



Dipartimento di Neuroscienze, Scienze Riproduttive ed Odontostomatologiche

Università Federico II di Napoli

Convegno SIN
Campania
Focus su novità
diagnostiche e
terapeutiche

Napoli, 13 Dicembre 2019

Nuove acquisizioni nella genetica delle epilessie

+ What's new?



New genes New pathways

DEPDC5 CDKL5

Novel genetic mechanisms

FAME

Precision/
personalized
medicine

KCNT1 KCNQ2

+ **DEPDC5** associated epilepsy

(disheveled Egl-10 and pleckstrin domain containing protein 5)

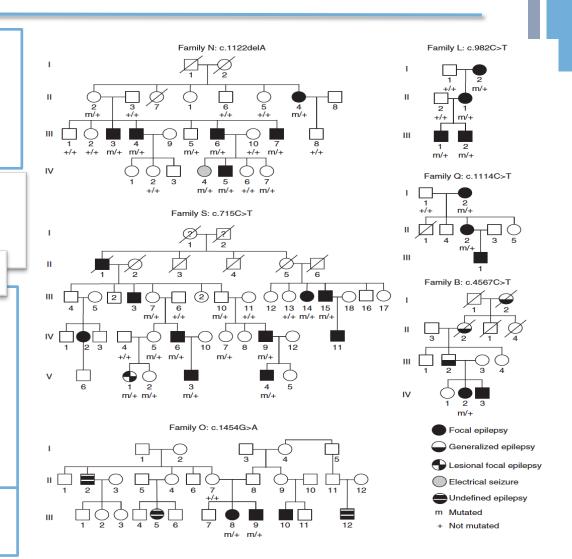
Firstly described by Dibbens et al (nature 2013) associated with familial focal epilepsy with variable foci

Mutations of *DEPDC5* cause autosomal dominant focal epilepsies

Saeko Ishida^{1,2}, Fabienne Picard³, Gabrielle Rudolf^{4,5}, Eric Noé^{1,2}, Guillaume Achaz^{2,6,7}, Pierre Thomas⁸, Pierre Genton^{9,10}, Emeline Mundwiller¹¹, Markus Wolff¹², Christian Marescaux⁴, Richard Miles^{1,2}, Michel Baulac^{1,2,13}, Edouard Hirsch⁴, Eric Leguern^{1,2,14} & Stéphanie Baulac^{1,2}

genetics

- Different lobes: frontal and temporal (both mesial and lateral)
- Variability within the same family
- NON lesional focal epilepsies
- Truncating mutations
- Loss of function of *DEPDC5*

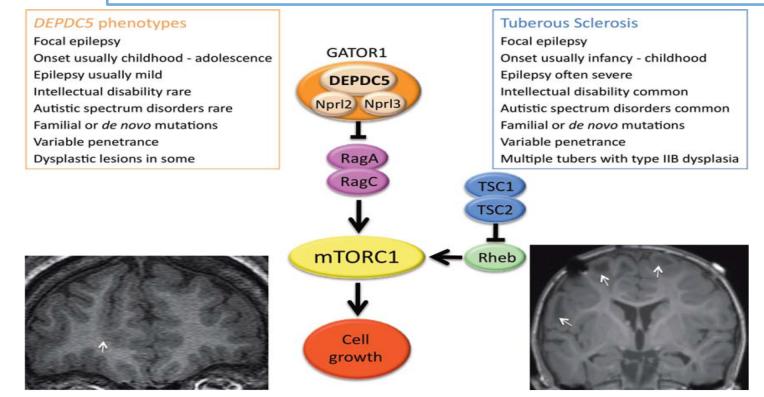


DEPDC5 associated epilepsy... mTORopathies

Mutations in Mammalian
Target of Rapamycin Regulator
DEPDC5 Cause Focal Epilepsy
with Brain Malformations

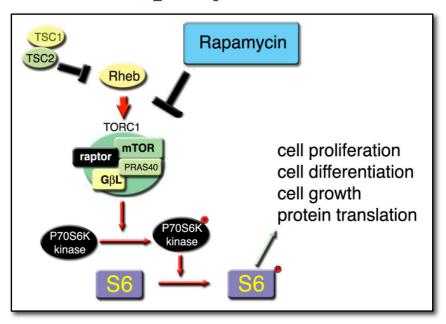
ANNALS of Neurology

Highly expressed in the developing and adult human brain Highly conserved across species Unknown function, possibly a G-protein Maybe involved in oncological processes (glioblastoma and hepatocellular carcinoma)



