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diagnosed with DS without mutations in the SCN1A [9,10]. There is a group of other genes giving DS-like phenotype, e.g. mutations in CHD2 recently described, but PCDH19 is still the first choice in girls [11]. The PCDH19 encodes the protein protocadherin-19, involved in cell adhesion. It is expressed during the brain development and plays important role in neuronal migration and formation of synaptic connections [12]. The ARX encodes the Aristless-related homeobox protein acting as a transcription factor modulating cerebral development and pattering. Mutations in this gene have been associated with syndromes exhibiting variable phenotypes, including idiopathic WS [13]. WS clinical picture differs significantly from SCN1A-related disorders; however, the single case of mutation in SCN1A was described as causative for infantile spasms [14].

All probands were also carriers of heterozygous mutation in the SCN1A – p.Thr1174Ser, which seems to modify the patients’ main phenotype. This substitution by itself has been causative for GEFS+ phenotype in one family and migraine in probands’ relatives. The purpose of our report is to present this mutation as a possibly causative factor of familial GEFS+ syndrome, but also as a factor potentially changing the phenotypes of the epileptic encephalopathies, caused by other mutations in the SCN1A, ARX or PCDH19.

Material and Method

Subjects

Five families (Figure1) with different types of epilepsy / epileptic encephalopathies were included into the study due to the presence of the p.Thr1174Ser (c.3521C>G) substitution in the SCN1A. Blood samples were collected from 16 affected individuals (5 probands) and their 6 asymptomatic relatives; this substitution was hereditary in all families. All families’ probands were among the patients referred for the SCN1A testing and clinically diagnosed with GEFS+ spectrum or DS (typical and atypical). This patients group included 250 probands representing the same number of families. Additional genes analysis was performed in two epileptic encephalopathy cases, leading to PCDH19 and ARX mutations identification.

<table>
<thead>
<tr>
<th>Genotype (gene, mutation)</th>
<th>Proband 1/Fam.1</th>
<th>Proband 2/Fam.2</th>
<th>Proband 3/Fam.3</th>
<th>Proband 4/Fam.4</th>
<th>Proband 5/Fam.5</th>
</tr>
</thead>
<tbody>
<tr>
<td>ARX</td>
<td>c.[1449-43_1448del][=] p.[?] [0]</td>
<td></td>
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<tr>
<td>PCDH19</td>
<td>c.[463G&gt;T] [=] p.[Asp155Tyr] [+]</td>
<td></td>
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</tbody>
</table>

| Gender | F | M | F | M | F |
| Age at investigation | 6 y. | 17 y. | 11 y. | 21 y. | 10 y. |
| Diagnosis | GEFS+ | Dravet syndrome | Dravet syndrome | Atypical West syndrome | EFMR |
| Family history (Pedigrees Figure 1) | intellectual impairment and migraine in mother; epilepsy in sister; intellectual impairment in sister and brother | migraine in mother and maternal grandmother | intellectual impairment and epilepsy in mother | emotional disturbances in mother | migraine in father, father’s sister and grandfather |
| Age at onset | 3 mo. | 8 mo. | 7 mo. | 3 mo. | 7 mo. |
| First seizure | tonic-clonic, febrile seizures | hemiconic during infection | febrile seizures (type unknown) | vaccination, loss of consciousness | tonic-clonic during infection |

