

GENETICA (parte 2)

Biomarcatori Genetici nelle Epilessie Idiopatiche

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Epilessie & “*Biomarcatori*” Genetici

“*Outline*”:

- ❖ “Epilessie Mendeliane”
- ❖ Canalopatie ed oltre ...
- ❖ Epilessie complesse
- ❖ Identificazione di “*Biomarcatori*” Genetici

Biomarcatore Genetico

- Definizione -

Si definisce **biomarcatore genetico** ogni *variante genetica (mutazione o polimorfismo)* correlata con l'insorgenza, lo sviluppo, la prognosi e/o la risposta alla terapia (farmacoresistenza) di una determinata malattia.

Epileptogenicity

- ❖ Refers to the **presence and severity** of an epilepsy condition
- ❖ **Goal:** To identify persistent, dynamic disturbances that indicate the presence of epileptogenicity and its severity
- ❖ **Tool:** Genetic, molecular, physiologic, and anatomic understanding of the epileptogenic abnormality

Epileptogenesis

- ❖ Refers to the **development and progression** of an epilepsy condition
- ❖ **Goal:** To identify persistent, dynamic disturbances that predict epileptogenesis
- ❖ **Tool:** Tracking the processes identified as underlying epileptogenesis

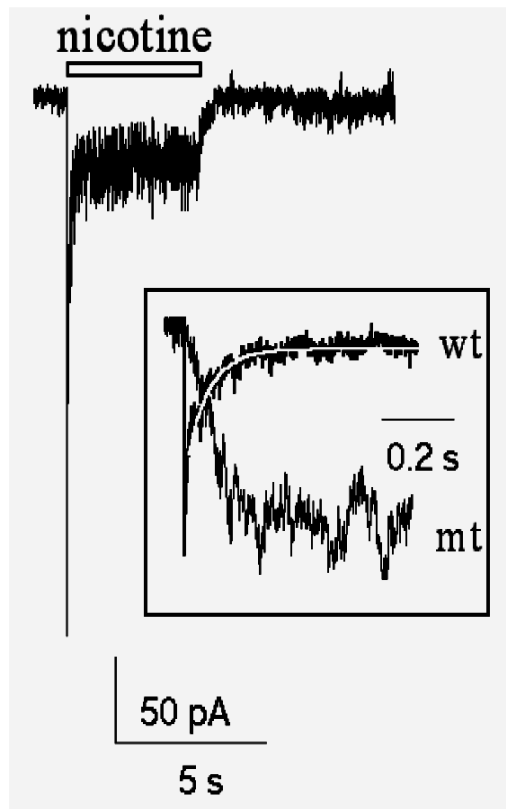
Genes for Monogenic Epileptic *Channelopathies*

Gene	Syndrome	Year of discovery
CHRNA4	ADNFLE	1995
KCNQ2	BFNS	1998
KCNQ3	BFNS	1998
SCN1B	GEFS ⁺	1998
SCN1A	GEFS ⁺ /SMEI	2000/(01)
CHRNA2	ADNFLE	2000
GABRG2	CAE/FS/GEFS ⁺	2001
SCN2A	GEFS ⁺ /BFNIS	2001/02
GABRA1	ADJME, CAE	2002/06
CLCN2	IGE	2003
CHRNA2	ADNFLE	2006
HCN2	IGE	2011
KCNT1	ADNFLE/MMPSI	2012
GRIN2A (NMDAR)	BECTS → LKS/ESES	2013

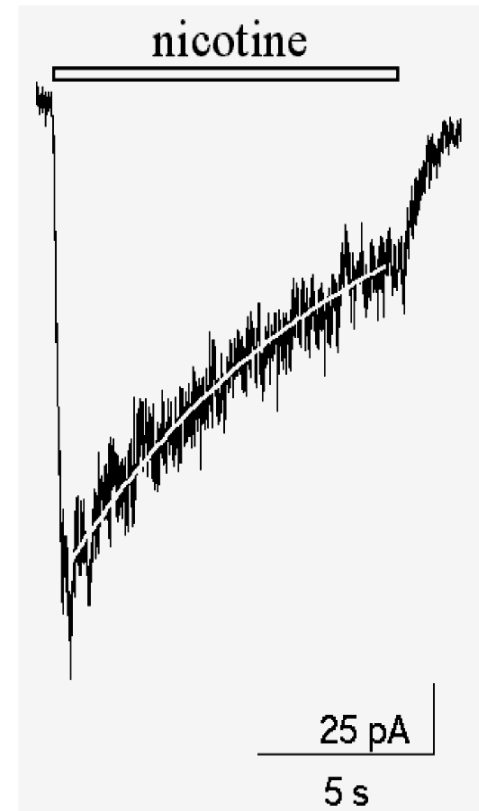
Non Ion-Channel Genes for Monogenic Idiopathic Epilepsies

Gene	Syndrome	Year of discovery
<i>LGI1</i>	ADLTLE	2002
<i>EFHC1</i>	JME	2004
<i>SLC2A1</i>	Early onset AE, IGE, GLUT1 deficiency	2009
<i>PRRT2</i>	BFIS/PKD	2011-'12
<i>DEPDC5</i>	FFEVF	2013
<i>DEPDC5</i>	FFEVF/Focal Epilepsies	2013
<i>STX1B</i>	Fever-associated epilepsy syndromes	2014

Electrophysiology of **wt** and **mutant** nicotinic receptors



wt



mutant

2013; 369:1502-1511

Clinical Whole-Exome Sequencing for the Diagnosis of Mendelian Disorders

Yang Y, Muzny DM, Reid JG, Bainbridge MN, Willis A, Ward PA, Braxton A, Beuten J, Xia F, Niu Z, Hardison M, Person R, Bekheirnia MR, Leduc MS, Kirby A, Pham P, Scull J, Wang M, Ding Y, Plon SE, Lupski JR, Beaudet AL, Gibbs RA, Eng CM.

Whole-exome sequencing identified the underlying genetic defect in **25%** of consecutive patients referred for evaluation of a possible genetic condition.

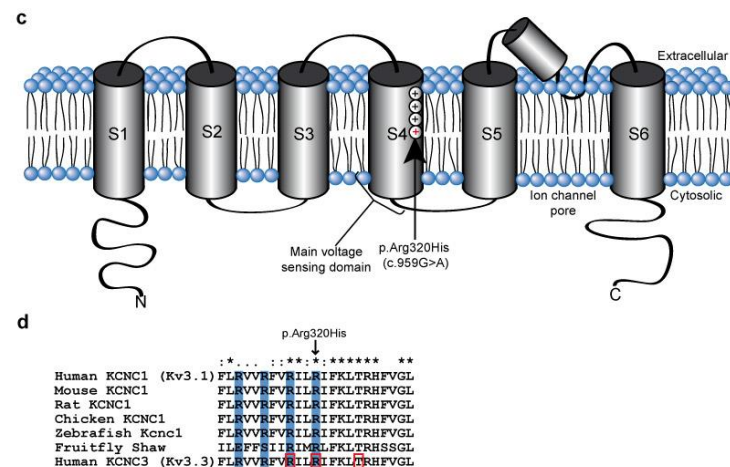
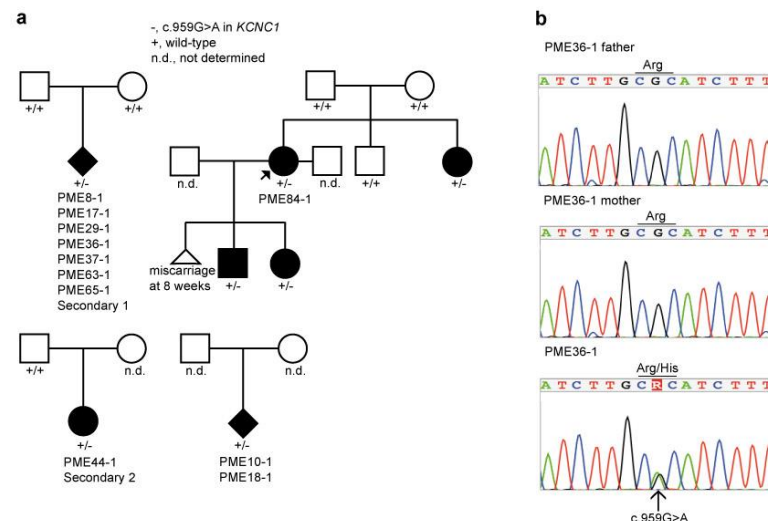
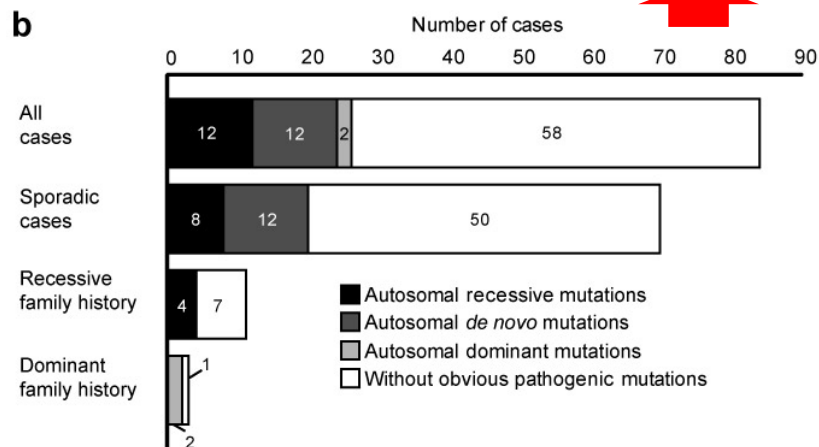
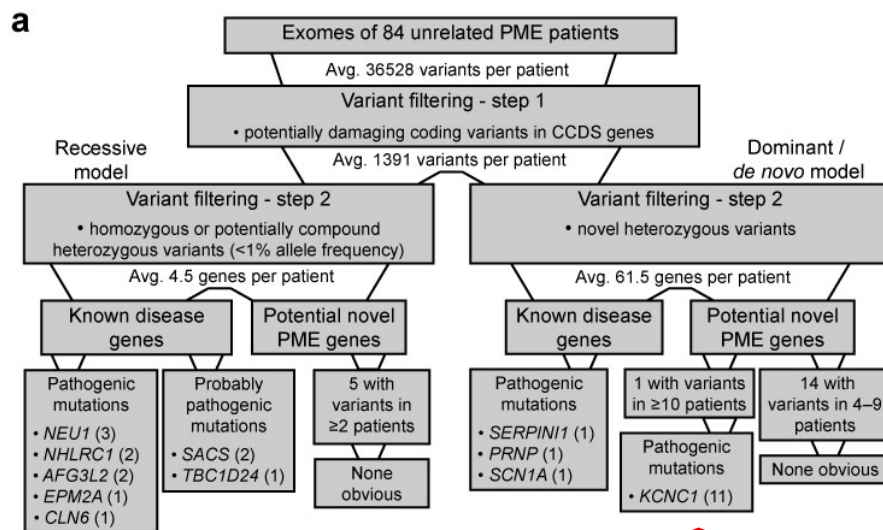


Table 5. Inheritance Pattern and Medical Presentation of Patients with Established Molecular Diagnosis.

Primary Phenotype Category	No. of Patients Tested	Positive Diagnosis					Rate of Positive Diagnosis (95% CI)
		Autosomal Dominant Trait	Autosomal Recessive Trait	X-Linked Trait	Two Traits	Total	

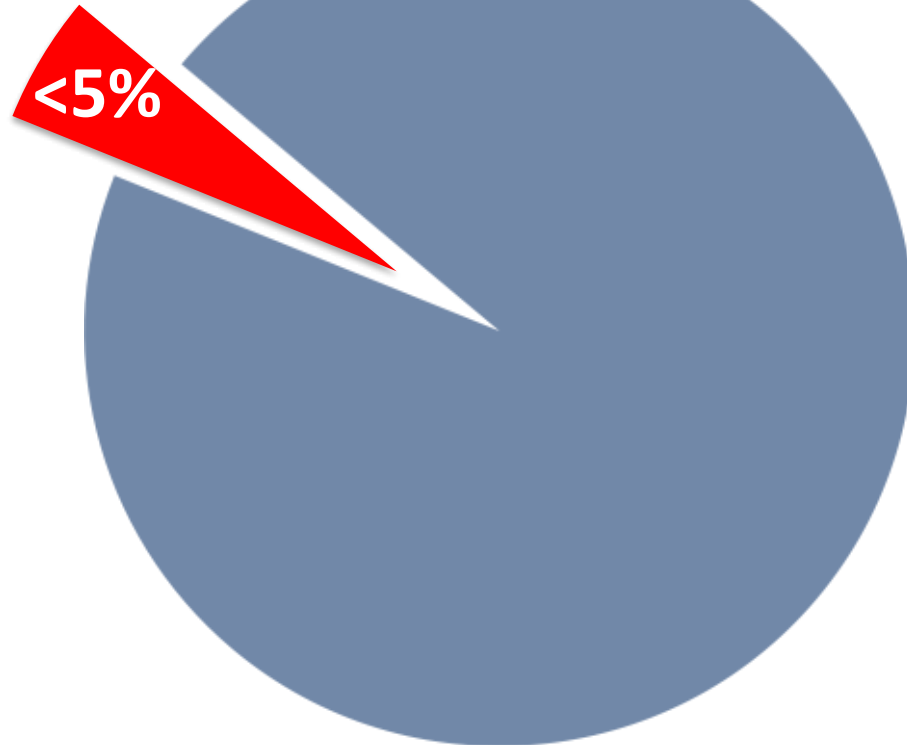
A recurrent *de novo* mutation in KCNC1 is a major cause of progressive myoclonus epilepsy

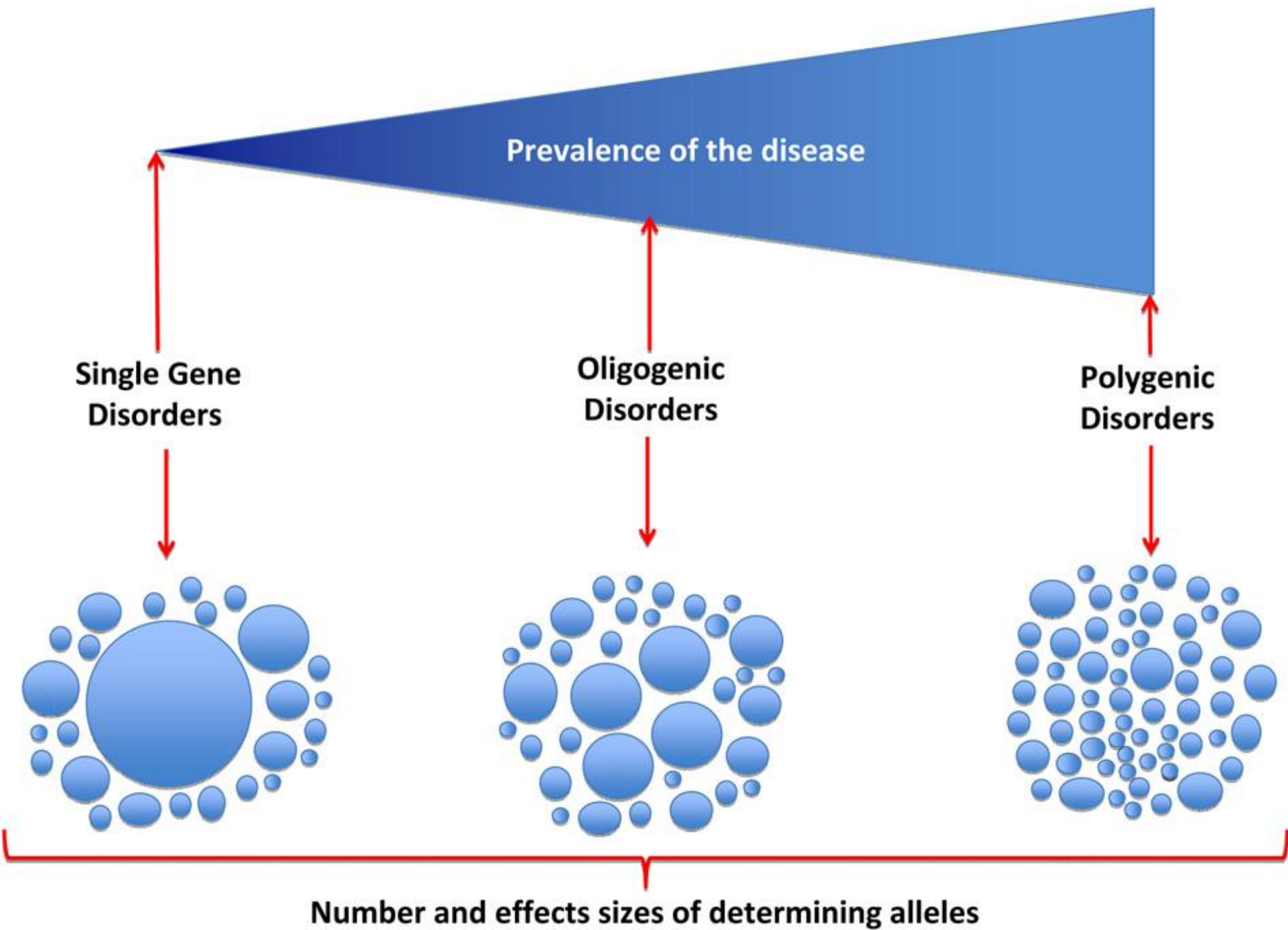
Muona M, Berkovic S, Dibbens L, Oliver K, Maljevic S, Bayly M, Joensuu T, Canafoglia L, Franceschetti S, Michelucci R, Markkinen S, Heron S, Hildebrand M, Andermann E, Andermann F, Gambardella A, Tinuper P, Licchetta L, Scheffer I, Criscuolo C, Filla A, Ferlazzo E, Ahmad J, Ahmad A, Baykan B, Said E, Topçu M, Riguzzi P, King M, Ozkara C, Andrade D, Engelsen B, Crespel A, Lindenau M, Lohmann E, Saletti V, Massano J, Privitera M, Espay A, Kauffmann B, Duchowny M, Steensbjerre Moller S, Straussberg S, Afawi Z, Ben-Zeev B, Samocha K, Daly M, Petrou S, Lerche H, Palotie A.



