 121–129, 2005.

[77] K. Sendrowski and W. Sobaniec, “Hippocampus, hippocampal sclerosis and epilepsy,” *Pharmacological Reports*, vol. 65, no. 3, pp. 555–565, 2013.

[78] C. Toma, L. Hervás, B. Torrico et al., “Analysis of two language-related genes in Autism: a case-control association study of FOXP2 and CNTNAP2,” *Psychiatric Genetics*, vol. 23, no. 2, pp. 82–85, 2013.

[79] T. D. Folsom and S. H. Fatemi, “The involvement of Reelin in neurodevelopmental disorders,” *Neuropharmacology*, vol. 68, pp. 122–135, 2013.

[80] E. Romano, C. Michetti, A. Caruso, G. Laviola, and M. L. Scattoni, “Characterization of neonatal vocal and motor repertoire of reelin mutant mice,” *PLoS ONE*, vol. 8, no. 5, Article ID e64407, 2013.

[81] S. Jeste, M. Sahin, P. Bolton, G. Ploubidis, and A. Humphrey, “Characterization of autism in young children with tuberous sclerosis complex,” *Journal of Child Neurology*, vol. 23, no. 5, pp. 520–525, 2008.

[82] D. C. Taylor, “Schizophrenias and epilepsies: why? When? How?,” *Epilepsy and Behavior*, vol. 4, no. 5, pp. 474–482, 2003.

[83] P. Qin, H. Xu, T. M. Laursen, M. Vestergaard, and P. B. Mortensen, “Risk for schizophrenia and schizophrenia-like psychosis among patients with epilepsy: population based cohort study,” *British Medical Journal*, vol. 331, no. 7507, pp. 23–25, 2005.

[84] Y.-T. Chang, P.-C. Chen, I.-J. Tsai et al., “Bidirectional relation between schizophrenia and epilepsy: a population-based retrospective cohort study,” *Epilepsia*, vol. 52, no. 11, pp. 2036–2042, 2011.

[85] M. C. Clarke, A. Tanskanen, M. O. Huttunen, M. Clancy, D. R. Cotter, and M. Cannon, “Evidence for shared susceptibility to epilepsy and psychosis: a population-based family study,” *Biological Psychiatry*, vol. 71, no. 9, pp. 836–839, 2012.

[86] N. G. Cascella, D. J. Schretlen, and A. Sawa, “Schizophrenia and epilepsy: is there a shared susceptibility?” *Neuroscience Research*, vol. 63, no. 4, pp. 227–235, 2009.

[87] A. Sette, A. Vitiello, B. Reherman et al., “The relationship between class I binding affinity and immunogenicity of potential cytotoxic T cell epitopes,” *Journal of Immunology*, vol. 153, no. 12, pp. 5586–5592, 1994.

[88] K. D. Moudgil and E. E. Sercarz, “Understanding crypticity is the key to revealing the pathogenesis of autoimmunity,” *Trends in Immunology*, vol. 26, no. 7, pp. 355–359, 2005.

[89] P. Eggleton, R. Haigh, and P. G. Winyard, “Consequence of neoantigenicity of the ‘altered self’,” *Rheumatology*, vol. 47, no. 5, pp. 567–571, 2008.

[90] D. Kanduc, “Peptide cross-reactivity: the original sin of vaccines,” *Frontiers in Bioscience*, vol. 4, pp. 1393–1401, 2012.