Finally (Table 1), probands were diagnosed with GEFS+ (1 subject, Fam.1), DS (2 sub., Fam. 2, 3), WS with atypical course (1 sub., Fam. 4) and EFMR (1 sub., Fam. 5). After mutations identification the clinical data were re-evaluated.
Subsequent seizure types | tonic-clonic, hemidonic, tonic with cyanosis | tonic-clonic, hemidonic, myoclonic seizures, tonic | tonic-clonic, hemidonic, tonic with cyanosis, absence, myoclonic | infantile spasms, atonic, hemidonic, myoclonic-tonic-clonic | tonic with apnoea, tonic-clonic
---|---|---|---|---|---
Seizure clusters | Yes | Yes | Yes | Yes | Yes
Status epilepticus | No | Yes | Yes | Yes | Yes
Acute encephalopathy | No | No | No | Yes | Yes
Seizure induced by | - | CBZ, LTG, VGB, TPM, GBP | CLN, VGB, OXC, LTG | VGB, TPM | LTG, VGB
Improvement with | VPA | VPA, CLB | LEV | VPA, BZD, LEV | STR
Remission age | 5 mo. | no | no | 12 y. | 8 y.
EEG | focal changes and then normal | generalized changes, slowing background | generalized and focal changes, slowing background | hypersynchronia, then generalized changes | focal and generalized changes, then normal
Neurological exam | normal | ataxia, tetraparesis | ataxia | tetraparesis | ataxia
Development | normal at onset; intellectual impairment at the age of 6 years | normal at onset; regression from the age of 2 years; severe intellectual impairment now | normal at onset; significant regression and autism at the age of 2 years | normal at onset; delayed in the first year of life; acute regression related to encephalopathy at the age of 6 years | normal at onset; start delayed in the second year of life; mild intellectual impairment now
Comments | Intellectual impairment is not related to SCN1A mutation; caused probably by other familial factors | Severe disease course was partially related to ineffective treatment, the presence of the SCN1A p.Trp1174Ser has no influence of phenotype as is monoallelic and localised 3’ to premature STOP codon | Severe phenotype with fast progressing intellectual impairment and autism might be related to coexistence of two mutations in SCN1A gene | Hemiclonic seizures triggered by fever and acute encephalopathy episode and treatment response might be related to additional mutation with SCN1A | Severe EFMR phenotype, treatment response and appearance of acute encephalopathy might be related to additional mutation in SCN1A.

| Table 1 | Characterization of the probands with p.Thr1174Ser substitution with/without additional pathogenic mutations in SCN1A or other gene, GEFS+ inclusion criteria: familial occurrence of classic febrile seizures, febrile seizures plus (with onset or persisting after 6 years of age, which are followed by afebrile tonic-clonic seizures), severe epileptic encephalopathy and other types of generalized or focal seizures [15].

Inclusion criteria for Dravet syndrome: normal development before onset, first seizures start in the first year of life in the form of generalized or unilateral febrile clonic / tonic-clonic seizures, secondary appearance of refractory different types of seizures (myoclonic, complex partial seizures and absences), often with photosensitivity, EEG often normal at first, but later characteristically shows generalized spike-wave activity, psychomotor development stagnates around the second year of life, and affected individuals show subsequent mental decline and other neurologic manifestations [16].

Phenotypes of epilepsies were verified and classified according to International League against Epilepsy (ILAE) classification system [17,18].

Ethics statement
The study was approved by the Ethics Committee of the Institute of Mother and Child, Warsaw (Poland). Written informed consent from all participants (parents and adult patients) was a criterion for the inclusion in the study.

Genetic testing
Molecular analysis was performed on genomic DNA extracted from subjects' venous blood, isolated using Genomic Maxi AX kit (A&A Biotechnology).

Analysis of the all relevant genes – SCN1A, PCDH19 and ARX – was performed by direct sequencing (Sanger method). The exons with exon / intron boundaries were sequenced with specific intronic primers (primers sequence, PCR conditions available on request). The ABI BigDye v.3.2 terminator sequencing kit (Applied Biosystems) was used. The multiplex ligation-dependent probe amplification (MLPA) was performed using commercially available MLPA probe mixes: P-137A2 SCN1A and P330-A1 PCDH19 (MRC-Holland) for rearrangements analysis in the SCN1A and PCDH19 genes.

Sequence data were analysed using Mutation Surveyor V3.24 software (Soft Genetics LLC.) in comparison to appropriate reference sequences NM_001165963 SCN1A; NM_001184880 PCDH19; NM_139058 ARX (all sequences according to GRCh37 Human Genome release). Variants were labelled according to numbering of the
longest transcript of cDNA accession number AB093548 (NCBI Ref Seq) in the case of the SCN1A gene identification.