Prevalence of Epilepsies & Genetics

Monogenic
epilepsies

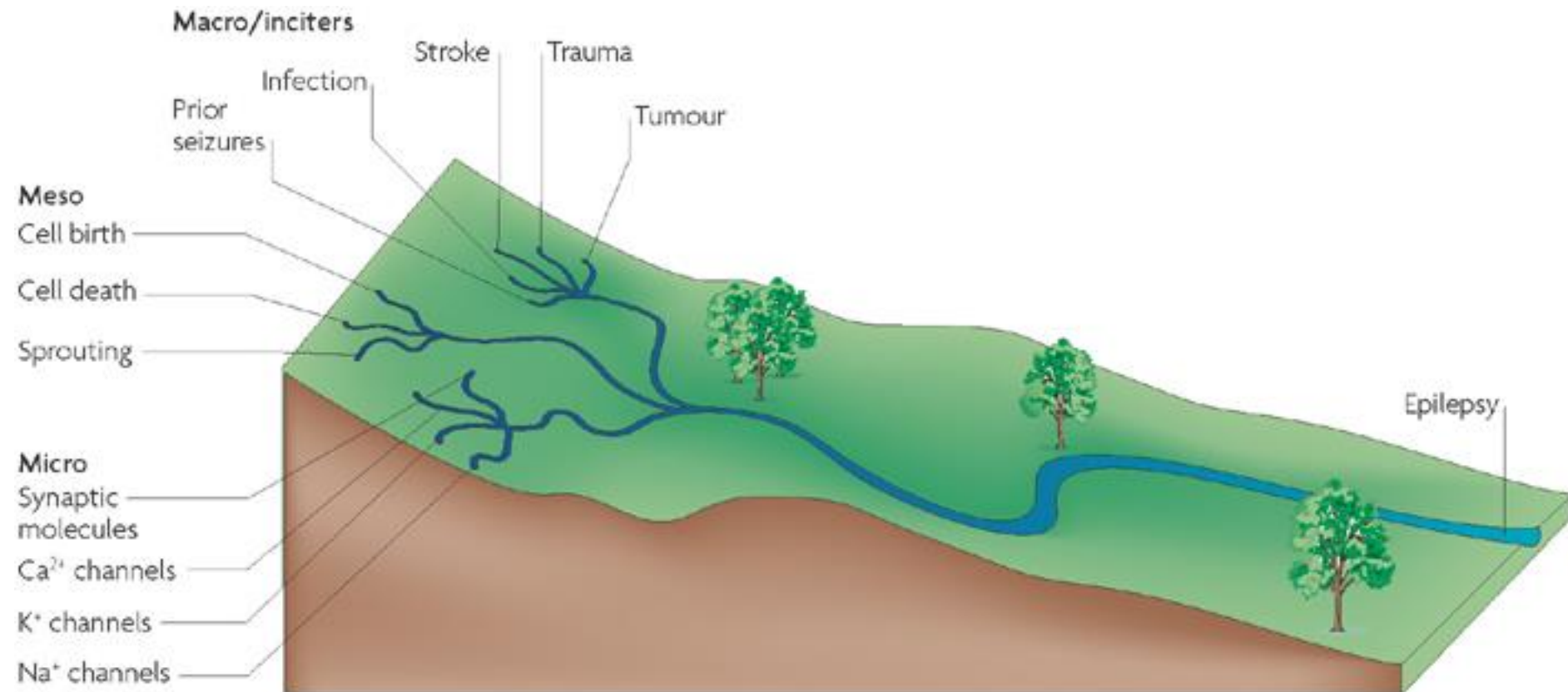




Sporadic epilepsy

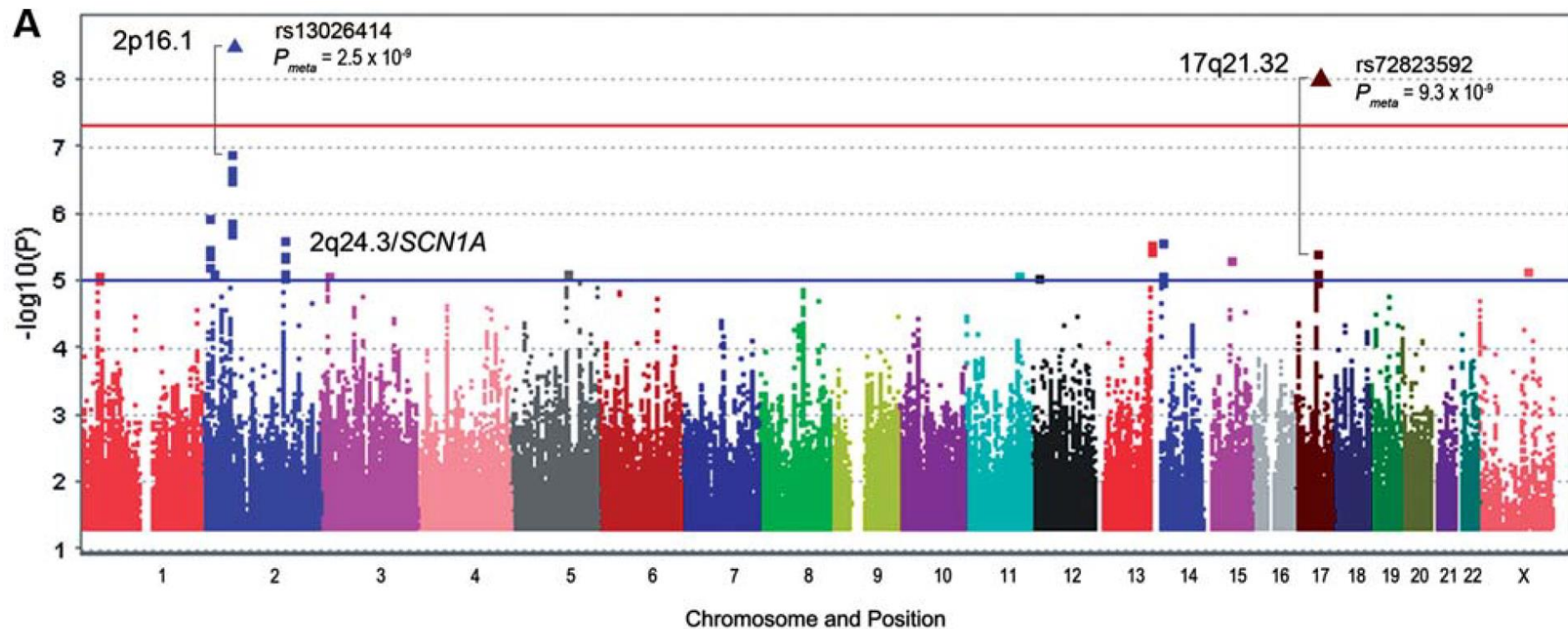
Polygenic/multifactorial disorder

The river of epilepsy (Lennox, 1950)



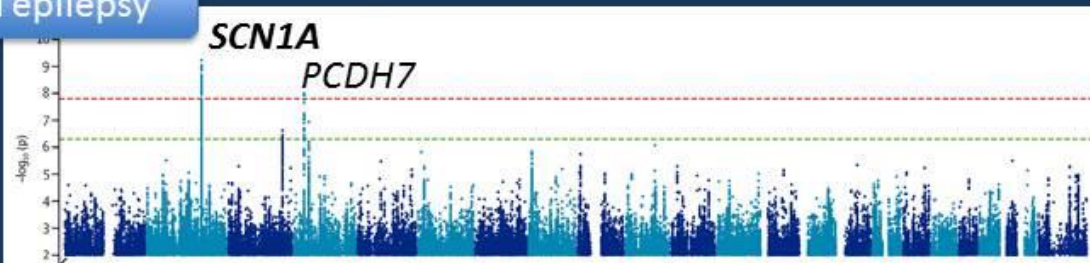
Genome-wide association analysis of genetic generalized epilepsies implicates susceptibility loci at 1q43, 2p16.1, 2q22.3 and 17q21.32.

EPICURE Consortium; EMINet Consortium, Steffens M, Leu C, Ruppert AK, Zara F, Striano P, Robbiano A, Capovilla G, Tinuper P, Gambardella A, Bianchi A, La Neve A, Crichton G, de Kovel CG, Kasteleijn-Nolst Trenité D, de Haan GJ, Lindhout D, Gaus V, Schmitz B, Janz D, Weber YG, Becker F, et al.

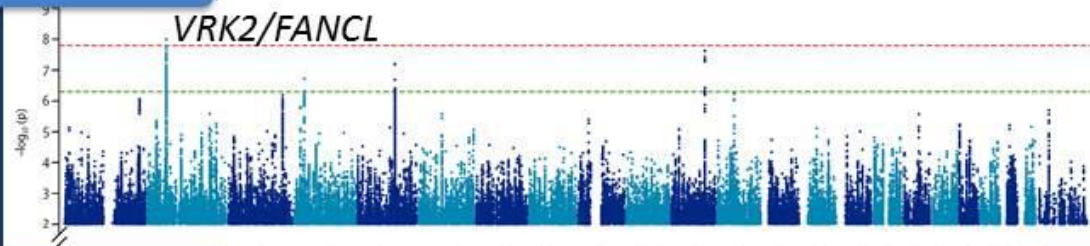


The ILAE Consortium genome-wide association study

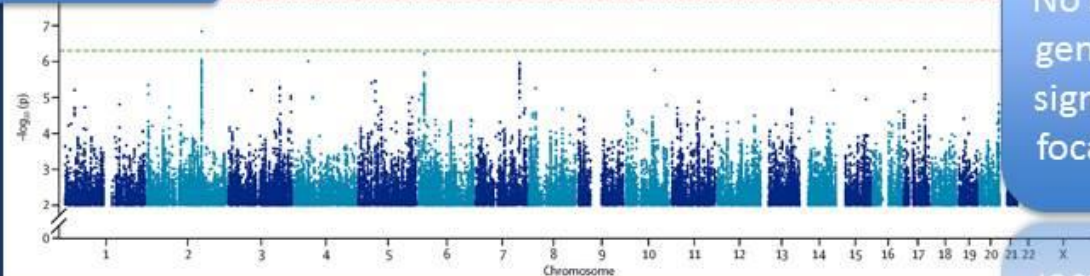
All epilepsy



IGE/GGE



Focal epilepsy

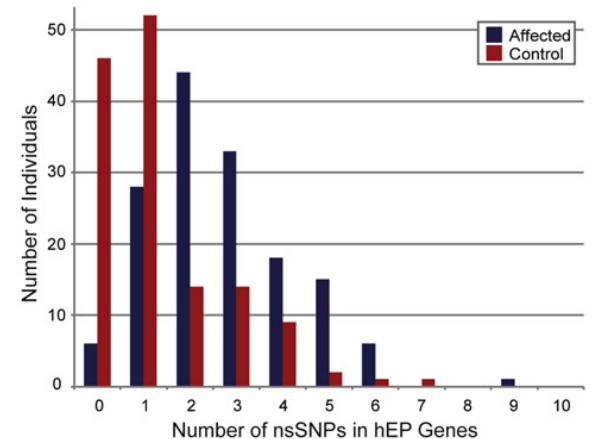
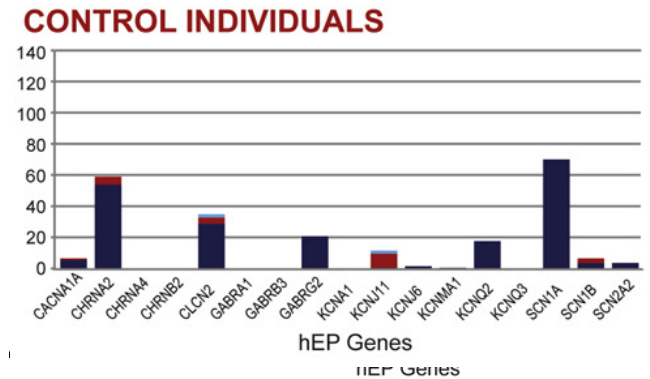
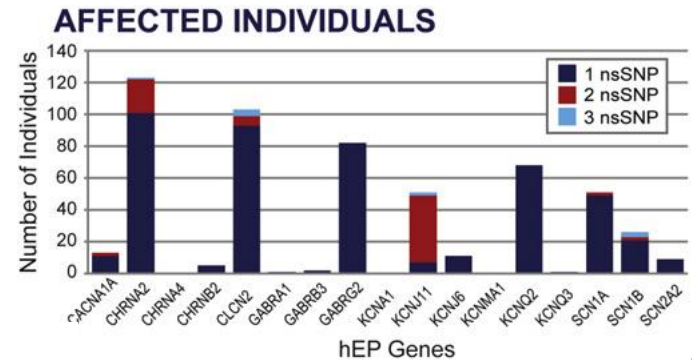
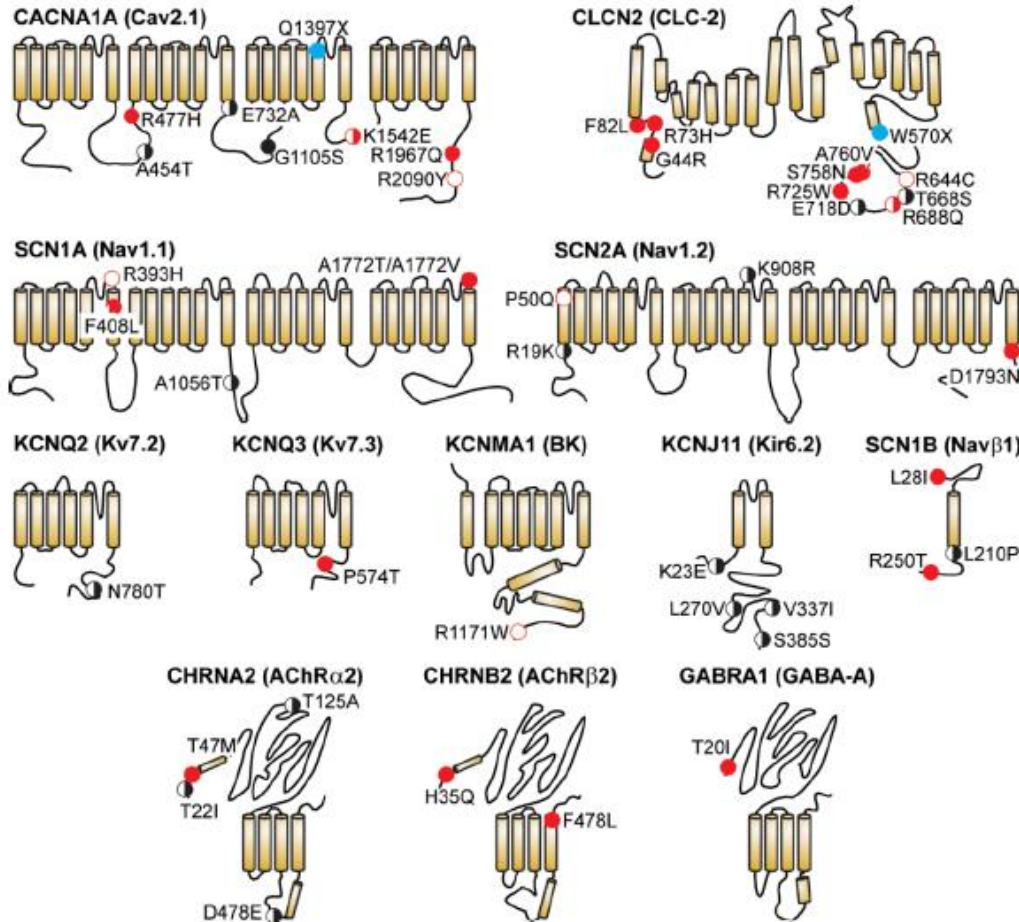


No signal with genome-wide significance in focal epilepsy

Exome sequencing of ion channel genes reveals complex profiles confounding personal risk assessment in epilepsy.

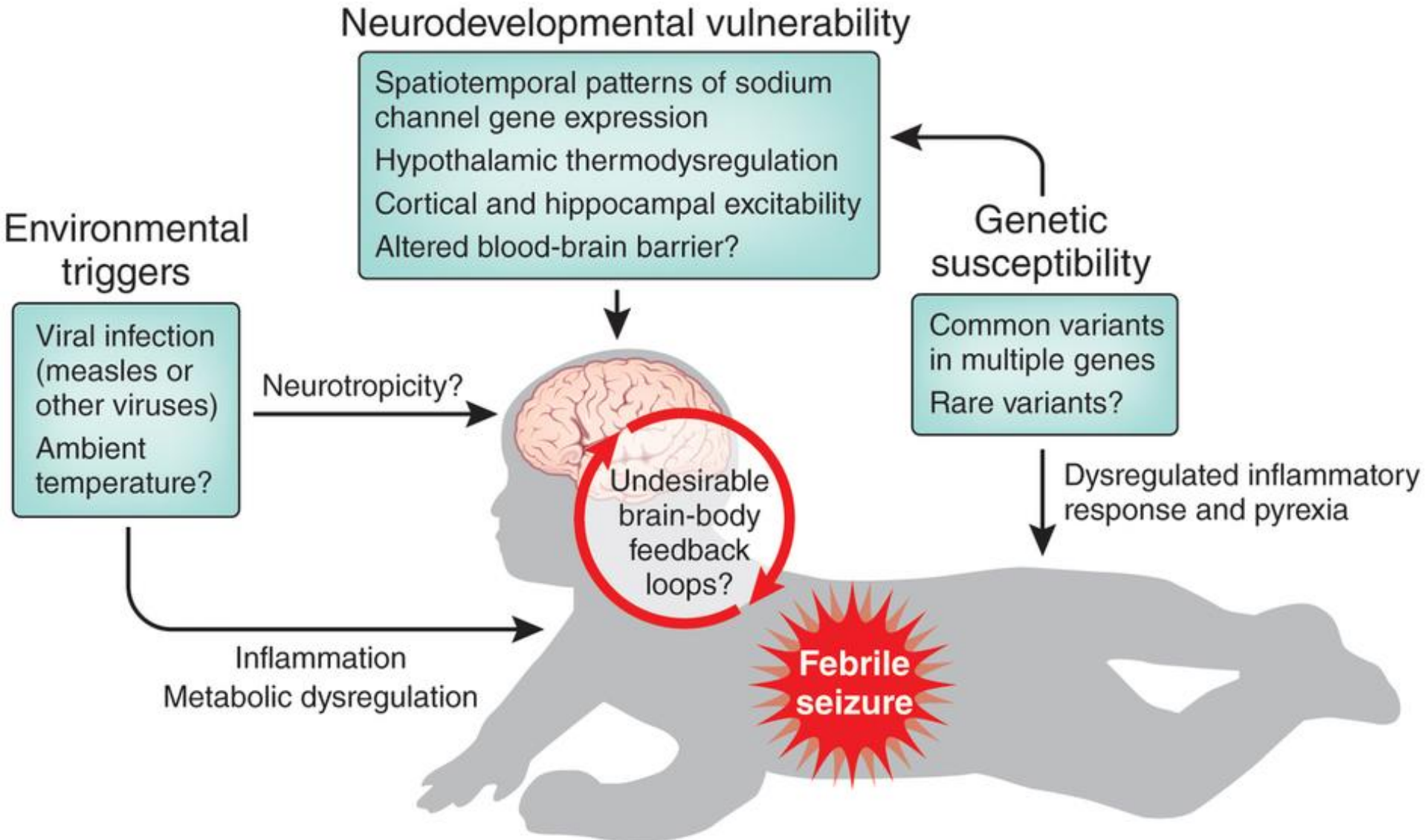
Klassen T, Davis C, Goldman A, Burgess D, Chen T, Wheeler D, McPherson J, Bourquin T, Lewis L, Villasana D, Morgan M, Muzny D, Gibbs R, Noebels J.