+ mTOR: TSC1/TSC2, and DEPDC5

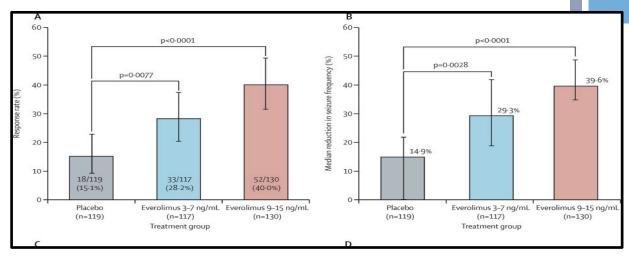
Rapamycin

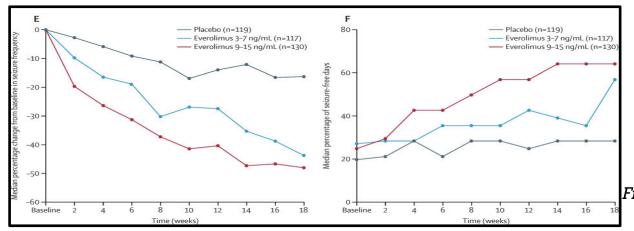


Rapamycin has shown seizures and SUDEP reduction in a TSC mouse model ((Zeng et al, 2008, Meikle et al, 2008)

Everolimus has been licensed for TSC-related epilepsy!

Everolimus





French et al. 2016

CDKL5 Hanefeld variant of Rett syndrome **EIEE2**

European Journal of Human Genetics (2013) 21, 266-273

The CDKL5 disorder is an independent clinical entity associated with early-onset encephalopathy

Stephanie Fehr¹, Meredith Wilson^{2,3}, Jenny Downs^{1,4}, Simon Williams⁵, Alessandra Murgia⁶, Stefano Sartori⁶,



- females (less frequent males);
- encephalopathy with early severe developmental delay (severely impairment gross motor function)
- early onset epilepsy, by 3 months; (infantile spasms, multifocal, myoclonic GTC)
 - hypotonia
 - sleep disturbances
 - -Dysmorphisms
 - negative brain MRI
 - -Honeymoon periods

+ CDKL5-related encephalopathy

CDKL5 gene-related epileptic encephalopathy: electroclinical findings in the first year of life

FEDERICO MELANI¹ | DAVIDE MEI¹ | TIZIANA PISANO¹ | SALVATORE SAVASTA² | EMILIO FRANZONI³ |

CDKL5 gene-related epileptic encephalopathy: electroclinical findings in the first year of life

WILLEM F M ARTS



Typical ictal electroclinical pattern: 'prolonged' generalized tonic—clonic-myoclonic seizures
This seizure type started with a **tonic—tonic/vibratory contraction**, followed by a **clonic** phase, after which a series of **spasms** ensued, gradually translating into rhythmic distal **myoclonic jerks.**It suggests that the thalamus or the brain stem is their generator



CDKL5: Honeymoon periods

ORIGINAL ARTICLE

CDKL5 mutations cause infantile spasms, early onset seizures, and severe mental retardation in female patients

H L Archer*, J Evans*, S Edwards, J Colley, R Newbury-Ecob, F O'Callaghan, M Huyton, M O'Regan, J Tolmie, J Sampson, A Clarke, J Osborne



Med Genet 2006:43:729-734. doi: 10.1136/ima.2006.04146

Epilepsy in Rett syndrome, and CDKL5- and FOXG1-gene-related encephalopathies

*†Renzo Guerrini and *Elena Parrini Epilepsia, 53(12):2067–2078, 2012

of life. For the remaining eight patients showing responses to the antiepileptic treatment, each showed a "honeymoon period," the duration of which lasted from 1 to 30 months (median 6 months). Follow-up of interictal EEG during this "honeymoon" period was available in five cases. This remained normal or showed a slight slow background activity until the median age of 6 months (range 5–24 months). Then, interictal EEG progressively deteriorated with slowing of the basal rhythm and disappearance of physiological sleep figures. For the remaining three patients (patients 4, 9, and 11), no information on the EEG during this transient seizure-free period was available.