MLPA data were analysed using the Gene Marker V1.8 software (Soft Genetics LLC.) with standard parameters.

Proband's parental and relatives samples were tested by direct PCR amplification and DNA sequencing of the appropriate exons in relevant genes (SCN1A and SCN1A/PCDH19 or SCN1A/ARX). In two cases of identified coexistence of two mutations in the SCN1A, their mono / biallelic localization was analysed. When both mutations (p.Arg1245* and p.Thr1174Ser) were inherited, inheritance analysis was performed. In the case when one of mutations was de novo (p.Arg712*), its origin – paternal or maternal was defined by SCN1A SNPs analysis. Referring to the dbSNP database the SNPs of the SCN1A close to mutations in the exon12 (introns 11 and 12) were selected (data on request).

The impact of discovered missense substitutions on the protein structure and functional changes were analysed with the PolyPhen-2 / HumVar model software and Mutation Taster Software [19,20]. Splice site mutation prediction was performed using Alamut Visual Splicing Predictions software (Alamut Visual v.2.5, Interactive Biosoftware).

Involvement of the identified mutations in the clinical phenotypes was checked by analysis of the Human Gene Mutation Database Professional (HGMD Professional v.2014.4).

**Results**

**Identification of pathogenic mutations**

All probands had got heterozygous mutation in the exon 17 of the SCN1A c.3521C>G, p.Trp1174Ser.

Based on HGMD data, this mutation has already been reported as pathogenic, and is associated mainly with hemiplegic migraine. However, there is still a question mark over this substitution pathogenicity, as it is also reported in dbSNP database (rs121918799), and in ExAC database with MAF = 0.27 for European Non-Finish population and 0.18 for general analysed population (ExAC). As the mutation p.Thr1174Ser shows variable penetrance, the mutation's carriers were not necessary free of undiagnosed / unreported seizures or migraine (individuals with severe paediatric diseases were excluded from the ExAC data set). We must be aware that this database was created from a variety of large-scale sequencing projects of various disease-specific (no epilepsy project included) and population genetic studies. According to ClinVar Database, the clinical significance of this substitution is also uncertain.

In all patients presented in the paper, c.3521C>G, p.Trp1174Ser substitution was heritable, and could be correlated in some families with migraine phenotype. Analysis of the SCN1A in family with GEFS+ (Fam.1), revealed only this one mutation.

Patients with DS had also got truncating mutations, we recognized as main pathogenic in SCN1A: c.2134C>T, p.Arg712* (Fam.2) and c.3733C>T, p.Arg1245* (Fam.3). Both had already been reported in HGMD as pathogenic and related to Myoclonic Epilepsy of Infancy. The first mutation - p.Arg712* was a novel one, the second p.Arg1245* - was inherited from less affected mother. The p.Arg712* mutation raised de novo on maternal allele and was monoallelic with p.Trp1174Ser (patient's SCN1A genotype c.[2134C>T;3521C>G];[=]).

In female EFMR patient heterozygous, de novo mutation c.463G>T, p.Asp155Tyr was identified in the PCDH19. This is a novel mutation, not reported in HGMD. It causes the substitution of highly conservative amino acid localised in extracellular, functional cadherin domain probably influencing the homophilic interactions of PCDH19 molecules. Substitution functional effect analysis using the prediction algorithms showed high scores, indicating it as a protein function damaging variant (PolyPhen-2, Mutation Taster). The p.Trp1174Ser mutation was in this case of paternal origin (patient's genotype PCDH19c.[463G>T];[=], SCN1A c.[3521C>G];[=]).