2011; 145: 1036–48



Feverish prospects for seizure genetics

Sanjay Sisodiya

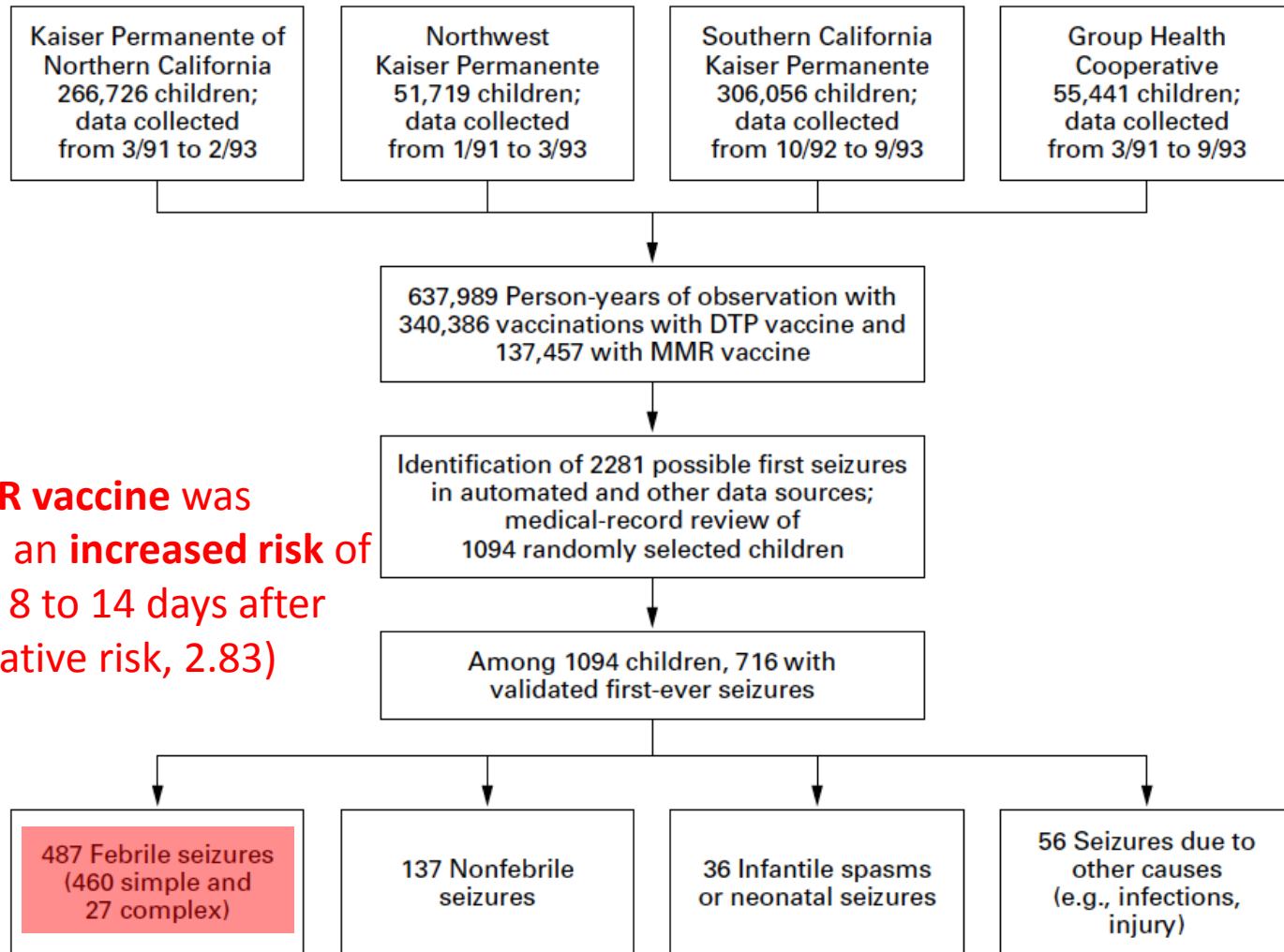




The risk of seizures after receipt of whole-cell pertussis or measles, mumps, and rubella vaccine.

Barlow WE, Davis RL, Glasser JW, Rhodes PH, Thompson RS, Mullooly JP, Black SB, Shinefield HR, Ward JI, Marcy SM, DeStefano F, Chen RT, Immanuel V, Pearson JA, Vadheim CM, Rebolledo V, Christakis D, Benson PJ, Lewis N; Centers for Disease Control and Prevention Vaccine Safety Datalink Working Group.

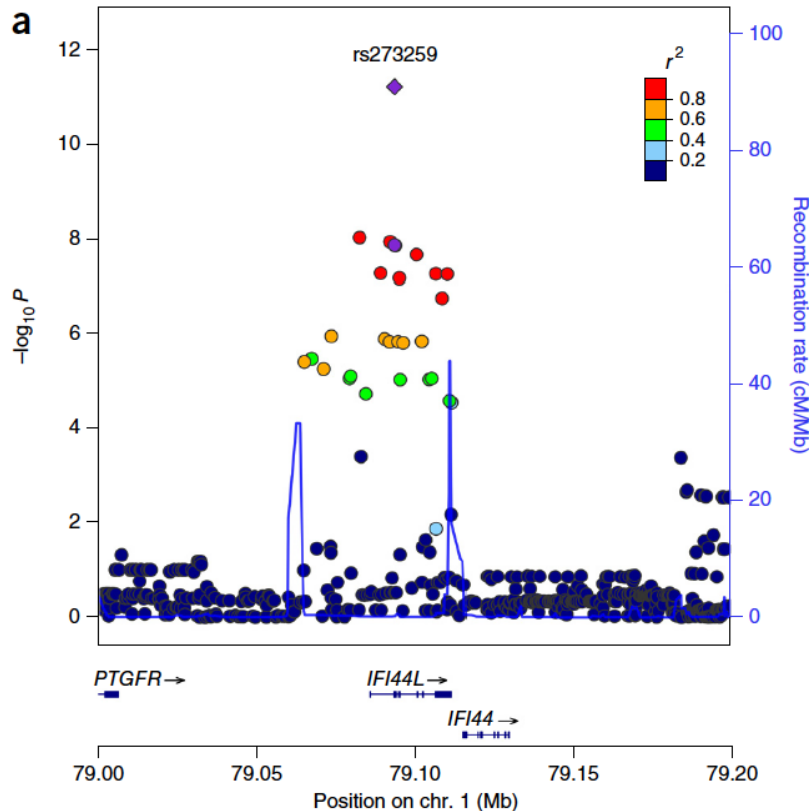
2001; 345:656-61.



Receipt of MMR vaccine was associated with an increased risk of febrile seizures 8 to 14 days after vaccination (relative risk, 2.83)

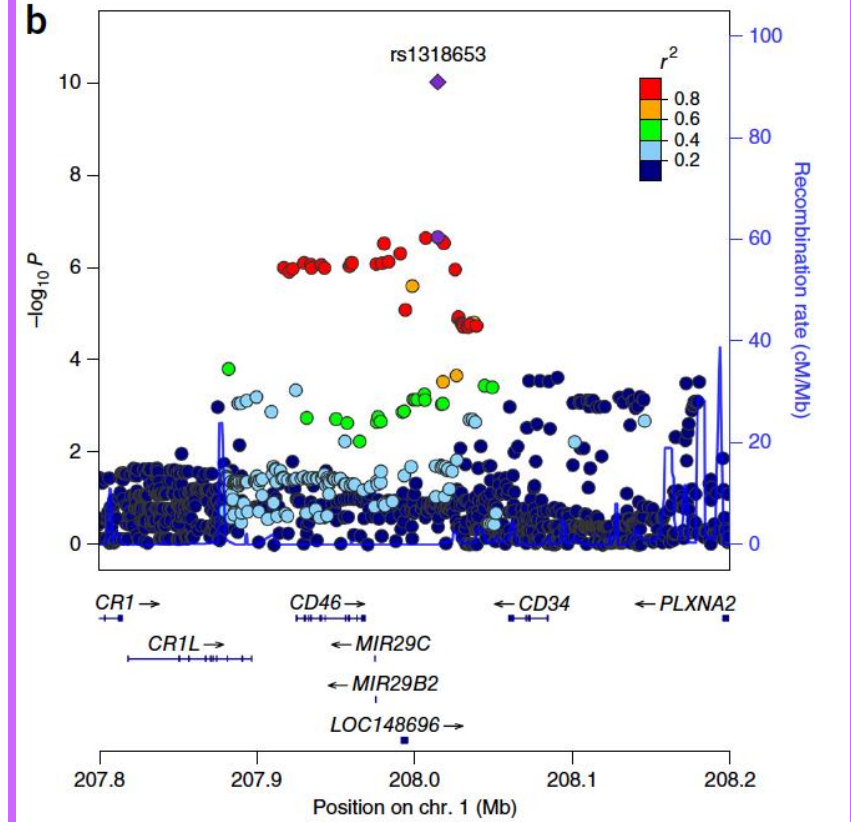
MMR-related febrile seizures

First locus on chromosome 1p31.1



The gene *IFI44L* belongs to the group of interferon-stimulated genes

Second locus on chromosome 1q32.2



The gene *CD46* encodes a membrane protein of the complement system

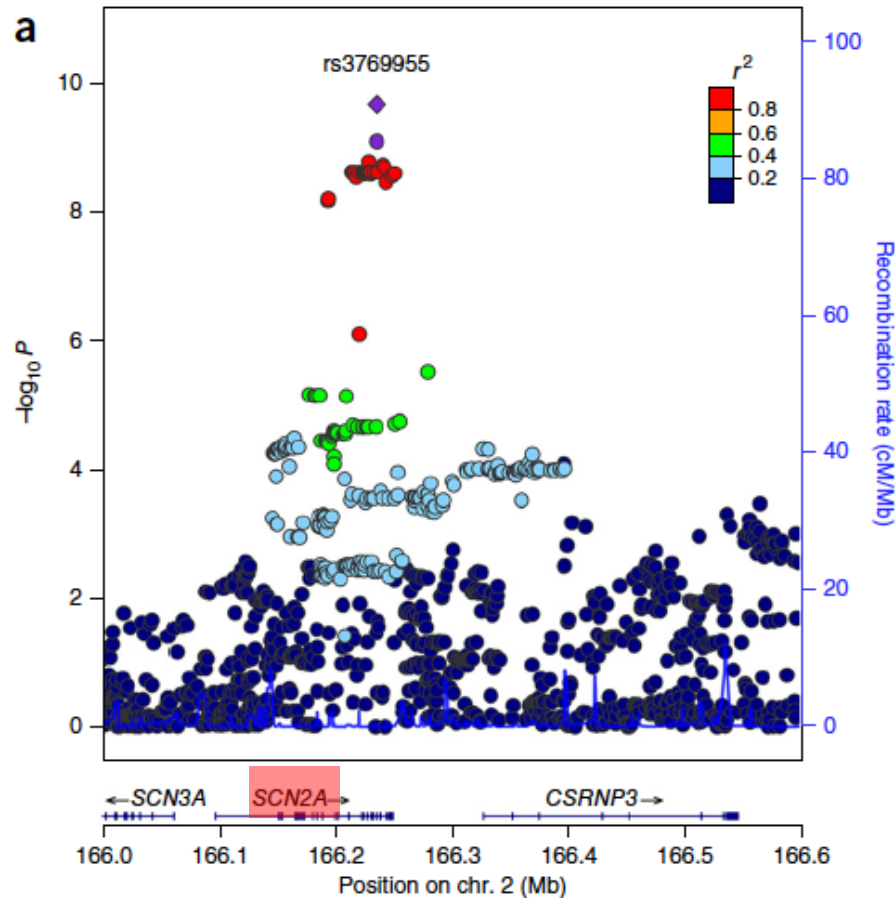
Common variants associated with general and MMR vaccine-related febrile seizures.

2014;46:1274-82

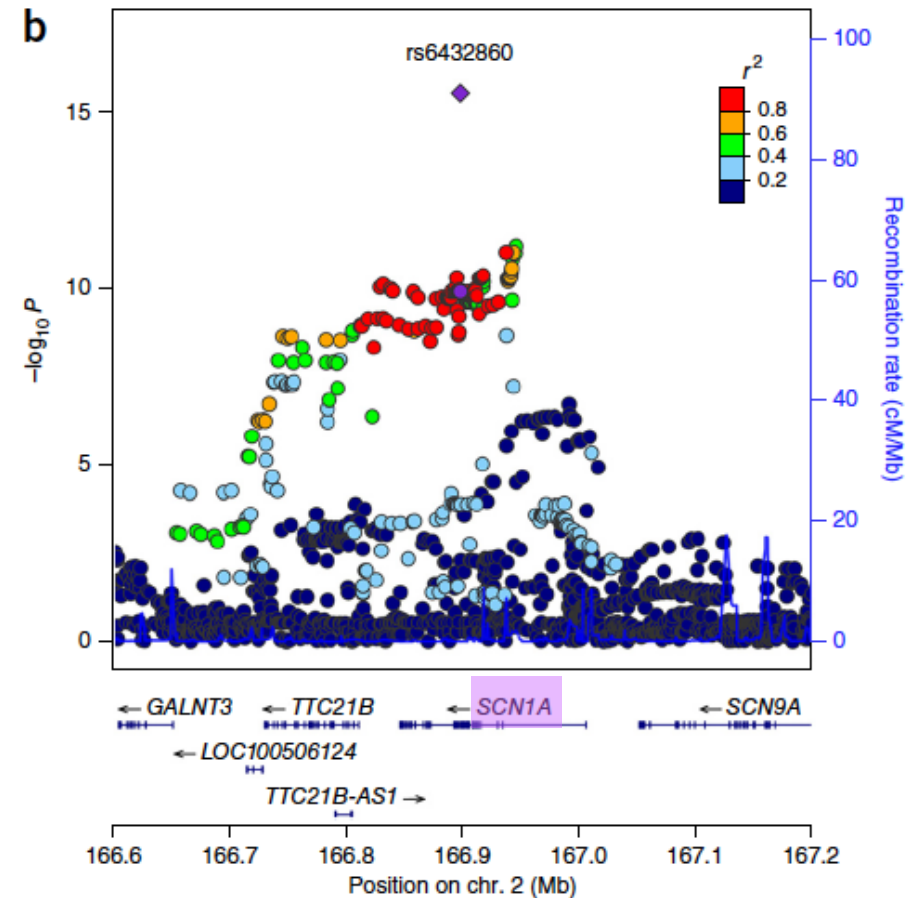
Feenstra B, Pasternak B, Geller F, Carstensen L, Wang T, Huang F, Eitson JL, Hollegaard MV, Svanström H, Vestergaard M, Hougaard DM, Schoggins JW, Jan LY, Melbye M, Hviid A.

MMR-*unrelated* febrile seizures

First locus on chromosome 2q24.3

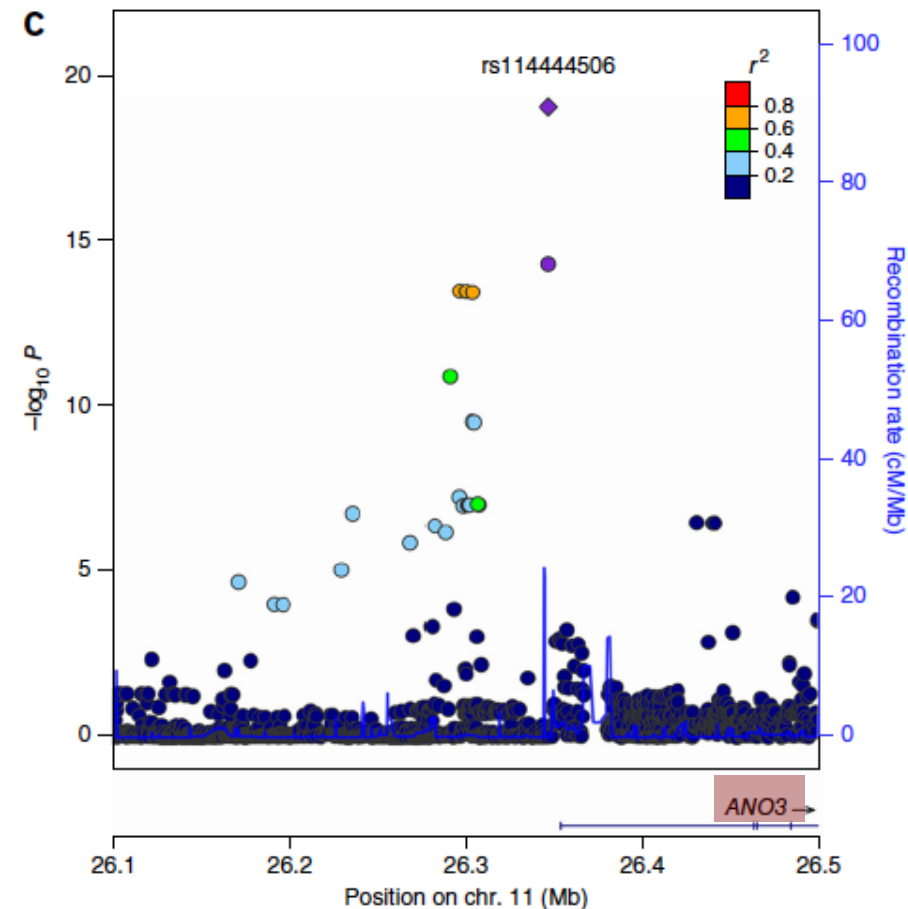


Second locus on chromosome 2q24.3

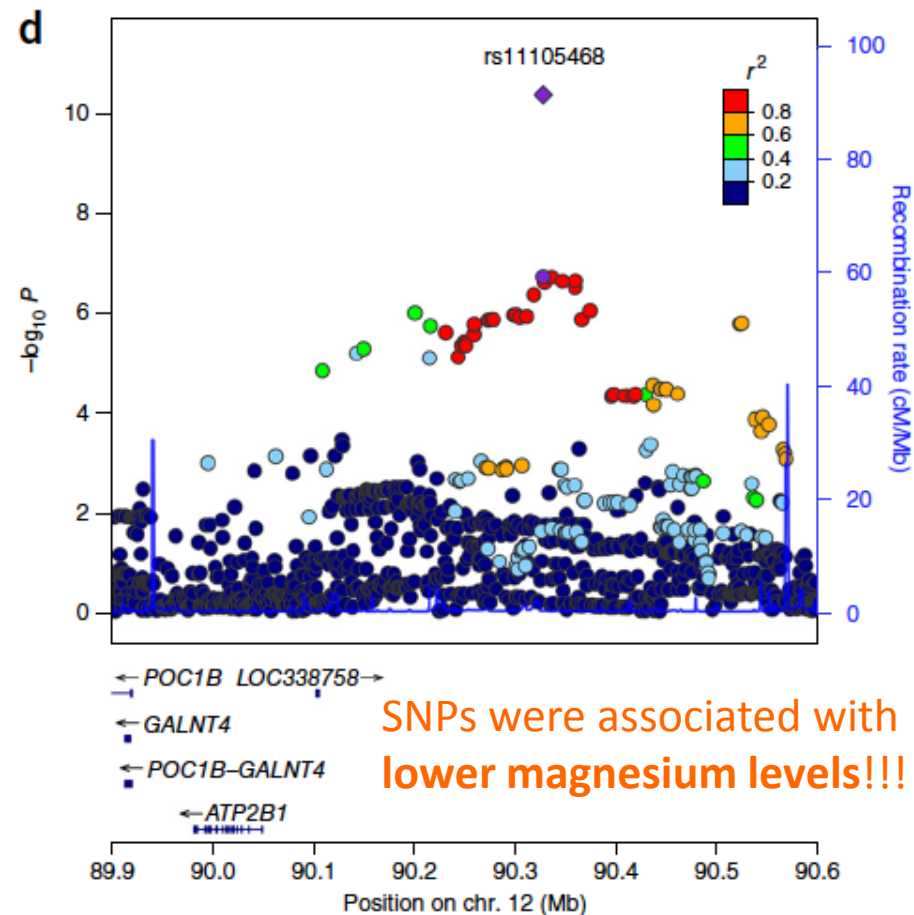


MMR-*unrelated* febrile seizures

Third locus on chromosome 11p14.2



Fourth locus on chromosome 12q21.33



Frequency of *HLA* alleles in patients with Stevens-Johnson syndrome:

Table 1 **Frequency of *HLA* alleles in patients with Stevens–Johnson syndrome**

<i>HLA</i> allele	CBZ–SJS	CBZ-tolerant	Normal
<i>B</i> *1502	44 (100%)	3 (3%)*	8 (8.6%)†
<i>Cw</i> *0801	41 (93.2%)	17 (16.8%)	13 (14%)
<i>A</i> *1101	36 (81.8%)	51 (50.5%)	53 (57%)
<i>DRB1</i> *1202	33 (75%)	12 (11.9%)	18 (19.4%)
<i>B</i> *1502, <i>Cw</i> *0801	41 (93.2%)	3 (3%)	7 (7.5%)
<i>B</i> *1502, <i>A</i> *1101	36 (81.8%)	2 (2%)	6 (6.5%)
<i>B</i> *1502, <i>DRB1</i> *1202	33 (75%)	1 (1%)	5 (5.4%)
<i>B</i> *1502, <i>Cw</i> *0801, <i>A</i> *1101, <i>DRB1</i> *1202	29 (66%)	0 (0%)	3 (3.2%)

Frequencies (by number and percentage) of individual or combined loci of the *B**1502 ancestral haplotype are shown in patients with carbamazepine-induced Stevens–Johnson syndrome (CBZ–SJS; $n = 44$), and in carbamazepine-tolerant ($n = 101$) and normal subjects ($n = 93$). For methods, see supplementary information.