ELSEVIER

Clinical Neurophysiology 117 (2006) 223-227

www.elsevier.com/locate/clin

Myoclonic encephalopathy in the CDKL5 gene mutation

Sabrina Buoni ^{a,e} Raffaella Zannolli ^{a,e} Vito Colamaria ^b Francesca Macucci ^a Rosanna

a daily basis. Four patients had a period without seizures in the second year of life, lasting between six weeks and nine months (patients 1, 2, 5, and 7). Honeymoon periods with new drugs were described in all patients but were followed by more severe seizures or by a change in seizure type. All but one had multiple seizure types and experienced one or more major seizures (such as generalised tonic-clonic or complex partial seizures) as well as numerous (up to 200) brief seizures (such as absences, drop fits, myoclonic jerks) every

Original Article

Historic, Clinical, and Prognostic Features of Epileptic Encephalopathies Caused by CDKL5 Mutations

Brian D. Moseley MD^{a,-}, Radhika Dhamija MBBS^b, Elaine C. Wirrell MD^{b,c}, Katherine C. Nickels MD^{b,c}

up. Although children with CDKL5 mutations can experience a "honeymoon" period when seizures become responsive to treatment (previously reported as lasting 1-30 months), their seizures invariably recur [12]. Similar to previous reports, we also

documented infantile snasms in our entire cohort. Although 4/6

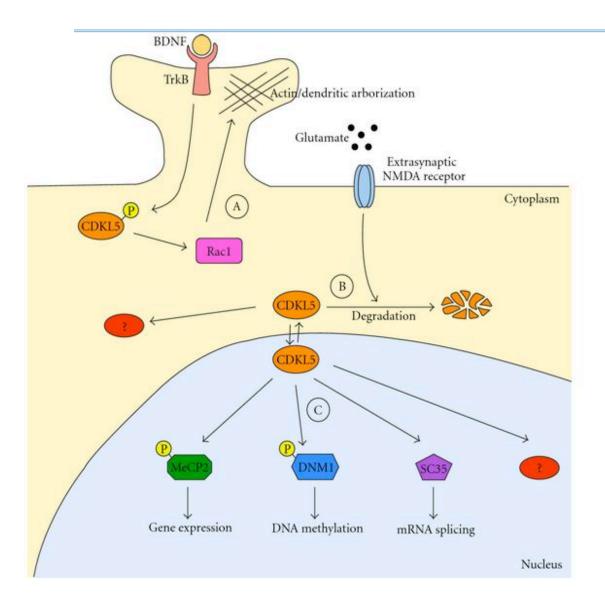
+ CDKL5-related encephalopathy







+ CDKL5 and MECP2



- Mutations affecting the Nterminal results in a more severe phenotype
- De novo
- Two functions (cytoplasmatic and nuclear)
- Defective CDKL5 protein influence phosphorylation of MECP2 and the trafficking of itself between the nucleus and the cytoplasm

+ What's new?



New genes New pathways

DEPDC5 CDKL5

Novel genetic mechanisms

FAME

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KCNT1 KCNQ2

+ Familial cortical tremor, myoclonus and epilepsy

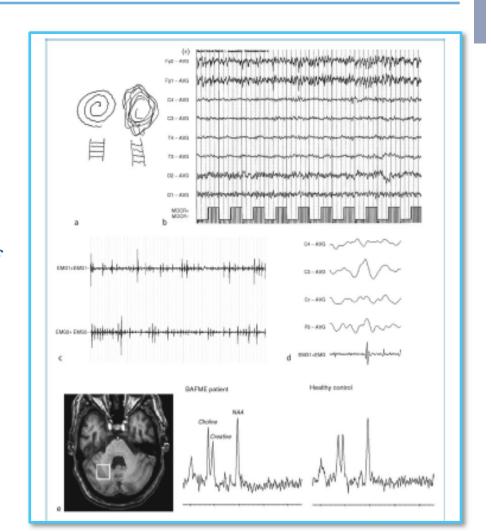
Firstly described by Uyuma in 1985 (FAME)