*Odds ratio (CBZ–SJS/CBZ-tolerant): 2,504 (95% CI, 126–49,522); corrected P value $P_c = 3.13 \times 10^{-27}$.

†Odds ratio (CBZ–SJS/normal): 895 (95% CI, 50–15,869); $P_c = 1.38 \times 10^{-21}$.

Strong association in Han Chinese between the human leukocyte antigen HLA-B*1502, and Stevens-Johnson syndrome induced by carbamazepine



Carbamazepine-Induced Toxic Effects and HLA-B*1502 Screening in Taiwan

Chen P, Lin JJ, Lu CS, Ong CT, Hsieh PF, Yang CC, Tai CT, Wu SL, Lu CH, Hsu YC, Yu HY, Ro LS, Lu CT, Chu CC, Tsai JJ, Su YH, Lan SH, Sung SF, Lin SY, Chuang HP, Huang LC, Chen YJ, Tsai PJ, Liao HT, Lin YH, Chen CH, Chung WH, Hung SI, Wu JY, Chang CF, Chen L, Chen YT, Shen CY; Taiwan SJS Consortium.

2011;364:1126-33.

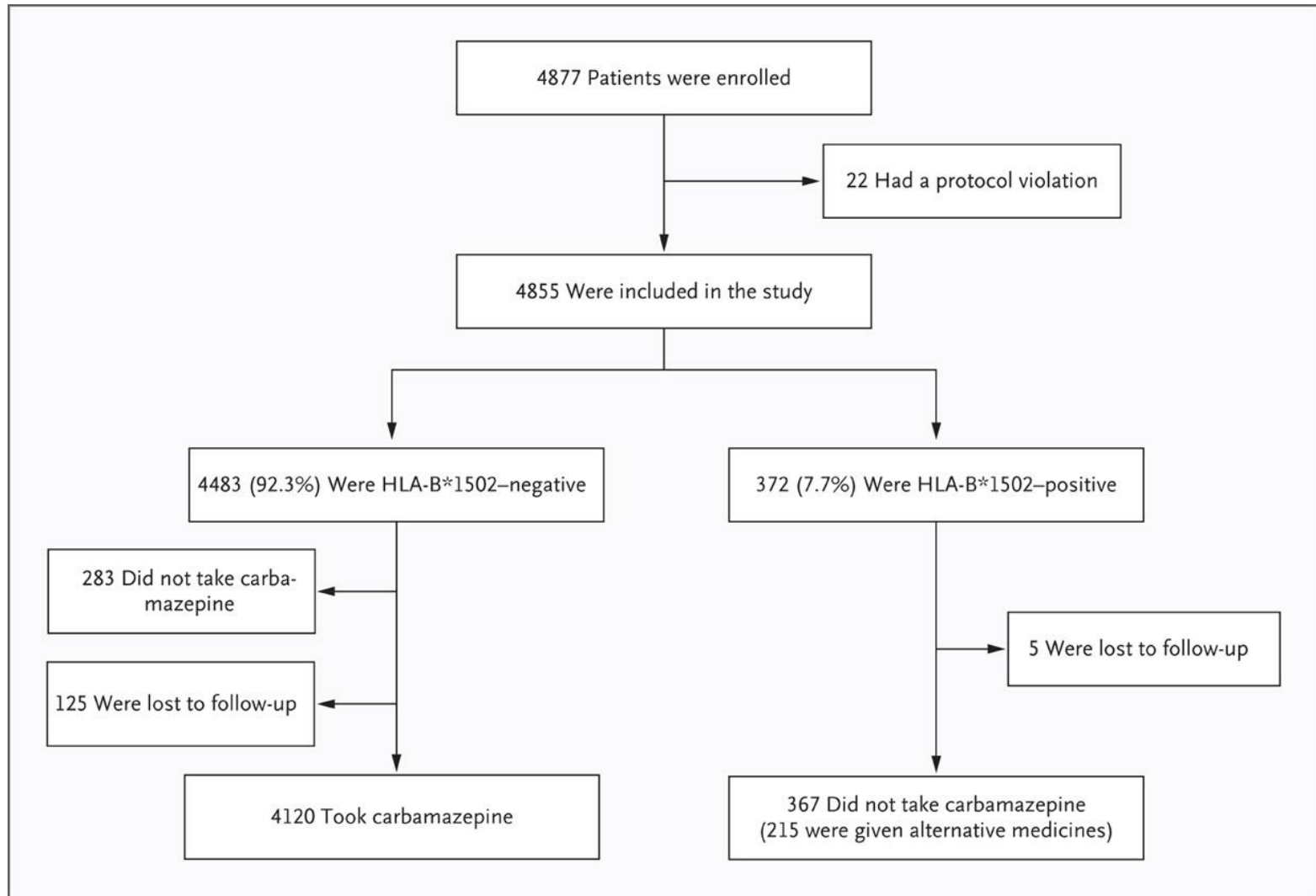


Table 2. Adverse Events during the 2-Month Follow-up.

Adverse Event	HLA-B*1502–Positive with Alternative Medication (N = 215)	HLA-B*1502–Negative with Carbamazepine (N = 4120) <i>number of events</i>	Total
Mild cutaneous events			
Rash and itching	5*	206	211
Rash, itching, and blisters	1†	20	21
Rash, itching, and oral ulcers	0	14	14
Rash, itching, blisters, and oral ulcers	0	7	7
Itching, blisters, and oral ulcers	0	2	2
Blisters and oral ulcers	0	3	3
Severe cutaneous events			
Maculopapular eruption	0	3	3
Hypersensitivity syndrome	0	2	2
Urticaria	1‡	1	2
Stevens–Johnson syndrome or toxic epidermal necrolysis	0	0	0
Other adverse events§			
Fever	1	92	93
Sore throat	4	126	130
Fatigue	16	818	834
Dizziness	10	497	507
Insomnia	5	197	202
Gastrointestinal symptoms	4	185	189

* Among these 5 subjects, the alternative drugs were gabapentin, lamotrigine, naproxen, imipramine, and prednisolone.

† This subject had rash, itching, and blisters after taking gabapentin as an alternative treatment. These symptoms were mild and disappeared in 7 days.

‡ This subject had taken oxcarbazepine before study enrollment.

§ Subjects may have had more than one adverse event. Adverse events with a low frequency are not listed.



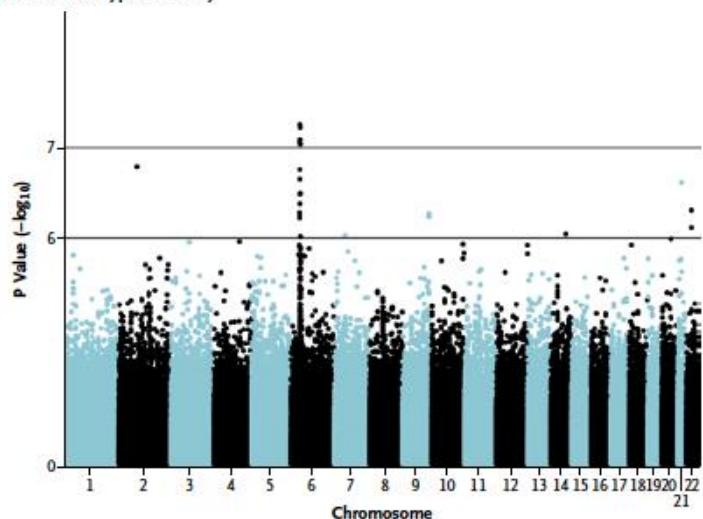
2011;364:1134-43.

HLA-A*3101 and Carbamazepine-Induced Hypersensitivity Reactions in Europeans

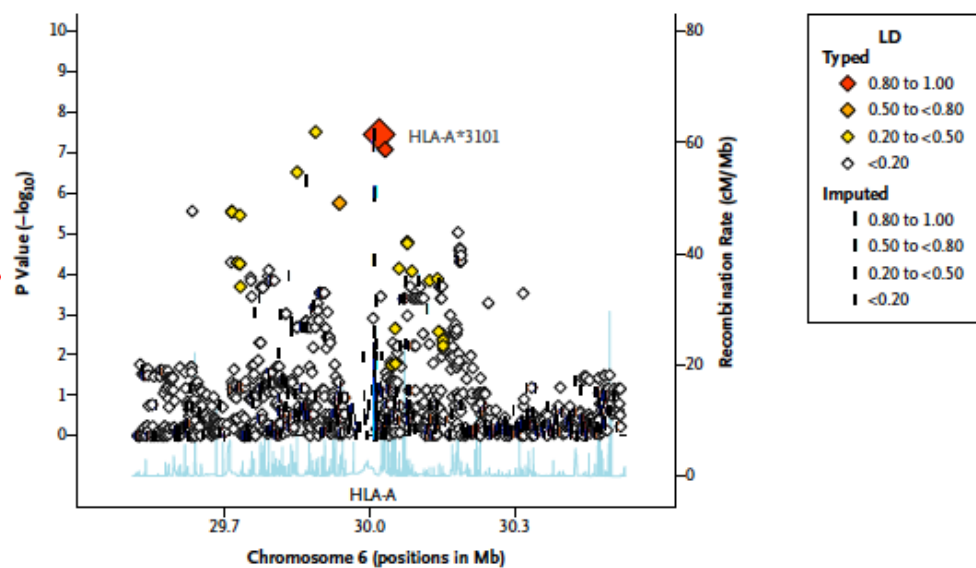
McCormack M, Alfirevic A, Bourgeois S, Farrell JJ, Kasperavičiūtė D, Carrington M, Sills GJ, Marson T, Jia X, de Bakker PI, Chinthapalli K, Molokhia M, Johnson MR, O'Connor GD, Chaila E, Alhusaini S, Shianna KV, Radtke RA, Heinzen EL, Walley N, Pandolfo M, Pichler W, Park BK, Depondt C, Sisodiya SM, Goldstein DB, Deloukas P, Delanty N, Cavalleri GL, Pirmohamed M

Genomewide Association Study of Samples from **22 Case Subjects with Carbamazepine-Induced Hypersensitivity Syndrome** and 2691 Control Subjects.

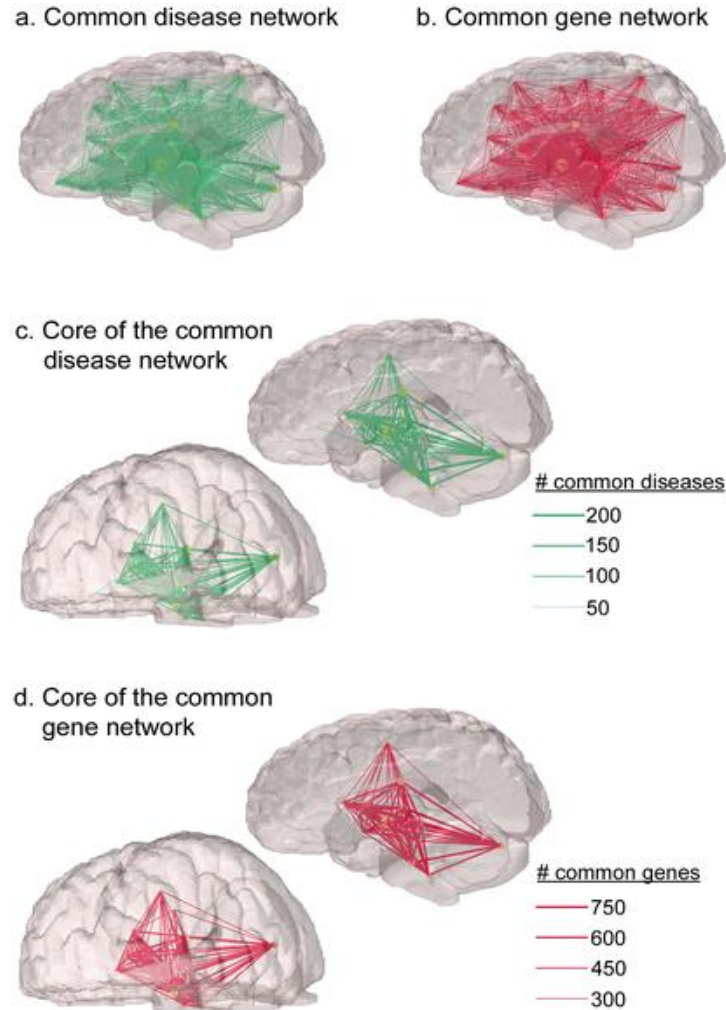
A Carbamazepine-Induced Hypersensitivity



B SNPs in the HLA-A Region



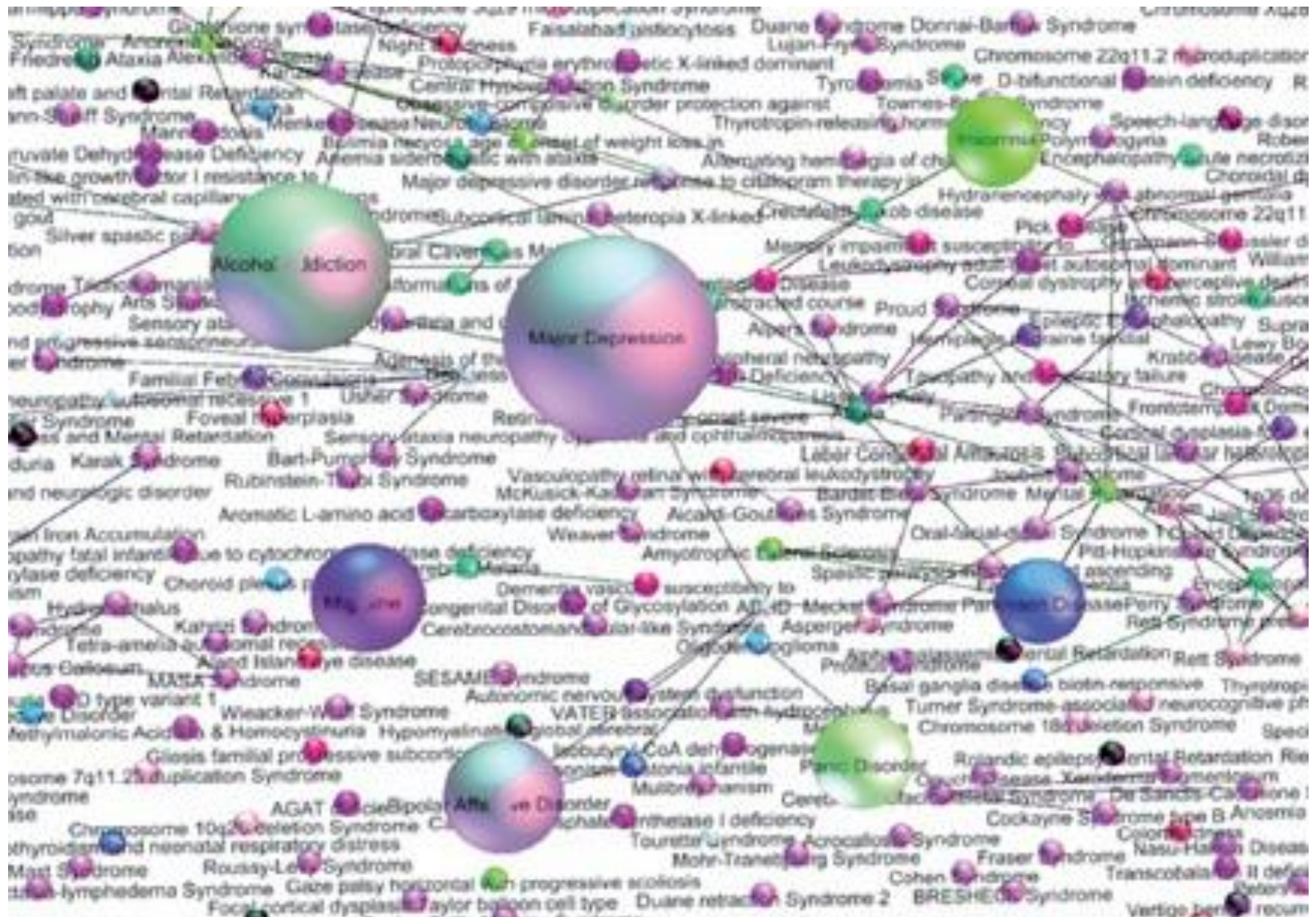
The common disease network and the common gene network.



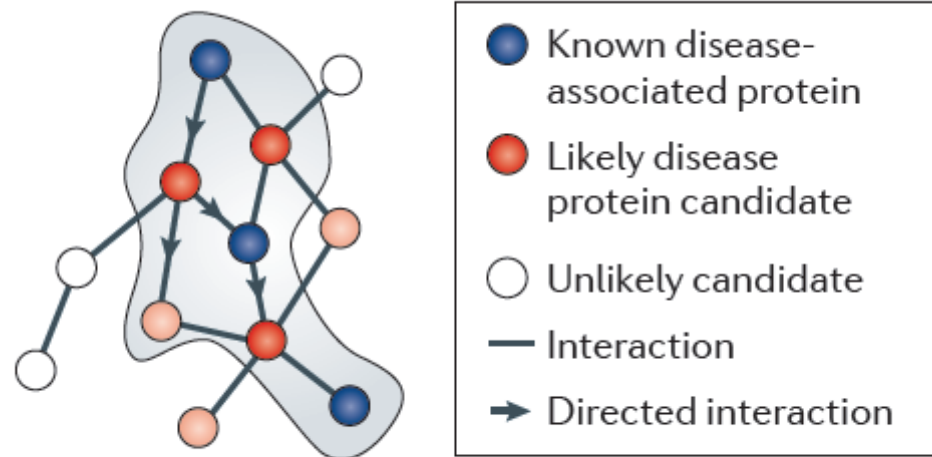
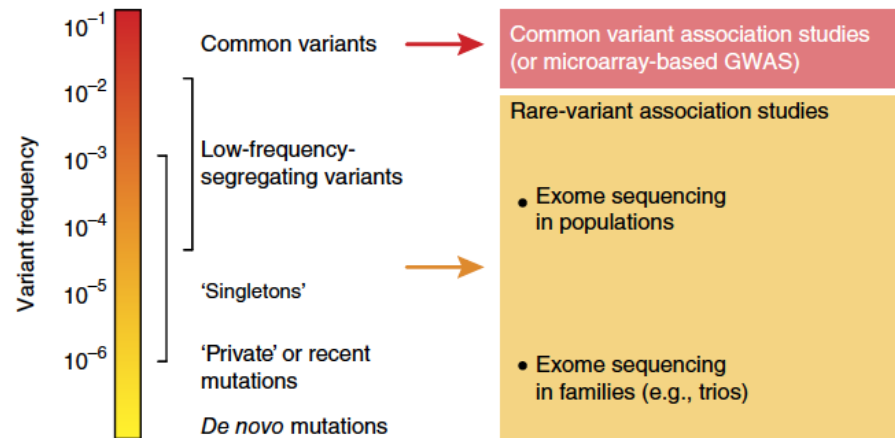
Hayasaka S, Hugenschmidt CE, Laurienti PJ (2011) A Network of Genes, Genetic Disorders, and Brain Areas. PLoS ONE 6(6): e20907. doi:10.1371/journal.pone.0020907

<http://www.plosone.org/article/info:doi/10.1371/journal.pone.0020907>

Neuropsychiatry *diseasome*



Biological pathway

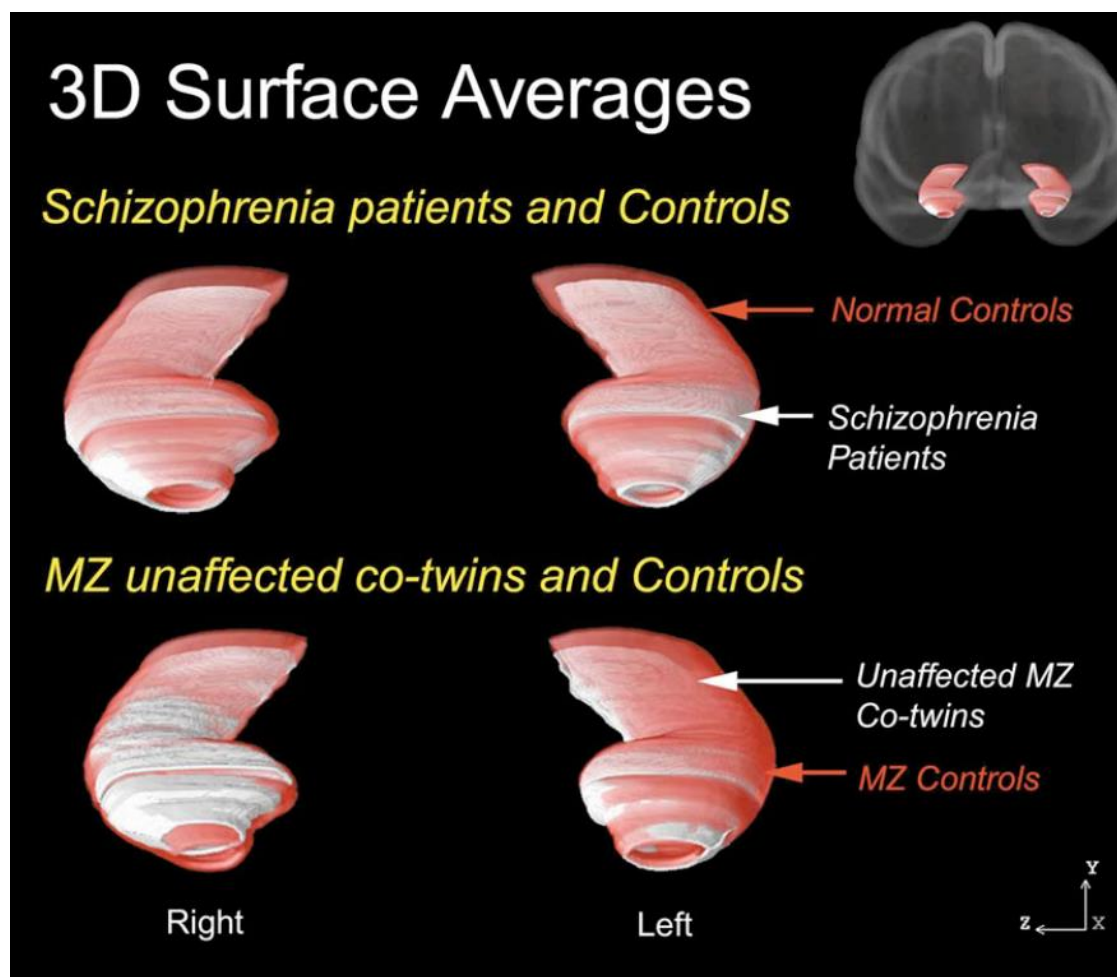


Predicted disease pathway

A twin study of genetic contributions to hippocampal morphology in schizophrenia.

Narr KL, van Erp TG, Cannon TD, Woods RP, Thompson PM, Jang S, Blanton R, Poutanen VP, Huttunen M, Lönngqvist J, Standerskjöld-Nordenstam CG, Kaprio J, Mazziotta JC, Toga AW.

Monozygotic, but not dizygotic, unaffected co-twins exhibited smaller left hippocampi

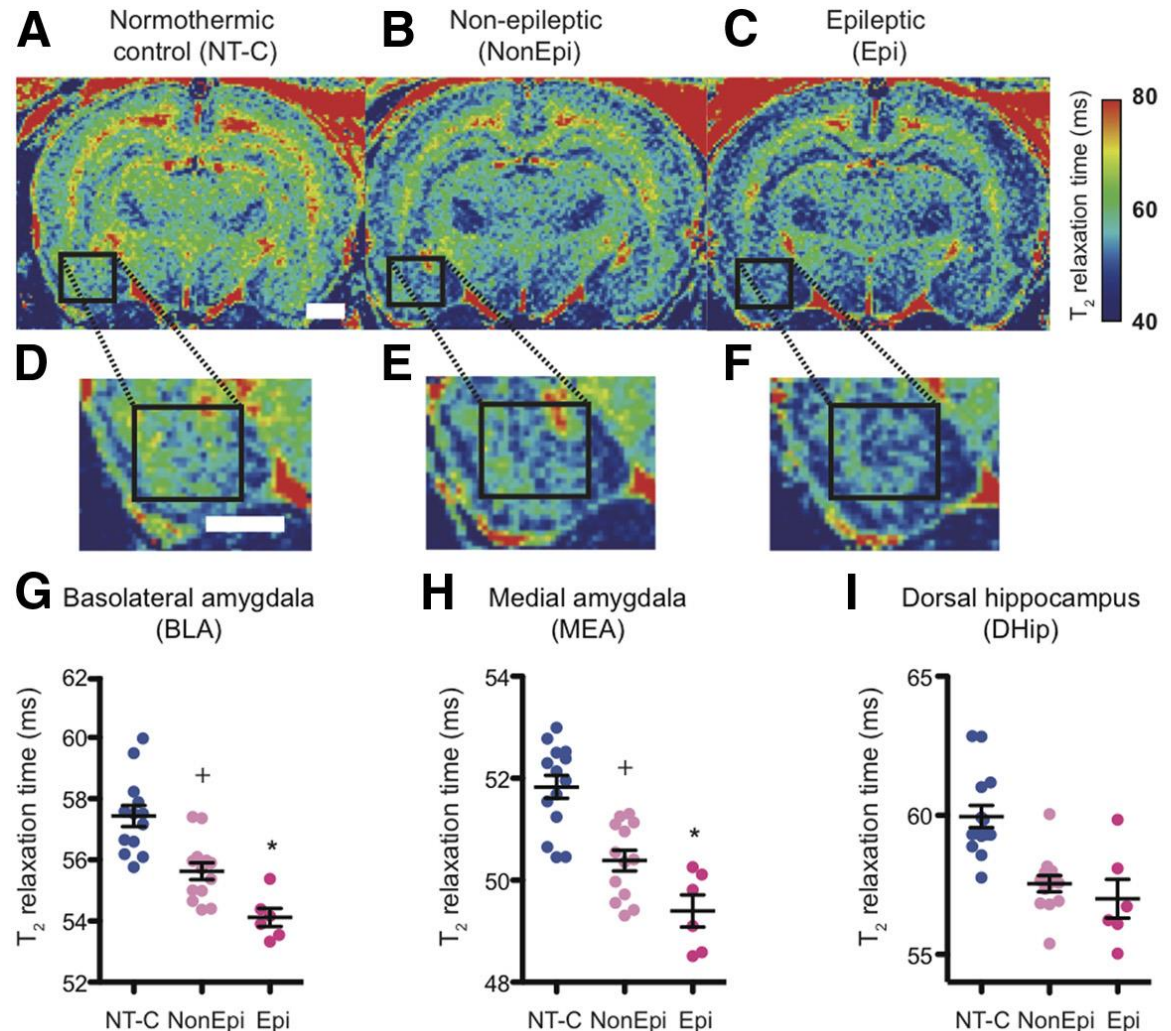


A novel, noninvasive, predictive epilepsy biomarker with clinical potential.

Choy M, Dubé CM, Patterson K, Barnes SR, Maras P, Blood AB, Hasso AN, Obenaus A, Baram TZ.

2014; 34:8672-84.

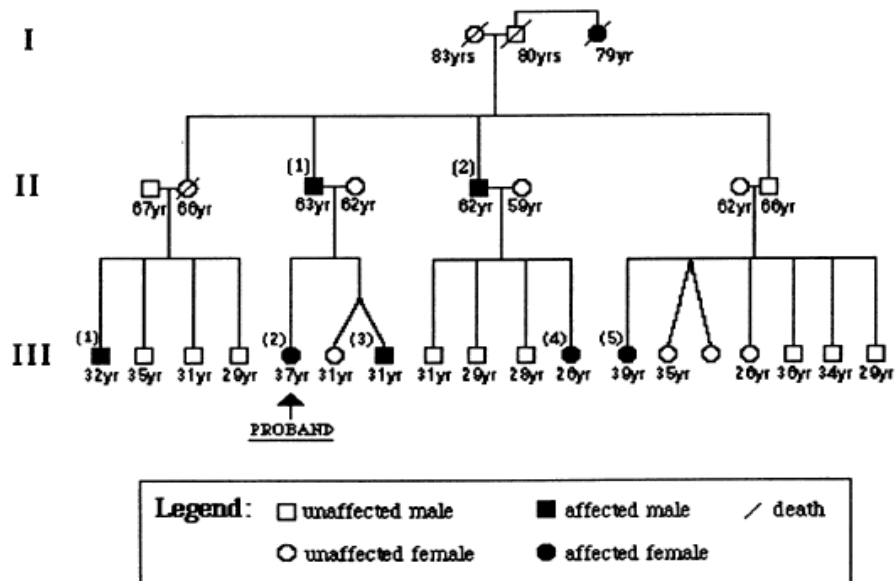
...reduced amygdala
T₂ relaxation times
in high-magnetic-
field MRI hours after
FSE predicted
experimental TLE.



We describe a new syndrome of familial temporal lobe epilepsy in **38 individuals from 13 unrelated white families**. The disorder was first identified in 5 concordant monozygotic twin pairs as part of a large-scale twin study of epilepsy. When idiopathic partial epilepsy syndromes were excluded, the 5 pairs accounted for 23% of monozygotic pairs with partial epilepsies, and 38% of monozygotic pairs with partial epilepsy and no known etiology. **Seizure onset for twin and nontwin subjects usually occurred during adolescence or early adult life**. Seizure types were simple partial seizures with **psychic or autonomic symptoms**, infrequent complex partial seizures, and rare secondarily generalized seizures. Electroencephalograms revealed sparse focal temporal interictal epileptiform discharges in 22% of subjects. **Magnetic resonance images appeared normal**. Nine affected family members (24%) had not been diagnosed prior to the study. Pedigree analysis suggested autosomal dominant inheritance with age-dependent penetrance. The estimated segregation ratio was 0.3, indicating an overall penetrance of 60% assuming autosomal dominant inheritance. **The mild and often subtle nature of the symptoms in some family members may account for lack of prior recognition of this common familial partial epilepsy**. This disorder has similarities to the El mouse, a genetic model of temporal lobe epilepsy with a major gene on mouse chromosome 9, which is homologous with a region on human chromosome 3.

Familial temporal lobe epilepsy Autosomal dominant inheritance in a large pedigree from Southern Italy[☆]

Antonio Gambardella ^{a,b,*}, Demetrio Messina ^a, Emilio Le Piane ^a,
R. Luciano Oliveri ^{a,b}, Grazia Annesi ^b, Mario Zappia ^a, Eva Andermann ^c,
Aldo Quattrone ^{a,b}, Umberto Aguglia ^a



Clinical, EEG and neuroradiological findings of the affected individuals

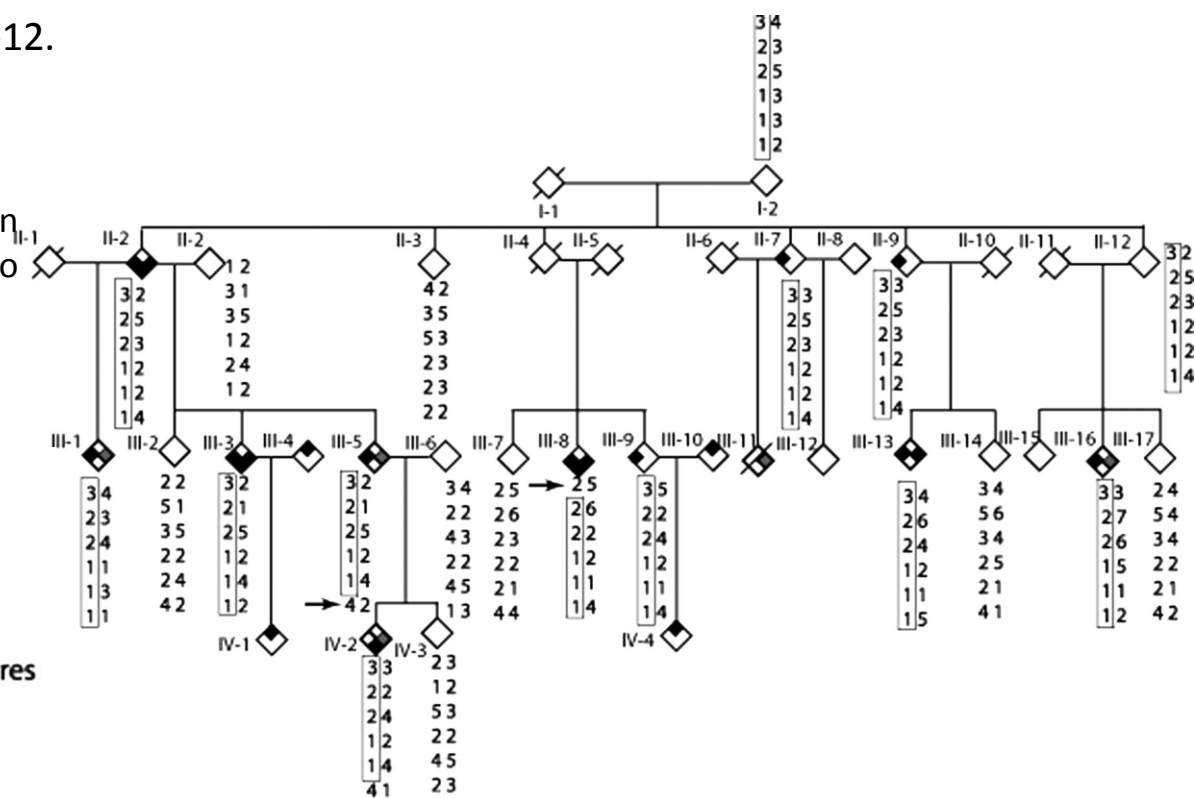
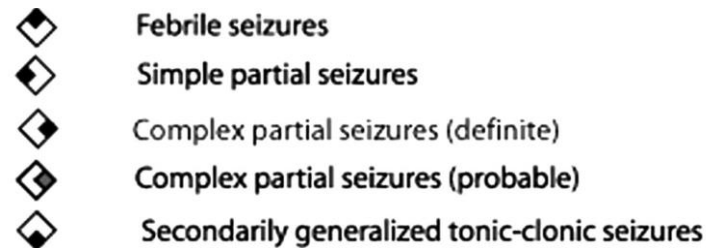
Patient n., age, sex	Antecedent factors	Age at onset of epilepsy	Seizures type	Frequency	Interictal EEG	Imaging study	Therapy	Prognosis (follow-up)
II-1, 63 years, male	None	52 years	Rising epigastric sensation	Weekly	Normal	Normal (CT scan)	None	–
II-2, 62 years, male	None	38 years	Fear, complex partial	Weekly 1/6–9 months	Left temporal delta waves	Normal (CT scan)	Carbamazepine (600 mg/daily)	sz. free (3 years)
III-1, 32 years, male	None	18 years	fear, confusion complex partial	Weekly, 3 in 9 years	Right temporal spiking	Normal (MR)	Phenytoin (300 mg/daily)	sz. free (3 years)
III-2, 37 years, female	Simple febrile convulsion (3 years)	17 years	Deja vu, complex partial, sec. Generalized	Weekly 1–3/ month, 2 in 19 years	Left temporal spiking	Normal (MR)	Carbamazepine (800 mg/daily)	sz. free (3 years)
III-3, 31 years, male	None	18 years	Fainting, deja vu, complex partial	2–3/6 months, 3 in 5 years	Normal	Normal (CT scan)	None ^a	sz. free (7 years)
III-4, 26 years, female	Head trauma with loss of consciousness (6 months)	19 years	Vegetative auras plus confusion, fear, complex partial, monthly, rare	Monthly, rare	Right temporal delta waves	Normal (MR)	Valproate (1.0 g/daily)	sz. free (3 years)
III-5, 39 years, female	None	30 years	Vegetative auras, complex partial	Weekly 1/3 years	Left temporal spiking	Normal (MR)	Carbamazepine (1.0 g/daily)	sz. free (4 years)

^a From the age of 25 years he stopped valproate.