BAFME: Benign Adult Familial Myoclonic Epilepsy (BAFME/FAME; OMIM:601068)

ADCME: Autosomal dominant cortical myoclonus, and epilepsy (ADCME/FCTME; OMIM:607876)

Other achronyms **FCMTE**, **FCTE**

- familial occurrence (autosomal dominant)
- postural and action-induced shivering movement of the hands mimicking essential tremor, but showing the electrophysiological findings of cortical reflex myoclonus [Ikeda et al., 1990; Striano et al., 2005, Uyama et al., 2005]
- Myoclonus of upper limbs and tonic-clonic seizures, often precipitated by sleep-deprivation or photic stimulation [Ikeda et al., 1990; de Falco et al., 2003; Striano et al., 2005]



Striano & Zara 2010; The Atlas of epilepsies

FAME History: loci



Expedited Publication

FAME1

Genetic localization of the familial adult myoclonic epilepsy (FAME) gene to chromosome 8q24

N.M. Plaster; E. Uyama, MD; M. Uchino, MD; T. Ikeda, MD; K.M. Flanigan, MD; I. Kondo, MD; and L.J. Ptáček, MD Neurology, 1999

FAME2

Brain (2001), 124, 2459-2475

Autosomal dominant cortical myoclonus and epilepsy (ADCME) with complex partial and generalized seizures

A newly recognized epilepsy syndrome with linkage to chromosome 2p11.1-q12.2

Renzo Guerrini, Paolo Bonanni, Andrea Patrignani, Peter Brown, Lucio Parmeggiani, Pascal Grosse. 2,6 Paola Brovedani, 3 Francesca Moro, 3 Paolo Aridon, 4 Romeo Carrozzo 4 and Giorgio Casari^{4,5}



Familial cortical myoclonic tremor with epilepsy

The third locus (FCMTE3) maps to 5p

FAME3

Neurology® 2010;74:2000-2003

- C. Depienne, PhD⁴ E. Magnin, MD*
- D. Bouteiller, MS
- G. Stevanin, PhD
- C. Saint-Martin, PhD
- M. Vidailhet, MD
- E. Apartis, MD
- E. Hirsch
- E. LeGuern, MD, PhD P. Labauge, MD, PhD

ABSTRACT

Background: Familial cortical mycolonic tremor with epilepsy (FCMTE) is defined by autosomal dominant adult-onset cortical myoclonus (CM) and seizures in 40% of patients. Two loci, 8g23.3q24.11 (FAME1/FCMTE1) and 2p11.1-q12.2 (FAME2/FCMTE2), were previously reported without an identified gene. Unlinked families argue for a third mutated gene.

Methods: A genome-wide scan was performed in a large FCMTE family using Linkage-12 microarrays (Illumina). Refinement of the locus on 5p was performed by genotyping 13 polymorphic microsatellite markers in the 45 available family members.

Results: This large French FCMTE family included 16 affected relatives. The first symptoms were CM in 5 patients (31.2%), seizures in 5 patients (31.2%), and both at the same time in 6 patients L. Rumbach, MD, PhD

A newly identified locus for benign adult familial myoclonic epilepsy on chromosome 3g26.32-3g28

Patra Yeetong^{1,2,3}, Surasawadee Ausavarat^{2,3}, Roongroj Bhidayasiri⁴, Krisna Piravej⁵, Nath Tayard Desudchit⁶, Chaipat Chunharas⁴, Jakrin Loplumlert⁴, Chusak Limotai⁴, Kanya Sur and Vorasuk Shotelersuk^{2,3}

FAME4



FAME5

Autosomal recessive cortical myoclonic tremor and epilepsy: association with a mutation in the potassium channel associated gene CNTN2

Elisabeth Stogmann, Eva Reinthaler, Salwa ElTawil, Mohammed A. El Etribi, Elisabeth Stogmann, Eva Reinthaler, Salwa ElTawil, Mohammed A. El Etribi, Mohammed A. Mahmoud Hemeda, ² Nevine El Nahhas, ² Ahmed M. Gaber, ² Amal Fouad, ² Sherif Edris, ³ Anna Benet-Pages, ⁴ Sebastian H. Eck, ⁴ Ekaterina Pataraia, ¹ Davide Mei, ⁵ Alexis Brice, ^{6,7,8,9} Suzanne Lesage, ^{6,7,8} Renzo Guerrini, ⁵ Friedrich Zimprich, ¹ Tim M. Strom ⁴ and Alexander Zimprich ¹