Five patients (II-2, III-2, III-3, III-4 and III-5) presented a history of migraine.

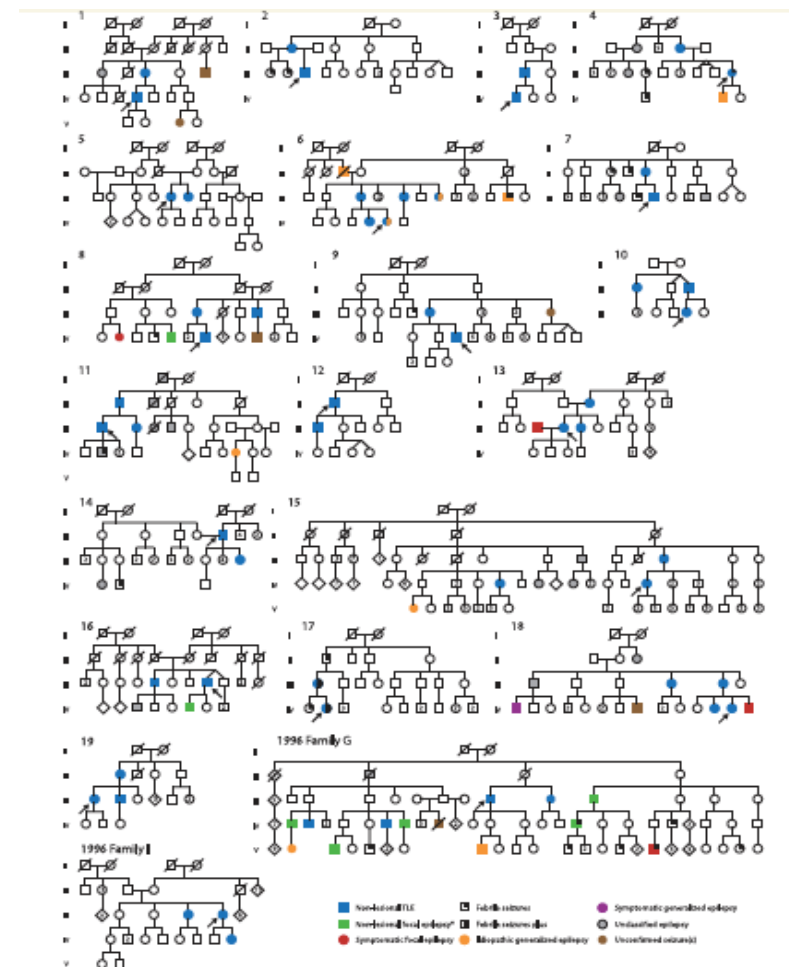
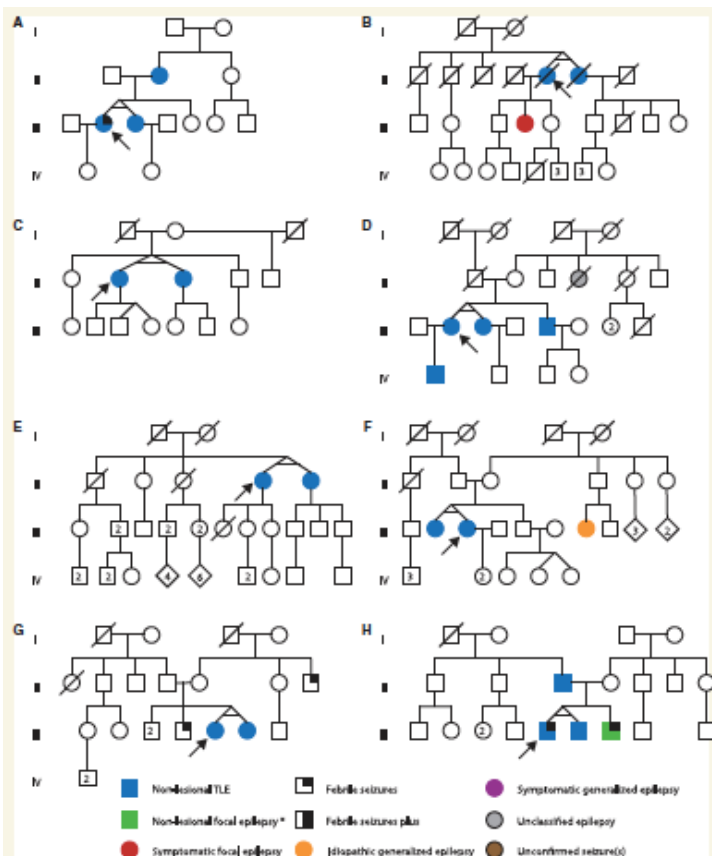
Familial mesial temporal lobe epilepsy maps to chromosome 4q13.2-q21.3

Hedera P, Blair MA, Andermann E, Andermann F, D'Agostino D, Taylor KA, Chahine L, Pandolfo M, Bradford Y, Haines JL, Abou-Khalil B.



- ❖ Inheritance was consistent with AD mode with reduced penetrance.
- ❖ Eleven individuals were classified as affected with FMTLE and we also identified two living asymptomatic individuals who had affected offspring.
- ❖ Seizure semiologies included predominantly SPS with déjà vu feeling, infrequent CPS, and rare secondarily generalized tonic-clonic seizures.
- ❖ No structural abnormalities, including hippocampal sclerosis, were detected on MRI performed on three individuals.
- ❖ Genetic analysis detected a group of markers with lod score >3 on chromosome 4q13.2-q21.3 spanning a 7 cM region.
- ❖ No ion channel genes are predicted to be localized within this locus.

.... These findings strongly suggest that **complex inheritance**, similar to that widely accepted in the idiopathic generalized epilepsies, is **the usual mode of inheritance in familial mesial temporal lobe epilepsy**.



Benign mesial temporal lobe epilepsy

Angelo Labate, Antonio Gambardella, Eva Andermann, Umberto Aguglia, Fernando Cendes, Samuel F. Berkovic and Frederick Andermann

Box 1 | Clinical features of bMTLE

- Onset in late adolescence or adulthood
- Normal neurological examination
- Normal cognitive examination
- Unremarkable past medical history
- ≈30% have positive family history of febrile seizures or epilepsy
- ≈15% have personal antecedents of simple febrile seizures
- Viscerosensory auras are the predominant symptoms
- Easily controlled with a single antiepileptic drug
- Misdiagnosis of panic attacks or gastrointestinal disturbances is very common

Abbreviation: bMTLE, benign mesial temporal lobe epilepsy.

A benign form of mesial TLE (bMTLE) does exist and represents a common but often unrecognized clinical entity...

Box 2 | EEG, MRI and genetics of bMTLE

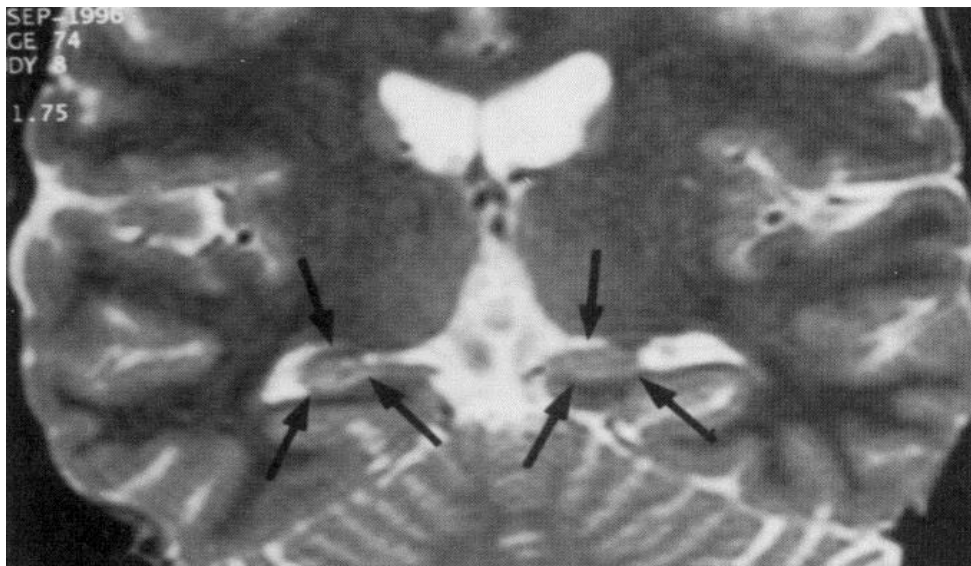
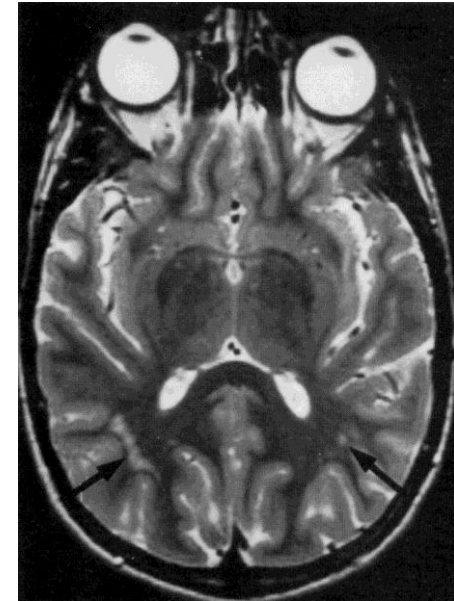
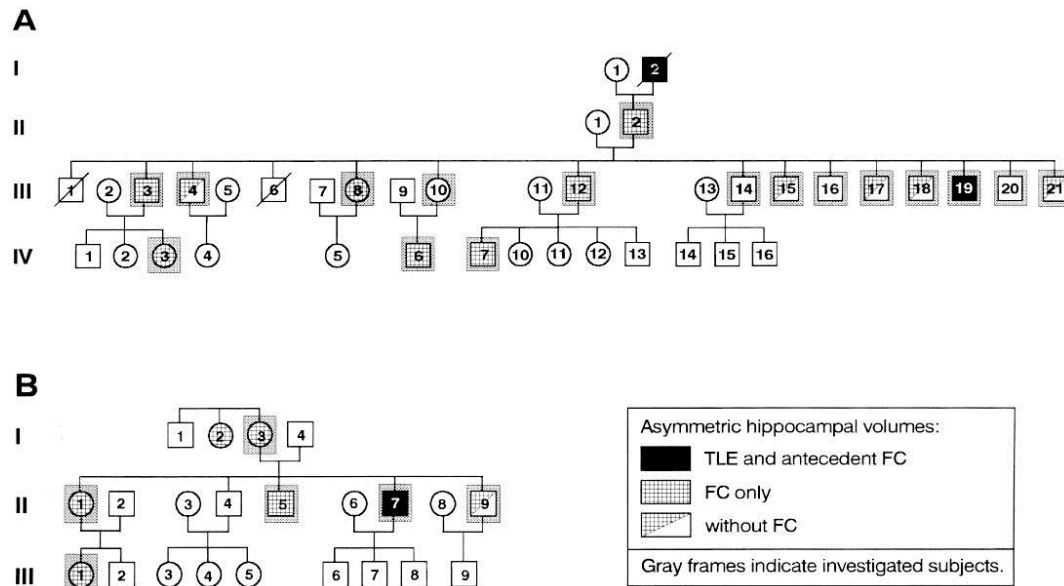
- ≥60% have normal interictal EEG
- Almost 40% have MRI evidence of hippocampal sclerosis
- Genetic predisposition is known to exist
- Remarkable intrafamilial and interfamilial phenotypic heterogeneity
- Autosomal dominant inheritance is rare

Abbreviation: bMTLE, benign mesial temporal lobe epilepsy.

Hippocampal malformation as a cause of familial febrile convulsions and subsequent hippocampal sclerosis

1998;50:909-17.

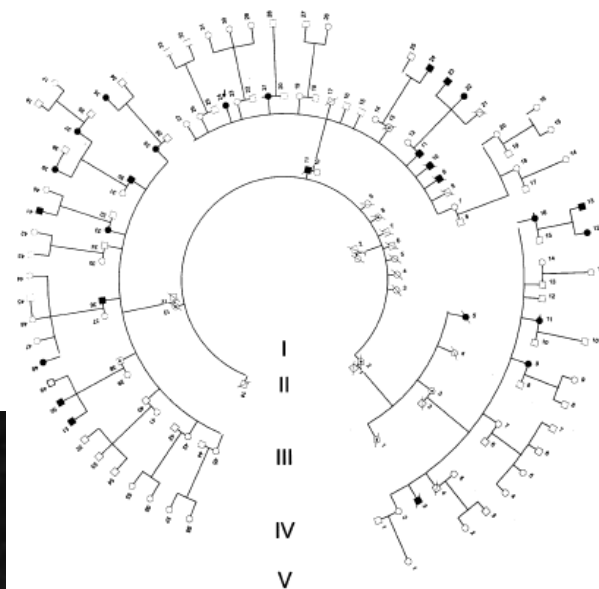
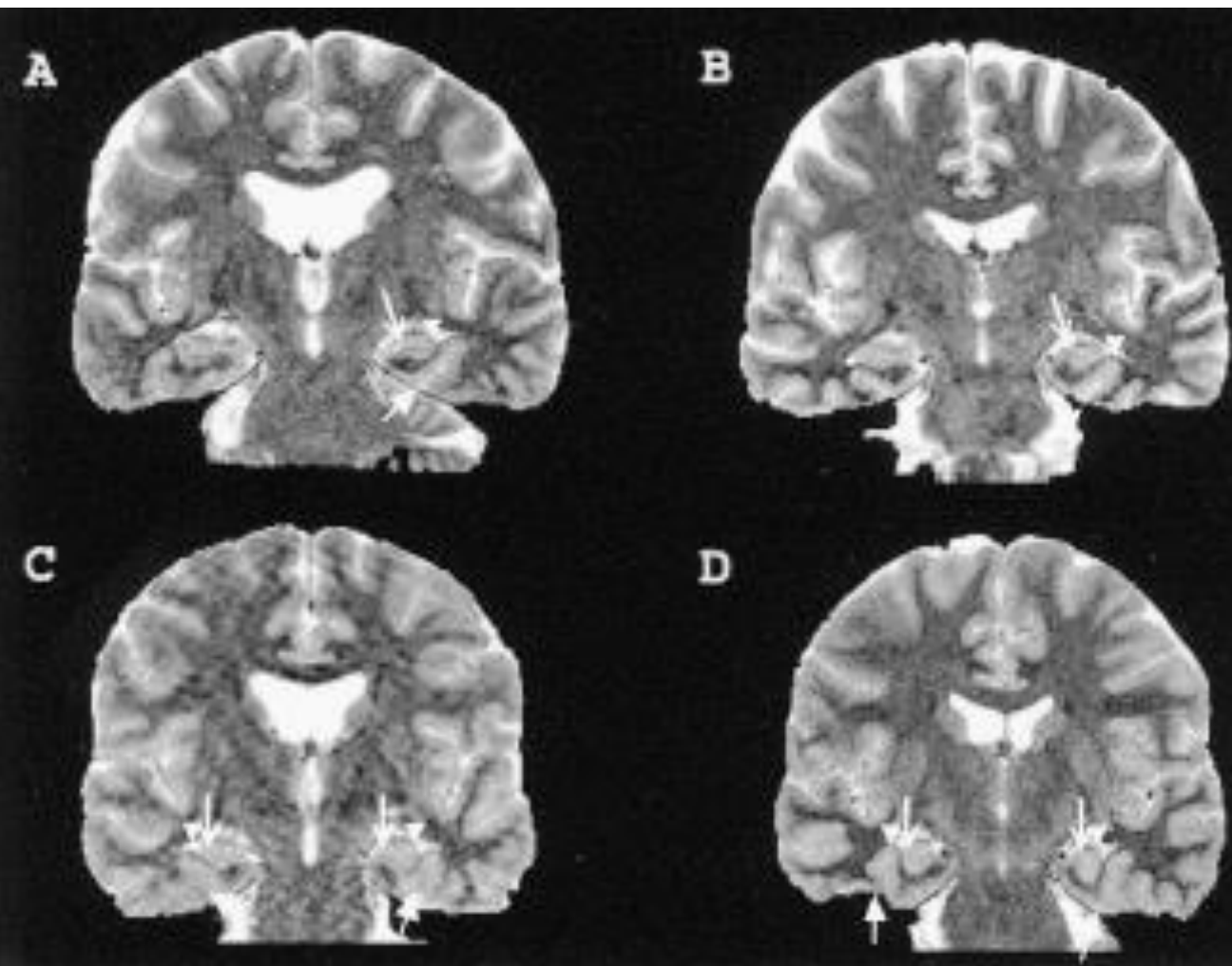
Fernández G, Effenberger O, Vinz B, Steinlein O, Elger CE, Döhring W, Heinze H J.



These findings suggest a subtle, pre-existing hippocampal malformation that may facilitate febrile convulsions and contribute to the development of subsequent HS.

Familial temporal lobe epilepsy with febrile seizures

Depondt C, Van Paesschen W, Matthijs G, Legius E, Martens K, Demaerel P, Wilms G.