+ FAME History: gene(s)

genetics

https://doi.org/10.1

Expansions of intronic TTTCA and TTTTA repeats in benign adult familial myoclonic epilepsy

Hiroyuki İshiura 1, Koichiro Doi², Jun Mitsui 1, Jun Yoshimura², Miho Kawabe Matsukawa¹, Asao Fujiyama², Yasuko Toyoshima⁴, Akiyoshi Kakita⁴, Hitoshi Takahashi⁴, Yutaka Suzuki⁵, Sumio Sugano⁴, Wei Qu², Kazuki Ichikawa², Hideaki Yurino², Koichiro Higasa⁵, Shota Shibata¹, Aki Mitsue¹, Masaki Tanaka¹, Yaeko Ichikawa⁰, Yuji Takahashi³o, Hidetoshi Date¹, Takashi Matsukawa¹, Junko Kanda¹, Fumiko Kusunoki Nakamoto¹, Mana Higashihara³, Koji Abe¹², Ryoko Koike¹³, Mutsuo Sasagawa¹⁴, Yasuko Kuroha¹³, Naoya Hasegawa⁵, Norio Kanesawa¹⁶, Takayuki Kondo¹², Takefumi Hitomi¹²¹8, Masayoshi Tada¹⁰, Hiroki Takano²⁰, Yutaka Saito²¹, Kazuhiro Sanpei²², Osamu Onodera 1, Masatoyo Nishizawa²³, Masayuki Nakamura²⁴, Takeshi Yasuda²⁵, Yoshio Sakiyama 1, Kayao Terao³⁰, Satomi Inomata-Terada¹, Masashi Hamada¹, Yuichiro Shirota¹, Akatsuki Kubota¹, Yoshikazu Ugawa³³, Kishin Koh³², Yoshihisa Takiyama³², Natsumi Ohsawa-Yoshida²³, Shoichi Ishiura³³³, Ayo Yamasaki¹⁵, Akira Tamaoka³⁶, Hiroshi Akiyama³³, Taisuke Otsuki³³, Akira Sano²⁴, Akio Ikeda³⁰, Jun Goto⁴₀, Shinichi Morishita² and Shoji Tsuji 1, Isuke Otsuki³³, Akira Sano²⁴, Akio Ikeda³⁰, Jun Goto⁴₀, Shinichi Morishita² and Shoji Tsuji 1, Isuke Otsuki³³,

Epilepsy is a common neurological disorder, and mutations in genes encoding ion channels or neurotransmitter receptors are frequent causes of monogenic forms of epilepsy. Here we show that abnormal expansions of TTTCA and TTTTA repeats in intron 4 of SAMD12 cause benign adult familial myocionic epilepsy (BAFME). Single-molocule, retime sequencing of BAC clones and nanopore sequencing of genomic DNA identified two repeat configurations in SAMD12. Intriguingly, in two families with a clinical diagnosis of BAFME in which no repeat expansions in SAMD12 were observed, we identified similar expansions of TTTCA and TTTTA repeats in introns of TMRC6A and RAPGEF2, indicating that expansions of the same repeat motifs are

id RAPGEF2, Indicatin

Intronic ATTTC repeat expansions in *STARD7* in familial adult myoclonic epilepsy linked to chromosome 2

Mark A. Corbett to et al.#

https://doi.org/10.1038/s41467-019-12671-y

Familial Adult Myoclonic Epilepsy (FAME) is characterised by cortical myoclonic tremor usually from the second decade of life and overt myoclonic or generalised tonic-clonic seizures. Four independent loci have been implicated in FAME on chromosomes (chr) 2, 3, 5 and 8. Using whole genome sequencing and repeat primed PCR, we provide evidence that chr2-linked FAME (FAME2) is caused by an expansion of an ATTTC pentamer within the first intron of STARD7. The ATTTC expansions segregate in 158/158 individuals typically affected

by EANAE from 22 and improve including 16 and involve and familiar and antital consideration

FAME 1: SAMD12

FAME 6:

TNRC6A
FAME 7:

RAPGEF2

FAME2 STARD7 doi:10.1093/brain/awz2

BRAIN 2019: 0: 1-7

BRAIN

REPORT

TTTCA repeat insertions in an intron of YEATS2 in benign adult familial myoclonic epilepsy type 4

©Patra Yeetong, Monnat Pongpanich, Adjima Assawapitaksakul, Santa
FAME4: YEATS2

I pilepsy is a common neurological disorder and identification of its causes is important for a better understanding of its pathogenesis. We previously studied a Thai family with a type of epilepsy, benign adult familial mynclomic epilepsy type 4 (BAFME4), and localized its gene to chromosome 326.5.3-q.28. Here, we used single-molecule real-time sequencing and found expansions of TITTA and insertions of TITCA repeats in intron 1 of YEATS2 in one affected member of the family. Of all the available members in the family—comprising 13 affected and eight unaffected—repeat-primed PCR and long-range PCR revealed the consergency of the control of the control subjects, none were found to harbour the TITCA repeats while four had the TITTA repeat expansions. Therefore, our findings suggest that BAFME4 is caused by the insertions of the intronic TITCA repeats in YEATS2. Interestingly, all four types of BAFME5 for which underlying genes have been found (BAFME5 1, 4, 6 and 7) are caused by the same molecular pathology, suggesting that the insertions of non-coding TITCA repeats para-invalued-in-tipeir pathogenesis.

Screon-Port

ARTICLE

https://doi.org/10.1038/s41467-019-12763-9

OPEN

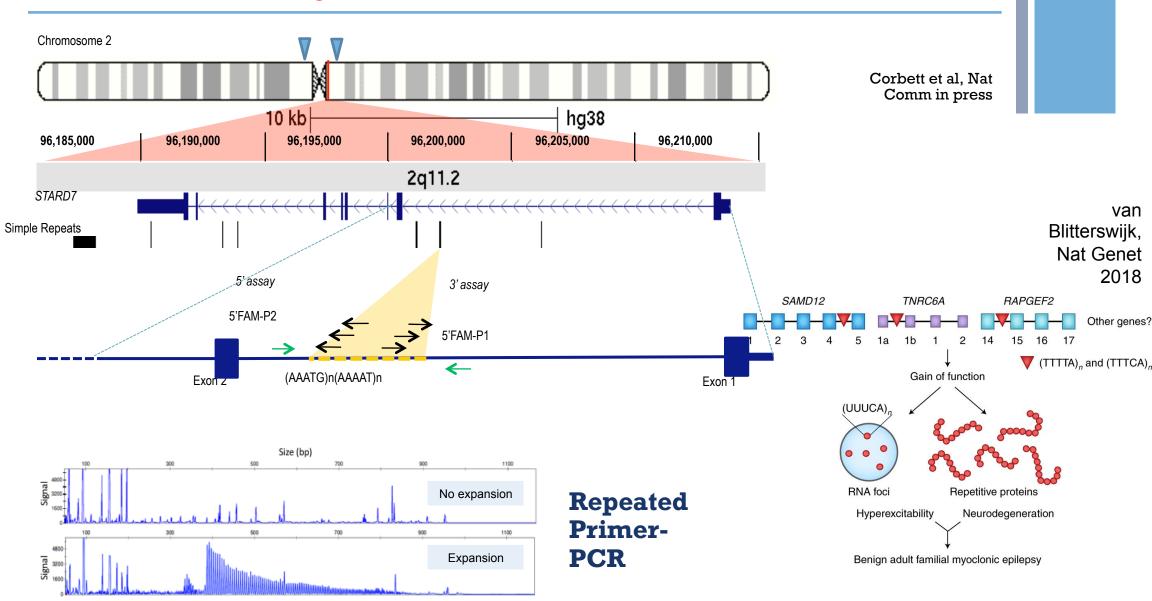
Unstable TTTTA/TTTCA expansions in *MARCH6* are associated with Familial Adult Myoclonic Epilepsy type 3

Rahel T. Florian et al.#

FAME3: MARCH6

Familial Adult Myoclonic Epilepsy (FAME) is a genetically heterogeneous disorder characterized by cortical tremor and seizures. Intronic TTTTA/TTTCA repeat expansions in SAMD12 (FAME1) are the main cause of FAME in Asia. Using genome sequencing and repeat-primed PCR, we identify another site of this repeat expansion, in MARCH6 (FAME3) in four European families. Analysis of single DNA molecules with nanopore sequencing and

+ FAME 2: *STARD7*



+ What's new?