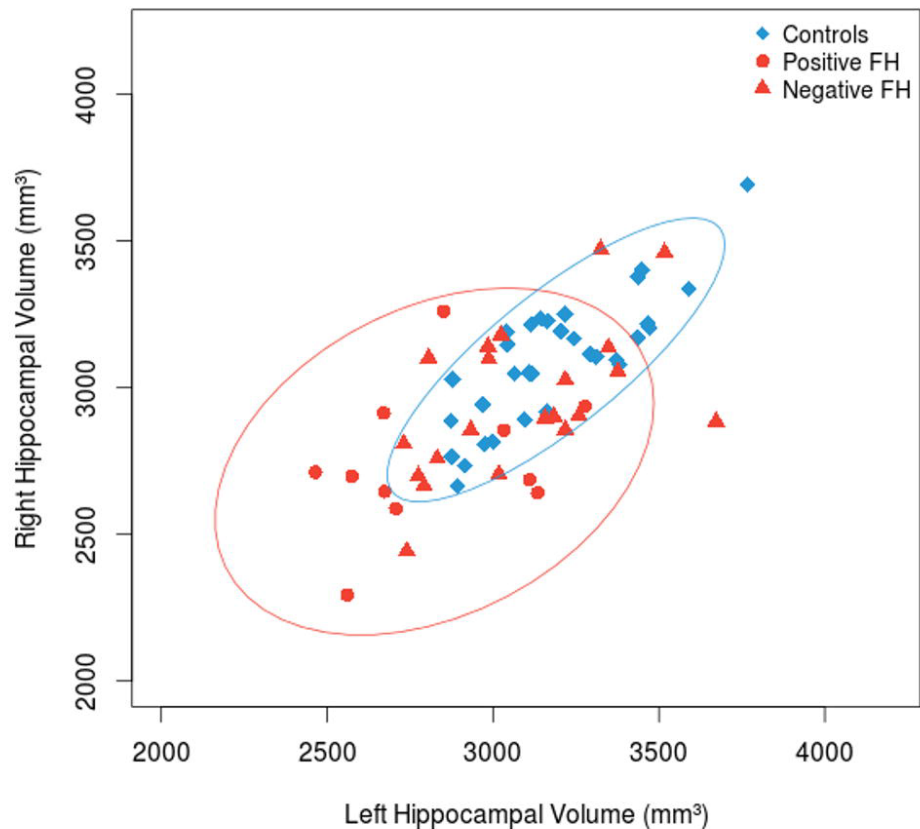
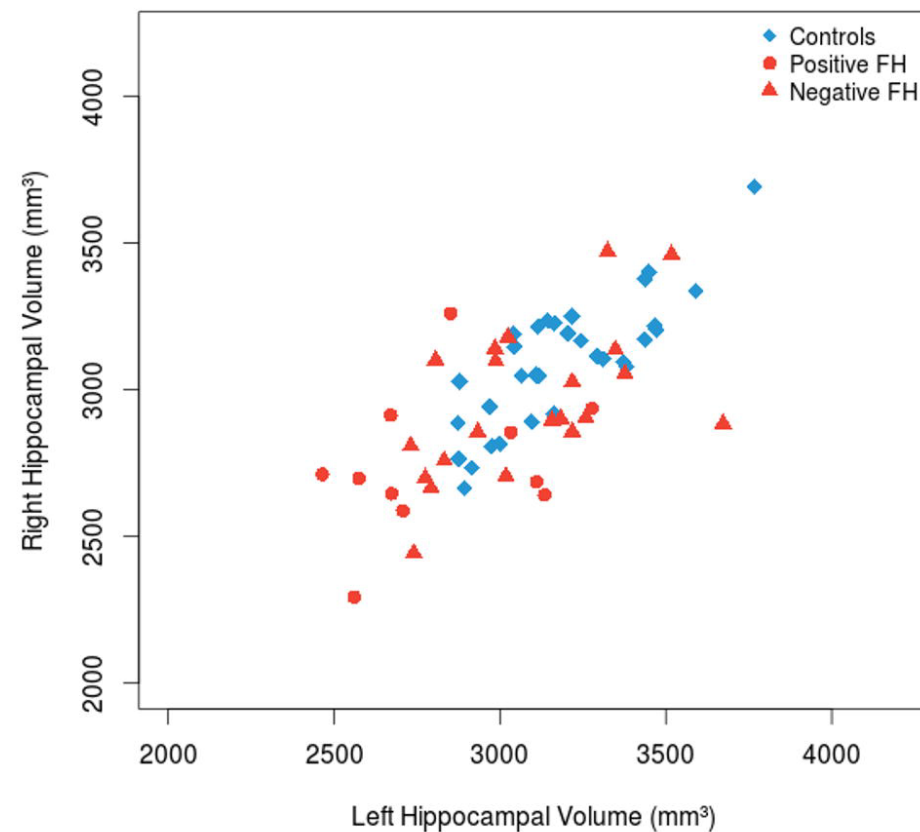


(A) and (B) show unilateral **left hippocampal malrotation (HIMAL)** and (C) and (D) **bilateral HIMAL**. Note the abnormally steep angles of the collateral sulci (small closed arrows), the abnormally rounded shapes of the hippocampi (large open arrows), and the abnormal configurations of the temporal horns (arrowheads).

Etiology of hippocampal sclerosis: evidence for a predisposing familial morphologic anomaly.

Tsai MH, Pardoe HR, Perchyonok Y, Fitt GJ, Scheffer IE, Jackson GD, Berkovic SF.

N^o 32 asymptomatic relatives from 15 families in which probands had TLE with HS and 32 age- and sex-matched controls



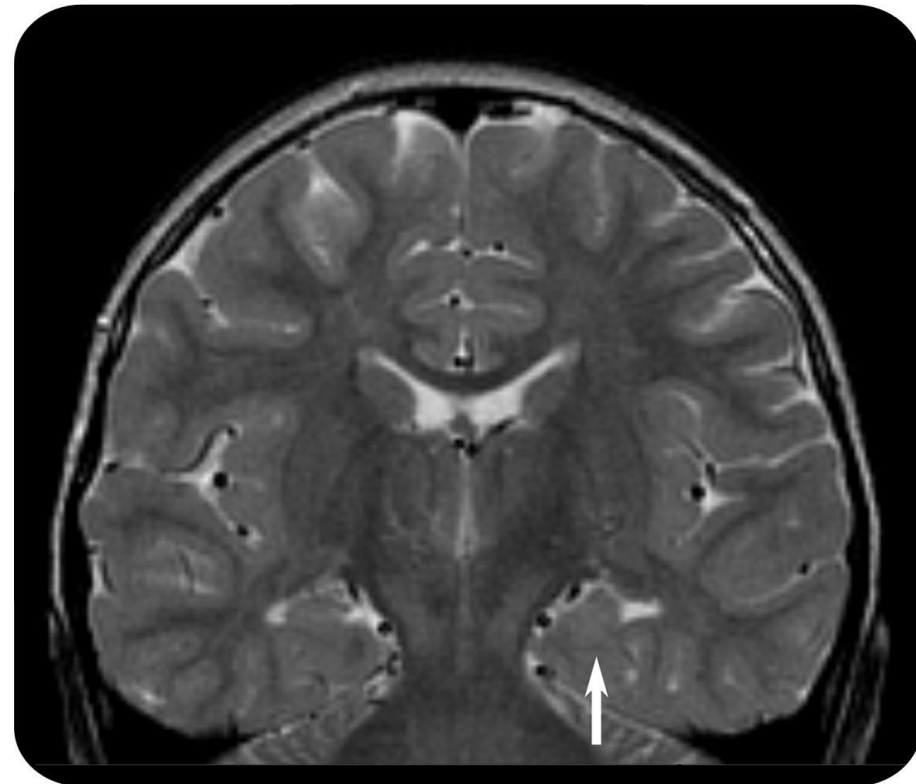
MRI abnormalities following febrile status epilepticus in children: the FEBSTAT study.

2012; 79(9):871-877

Shinnar S, Bello JA, Chan S, Hesdorffer DC, Lewis DV, Macfall J, Pellock JM, Nordli DR, Frank LM, Moshe SL, Gomes W, Shinnar RC, Sun S; FEBSTAT Study Team

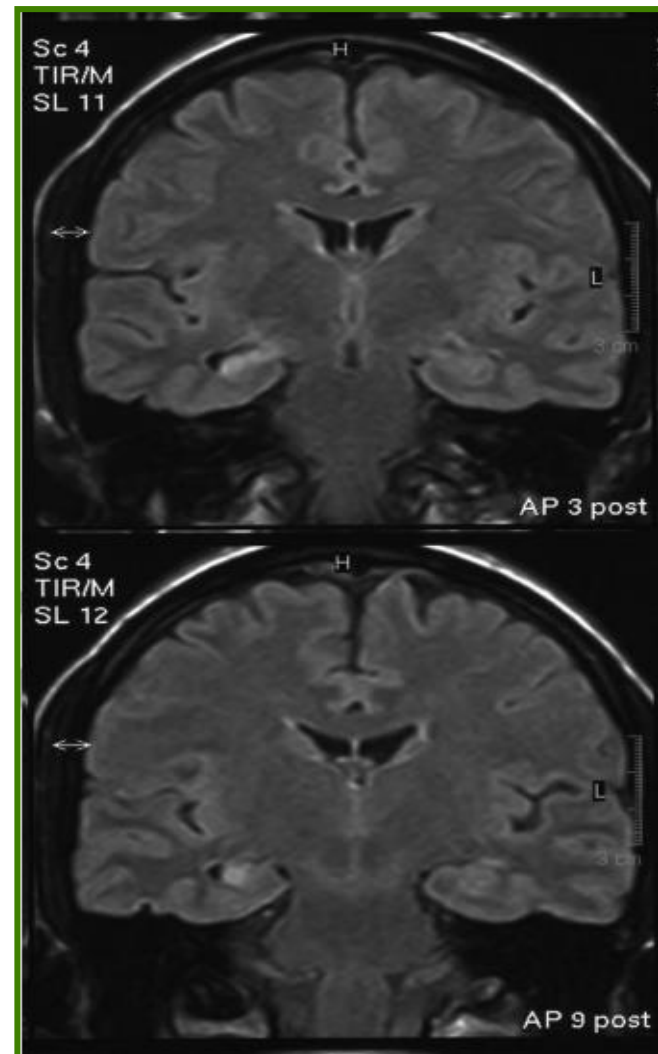
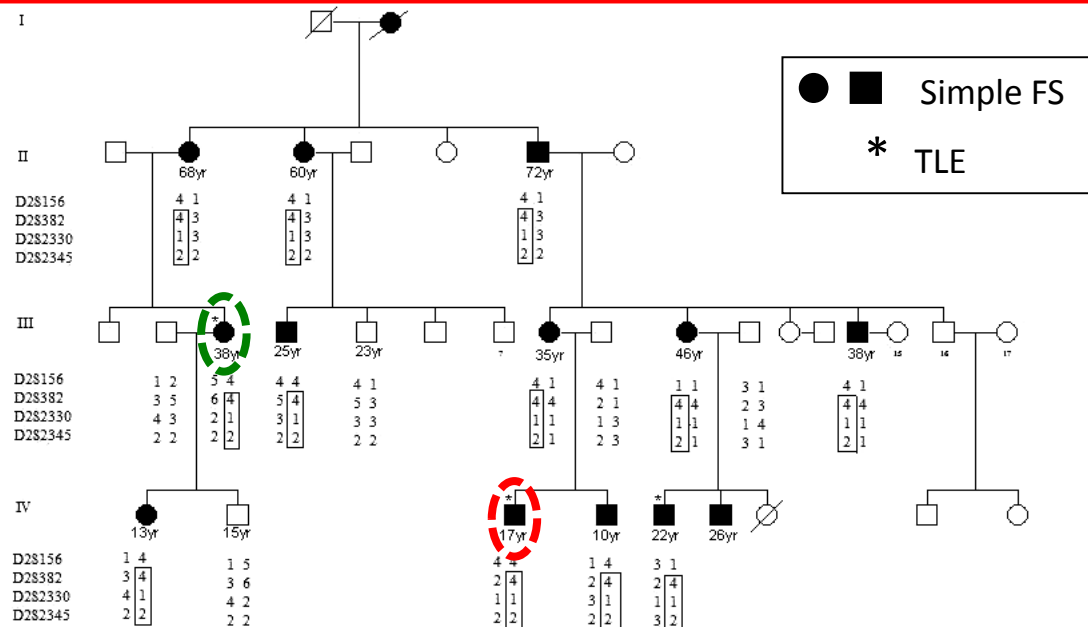
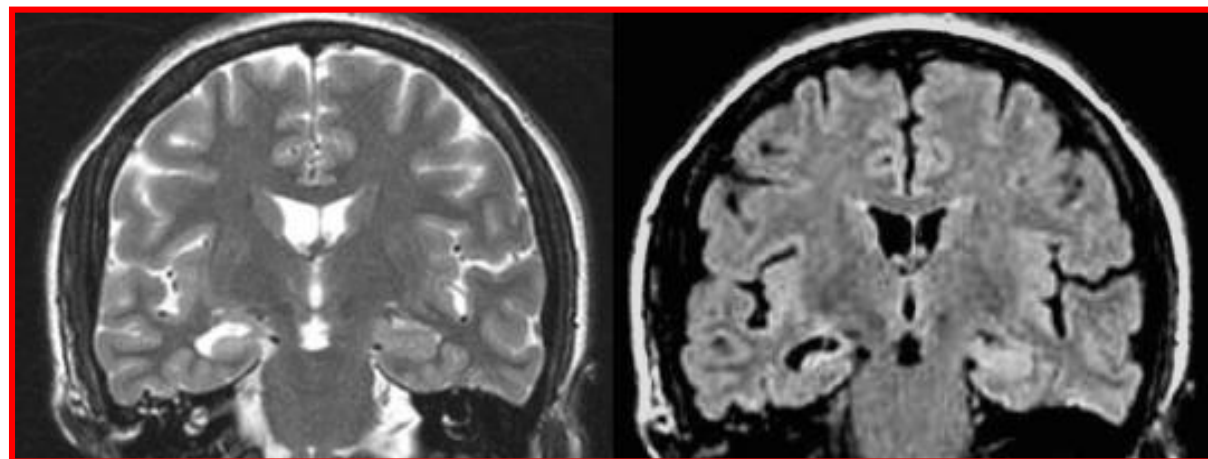
Developmental abnormalities of the hippocampus were more common in the FSE group (n 20, 10.5%) than in controls (n 2, 2.1%) (p 0.0097) with *hippocampal malrotation being the most common* (15 cases and 2 controls).

Hippocampal malrotation in a 40-month-old child with febrile status epilepticus

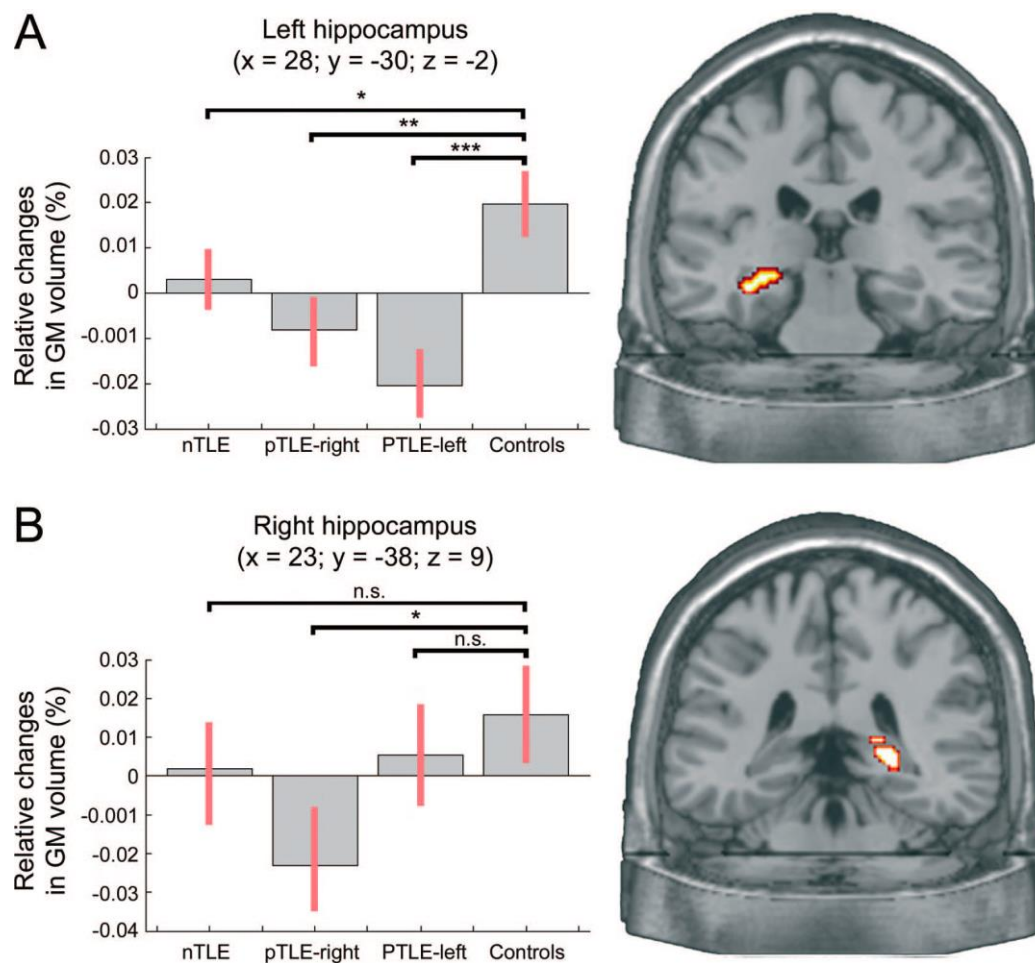


Electroclinical Features of a Family with Simple Febrile Seizures and Temporal Lobe Epilepsy Associated with SCN1A Loss-of-Function Mutation

Colosimo E, Gambardella A, Mantegazza M, Labate A, Rusconi R, Schiavon E, Annesi F, Cassulini RR, Carrideo S, Chifari R, Canevini MP, Canger R, Franceschetti S, Annesi G, Wanke E, Quattrone A.



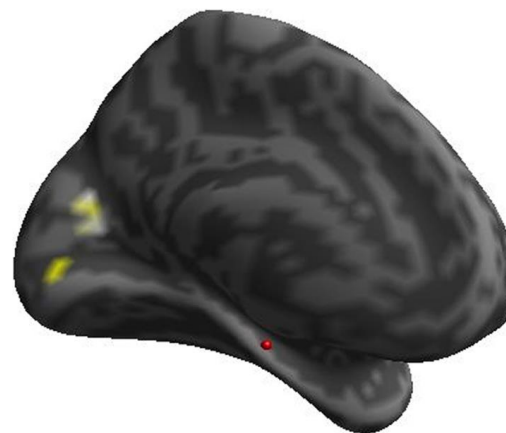
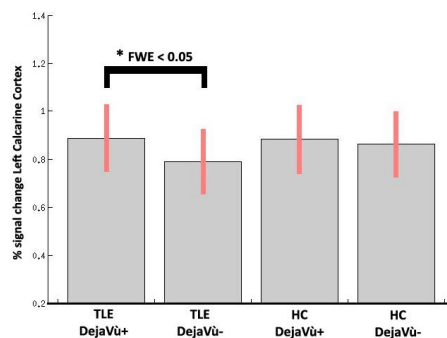
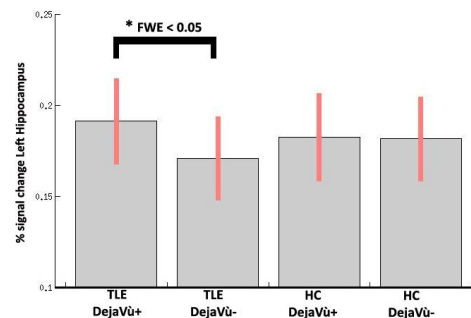
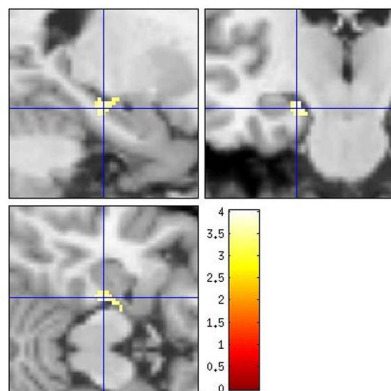
Volume of (A) left (peak voxel x, y, z28, 30, 2) and
(B) right hippocampus (peak voxel x, y, z23, 38, 9)



Neuro-anatomical differences among epileptic and non-epileptic déjà-vu

Labate A, Cerasa A, Mumoli L, Ferlazzo E, Aguglia U, Quattrone A, Gambardella A.

TLE patients with DV display **an abnormal increase of the gray matter in the left hippocampus** and calcarine cortex volume in comparison with those without DV.



Experiential phenomena occurring in spontaneous seizures or evoked by brain stimulation were reported by **18 of 29 patients** who were investigated with chronic, stereotactically implanted intracerebral electrodes.

Topographical distribution of responses obtained with electrical stimulations applied to adjacent pairs of contacts

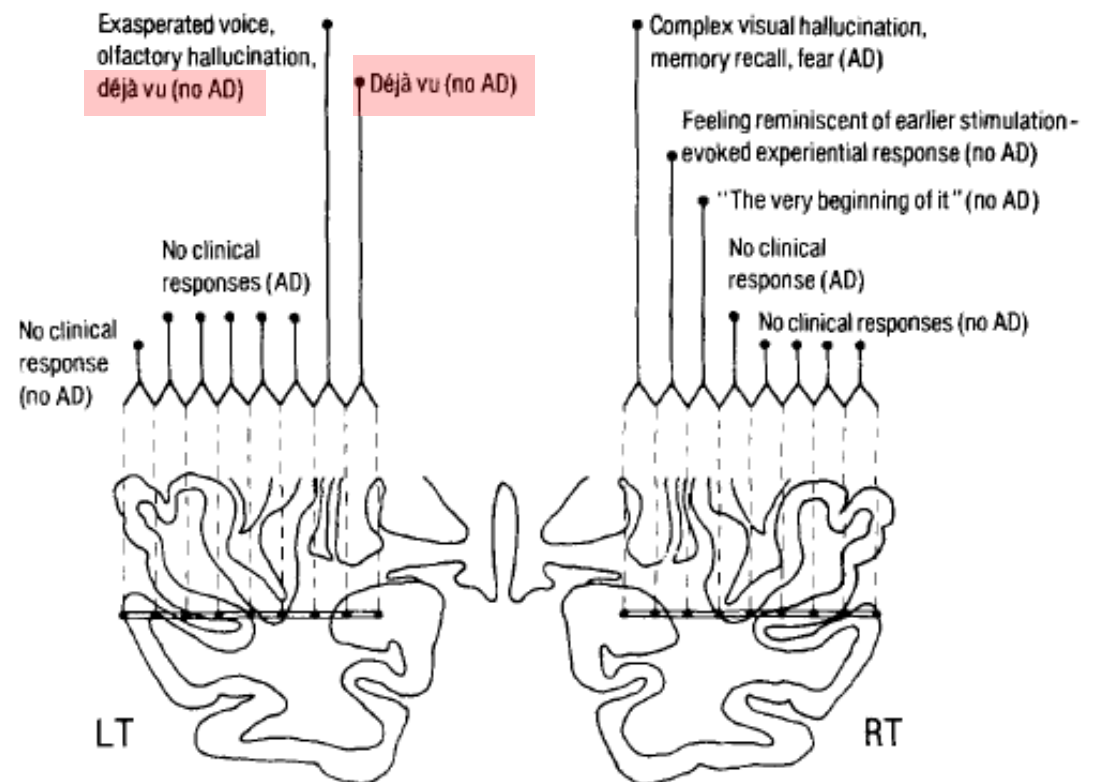


Table 1. Experiential Illusions and Hallucinations Observed with Stereotaxic Exploration of the Temporal Lobes

Experience	No. of Observations	No. of Patients
Visual illusions	9	3
Elementary visual hallucinations (phosphenes)	15 ^a	3
Complex visual hallucinations	18	5
Auditory illusions	0	0
Elementary auditory hallucinations	0	0
Complex auditory hallucinations	3	2
Olfactory hallucinations	2	1
Familiarity (déjà vu)	23	4
Unfamiliarity (jamais vu)	0	0
Memory recall	19	5
Forced thinking	10	2
Fear	>49	7
Anger	1 ^b	1
Irritation	>3	1
Emotional distress (depression, guilt, etc)	6 ^c	3
Far-away feeling	>3	1
Feeling of someone being nearby	1	1
Pleasant emotion	0	0
Sexual emotion	0	0
Thirst	10 ^d	2
Hunger	0	0
Feeling of bodily distortion	2	1
Strange, indescribable feeling (mental)	2	2
Floating sensation (excitement? startle?)	7	1

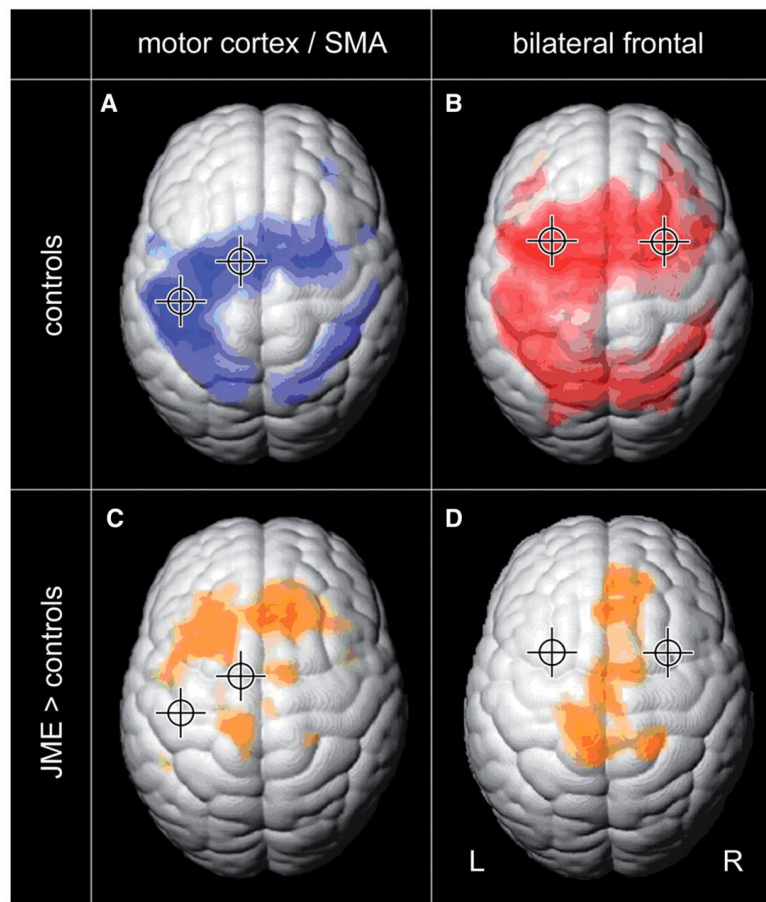
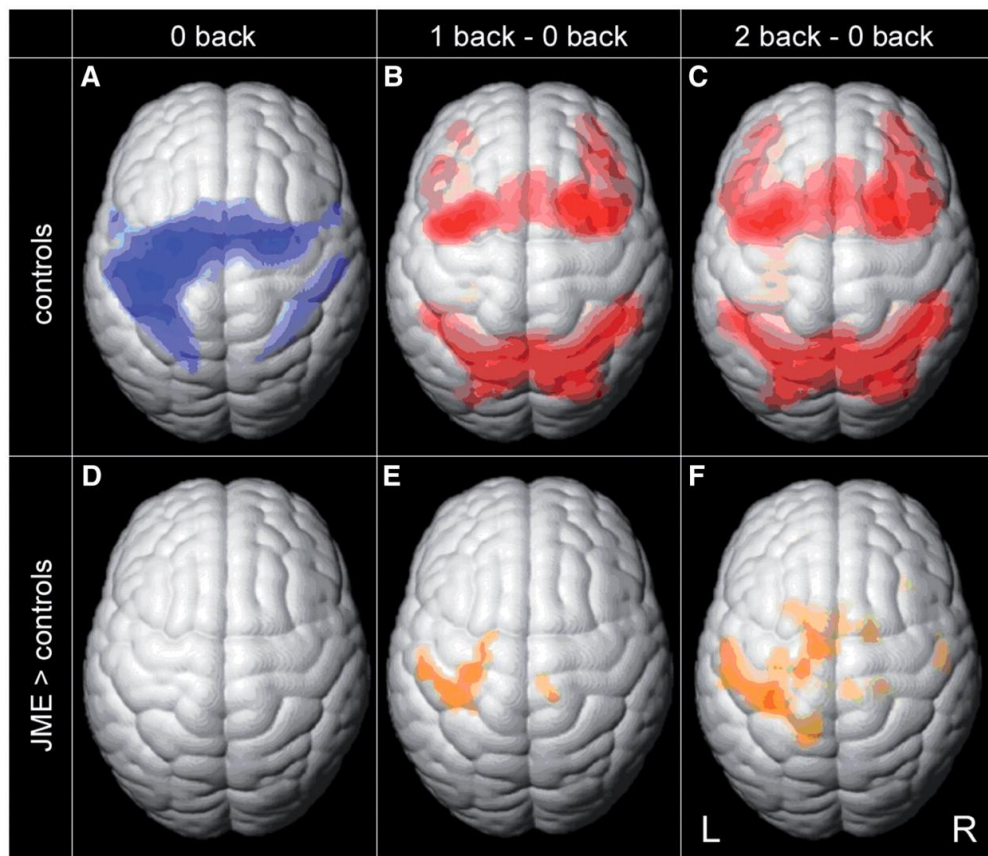
Motor system hyperconnectivity in juvenile myoclonic epilepsy: a cognitive functional magnetic resonance imaging study.

2011;135:3635-44

Vollmar C, O'Muircheartaigh J, Symms MR, Barker GJ, Thompson P, Kumari V, Duncan JS, Janz D, Richardson MP, Koepp MJ.

Functional connectivity is increased in JME.

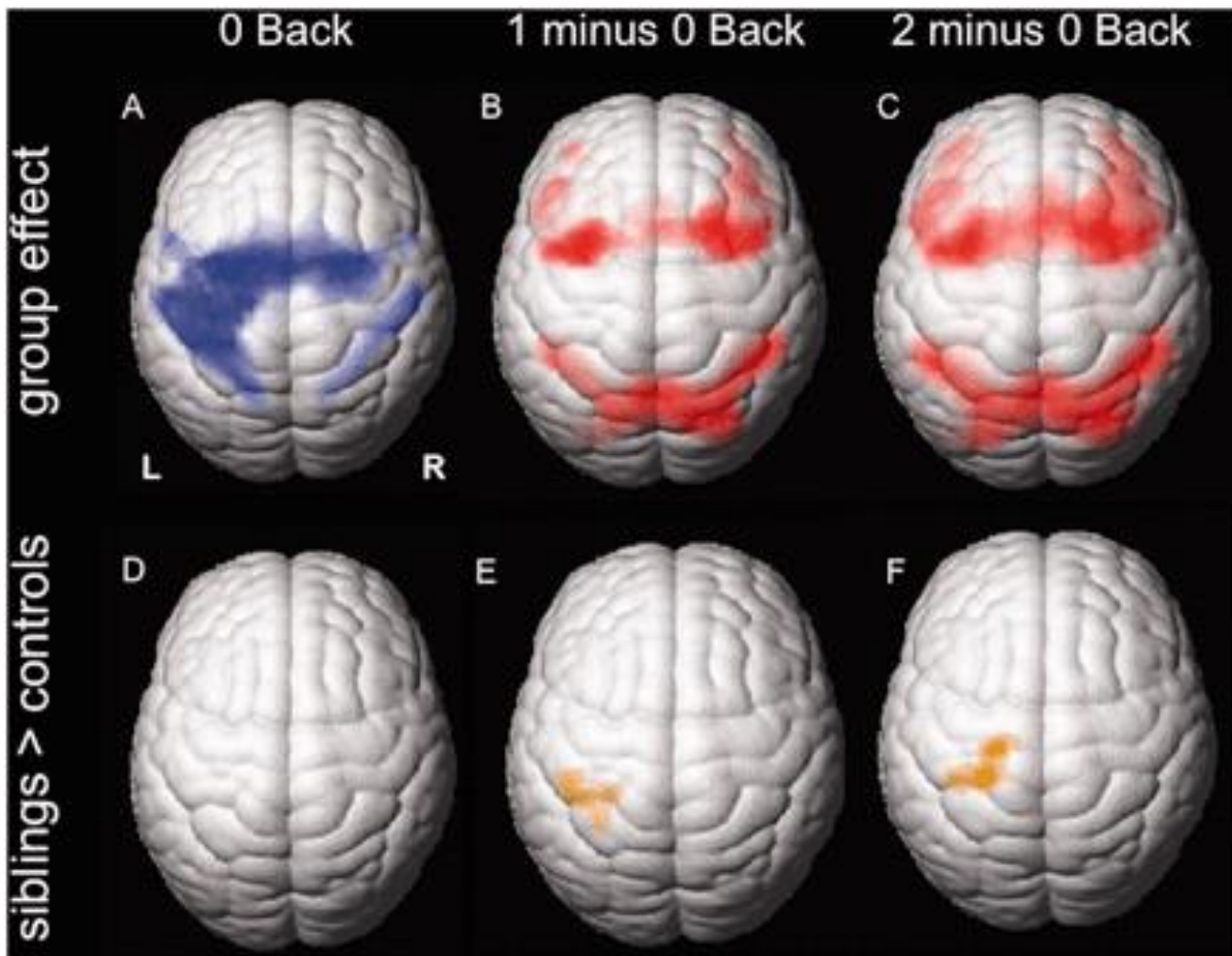
Functional MRI activation from working memory task in controls and group differences.



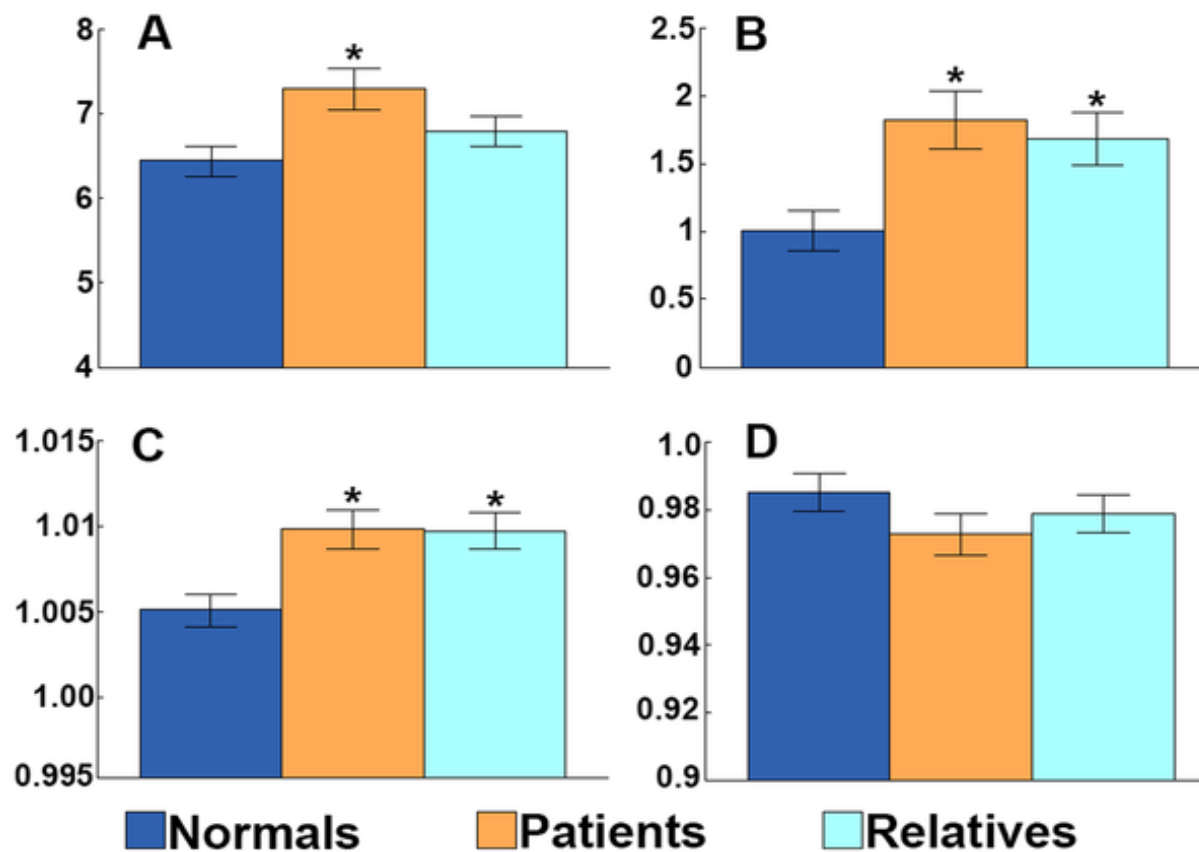
Motor co-activation in siblings of patients with juvenile myoclonic epilepsy: an imaging endophenotype?

2014;137:2469-79 Wandschneider B, Centeno M, Vollmar C, Symms M, Thompson PJ, Duncan JS, Koepp MJ.

Functional MRI activation from working memory task in controls and group differences.



An abnormal EEG network topology is present in IGE patients and first-degree relatives.



(A) mean degree K , (B) mean degree variance D , (C) clustering coefficient, and (D) normalised path length, in the 6–9 Hz band

Conclusioni:

- ✓ Nelle **epilessie idiopatiche mendeliane**, le nuove tecniche biomolecolari (GWAS, Exome Sequencing, etc.) consentono di identificare spesso mutazioni non solo di **geni canale** ma anche di altri **geni “non-canale”** (*DEPDC5*, *LGI1*, *PPRT2*, etc.).
- ✓ Molto più difficile e complessa è l'identificazione dei fattori genetici coinvolti nelle **epilessie sporadiche, multifattoriali**, nelle quali sono stati finora identificati svariati loci e/o varianti geniche di incerto significato.
- ✓ Il **link tra deficit molecolare e fenotipo clinico rimane spesso elusivo**, inoltre una considerevole eterogeneità genetica e fenotipica è evidente. Ancora più importante è l'**eterogeneità funzionale dei canali mutati**, indicando una relazione ancora più complessa tra fenotipo clinico e comportamento biofisico del canale.
- ✓ L'estrema eterogeneità genetica e fenotipica suggerisce che differenti meccanismi possono interferire su **specifici network di ipereccitabilità** capace di produrre un determinato fenotipo.
- ✓ L'identificazione di **biomarcatori specifici** è essenziale per la caratterizzazione di network epilettogeni e la comprensione dei meccanismi di epilettogenesi, con possibilità di sviluppare nuovi e affidabili protocolli diagnostici nonché nuove strategie terapeutiche.