New genes New pathways

DEPDC5 CDKL5

Novel genetic mechanisms

FAME

Precision/ personalized medicine

KCNT1 KCNQ2

+ *KCNT1* mutations: Migrating partial seizures of infancy





Quinidine

antiarrhythmic, partial antagonist of *KCNT1*previously used to reverse the hyperactivity of the mutant *KCNT1* in Xenopus oocytes

Targeted Treatment of Migrating Partial Seizures of Infancy with Quinidine

Gain of function!

David Bearden, MD,¹
Alanna Strong, PhD,²
Jessica Ehnot, PharmD,³
Marissa DiGiovine, MD,¹
Dennis Dlugos, MD, MSCE,¹ and Ethan M. Goldberg, MD, PhD¹

Migrating partial seizures of infancy is an early onset epileptic encephalopathy syndrome that is typically resistant to treatment. The most common cause is a gain of function mutation in the potassium channel *KCNT1*. The antiarrhythmic drug quinidine is a partial antagonist of *KCNT1* and hence may be a candidate drug for treatment of this condition. We report the

infancy secondary to an activating mutation in KCNT1 treated with quinidine. Treatment with quinidine was correlated with a marked reduction in seizure frequency and improved psychomotor development.

ANN NEUROL 2014;76:457-461



+ KCNT1 mutations: "ADNFLE"

Quinidine: antiarrhythmic, partial antagonist of KCNT1

Precision therapy for epilepsy due to KCNT1 mutations

A randomized trial of oral quinidine

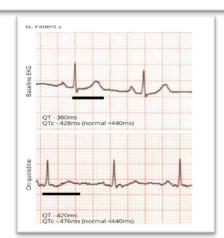
Saul A. Mullen, MBBS, PhD, Patrick W. Carney, MBBS, PhD, Annie Roten, BAppSc, Michael Ching, MPharm, PhD, Paul A. Lightfoot, BSc, Leonid Churilov, PhD, Umesh Nair, BSc, Melody Li, PhD, Samuel F. Berkovic, MBBS, MD, Steven Petrou, PhD, and Ingrid E. Scheffer, MBBS, PhD

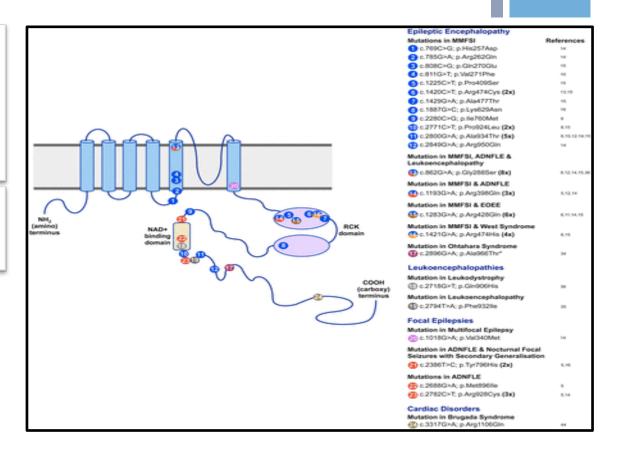
Neurology® 2018;90:e1-6. doi:10.1212/WNL.000000000004769

Conclusion

Quinidine did not show efficacy in adults and teenagers with ADNFLE. Dose-limiting cardiac side effects were observed even in the presence of low measured serum quinidine levels. Although small, this trial suggests use of quinidine in ADNFLE is likely to be ineffective coupled with considerable cardiac risks.







Lim et al. 2015



+ KCNQ2:Early-onset epileptic encephalopathy

KCNQ2 Encephalopathy: Emerging Phenotype of a Neonatal Epileptic Encephalopathy

Sarah Weckhuysen, MD, ^{1,2,3} Simone Mandelstam, MB ChB, ^{4,5} Arvid Suls, PhD, ^{1,2} Dominique Audenaert, PhD, 1,2,6 Tine Deconinck, MSc,1,2 Lieve R.F. Claes, PhD, 1,2 Liesbet Deprez, PhD, 1,2 Katrien Smets, MD, 1,2,7 Dimitrina Hristova, MD, 8 Iglika Yordanova, MSc, 9 Albena Jordanova, PhD, 1,2 Berten Ceulemans, MD, PhD, 2,10 An Jansen, MD, PhD, 11,12 Danièle Hasaerts, MD, 11 Filip Roelens, MD, 13 Lieven Lagae, MD, PhD, 14 Simone Yendle, BSc (Hons), 15 Thorsten Stanley, MD, 16 Sarah E. Heron, PhD,¹⁷ John C. Mulley, PhD,^{18,19} Samuel F. Berkovic, MD, FRS,¹⁵ Ingrid E. Scheffer, MBBS, PhD, 4,15,20 and Peter de Jonghe, MD, PhD1,2,7

ANN NEUROL 2012;71:15-25

Children with neonatal and/or infantile convulsions of unknown origin, neuropsychomotor delays, and peculiar neuroradiologic features

Whole Exome Sequencing Identifies KCNQ2 Mutations in Ohtahara Syndrome

Hirotomo Saitsu, MD, PhD,¹ Mitsuhiro Kato, MD, PhD,² Ayaka Koide, MD, PhD,³ Tomohide Goto, MD, PhD,³ Takako Fujita, MD,4 Kiyomi Nishiyama, PhD,1 Yoshinori Tsurusaki, PhD,¹ Hiroshi Doi, MD, PhD,¹ Noriko Miyake, MD, PhD,¹ Kiyoshi Hayasaka, MD, PhD,² and Naomichi Matsumoto, MD, PhD¹

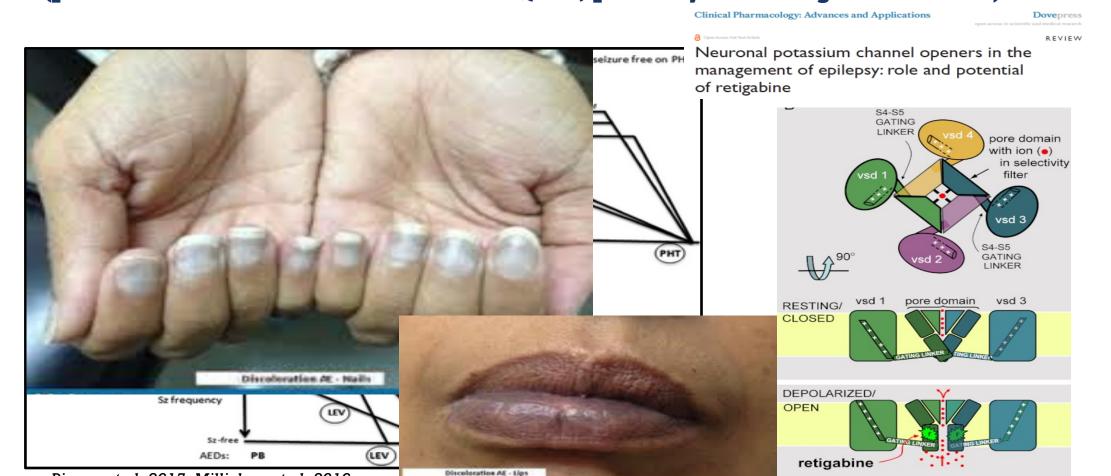
ANNALS of Neurology

2012; 72:298-300

Children with Ohtahara Syndrome (or Early Infantile Epileptic **Encephalopathy with Suppression-**Burst), the most severe and early onset epileptic encephalopathy

+ KCNQ2:Early-onset epileptic encephalopathy

Sodium channel blockers Retigabine (positive allosteric modulator of KCNQ2-5, partially reversing LOF in vitro)



+ Highlights and take home messages

- √New genes
- √New genetic mechanisms

✓ Precision medicine is the future

√ Counselling





GENETICS

This is how it works

Thanks for your attention!

HI DOC, GOOD THING THAT PERSONALIZED MEDICINE!!

STANDARD TREATMENTS NEVER WORKED FOR ME!!