The male patient finally diagnosed with WS with atypical course, was referred twice as having epilepsy of unknown aetiology and later as DS-like. He had got the novel, not previously described mutation in the X-linked ARX, deletion of the 79nt in IVS4 and Ex5, c.1449-43_1448del [HGMD]. This mutation alters the acceptor splice site of exon 5, probably causing the last exon skipping and synthesis of truncated protein (Alamut Visual Splicing Predictions). Mutation in the ARX was of maternal and SCN14 p.Trp1174Ser of paternal origin (patient's genotype ARX c.[1449-43_1448del];[0], SCN1A c.[3521C>G];[=]).

**Clinical features of patients with identified mutations**

All probands development was within normal range till disease occurrence, and pregnancy history was not complicated with the exception of proband from the Fam.1, born by caesarean section (Apgar 10), due to pregnancy complicated by diabetes.

**Case 1: GEFS+ (SCN1A p.Thr1174Ser)**

GEFS+ family proband (Table1; Figure1, Fam.1 II-4) was the 6-year-old girl, who at the age of 3-5 months presented tonic-clonic, and tonic seizures with cyanosis, and hemiclonic fits, appearing on both sides alternatively. Seizures were related to infections and high fever in initial period, then without fever, clustered, but short lasting (approx. 1 min), ceasing spontaneously. Focal spikes in temporo-parieto-occipital were observed in ictal EEG. Neurological examination, MRI and metabolic tests were within normal range. Seizures ceased under valproate (VPA) treatment. EEG normalization was observed during the following years. Cognitive development regressed from 100 (Brunet-Lezine scale) in the second year of life to 60 points (Leiter test) at the age of 6 years.

Proband's sister (II-3) with normal IQ, developed afebrile generalized tonic – clonic seizures (GTCS) and complex partial seizures with cyanosis, and hemiclonic fits, appearing on both sides alternatively. Seizures were related to infections and high fever in initial period, then without fever, clustered, but short lasting (approx. 1 min), ceasing spontaneously. Focal spikes in temporo-parieto-occipital were observed in ictal EEG. Neurological examination, MRI and metabolic tests were within normal range. Seizures ceased under valproate (VPA) treatment. EEG normalization was observed during the following years. Cognitive development regressed from 100 (Brunet-Lezine scale) in the second year of life to 60 points (Leiter test) at the age of 6 years.

**Case 2: DS (SCN1A monoallelic p.Arg712 and p.Thr1174Ser)**

The proband was 17-year-old male (Table 1; Figure 1 Fam.2 III-1). He has displayed febrile hemiconic seizures (appearing on both sides alternatively) and GTCS since the age of 8 months. He was treated with phenobarbital (PB), carbamazepine (CBZ), VPA, vigabatrin (VGB),

topiramate (TPM), and lamotrigine (LTG), and clobazam (CLB) in different combinations. Seizures were refractory – long lasting GTCS and CPS were observed several times. Myoclonic seizures occurred after gabapentin (GBP) introduction at the age of 7 years. Seizure worsening was observed during ketogenic diet. Dravet syndrome was diagnosed at the age of 9 years. Parents did not consent for stiripentol. IQ to severe impairment. Neurological examination showed ataxia and mild spastic paraparesis. MRI was normal. Family history analysis revealed migraine without aura in proband’s mother (II-2) and maternal grandmother (I-2) who were heterozygous SCN1A p.Thr1174Ser substitution carriers.

**Case 3: DS (SCN1A biallelic p.Arg1245 and p.Thr1174Ser)**

The proband was a 11-year-old girl (Table 1, Figure Fam3 II-1). Her first febrile seizures occurred during otitis at the age of 7 months and they were recurrent during the first two years of life. Hemiconic seizures were appearing on both sides alternatively and tonic-clonic seizures have been observed since the age of 2 years, accompanied by tonic seizures with cyanosis during its age of 4 years and absence seizures from the age of 5 years. Myoclonic seizures occurred when she was 7 years old. Seizures are still polymorphic, very frequent, in clusters and last several hours. VGB, oxcarbazepine (OXC) and LTG triggered seizure appearance. VPA, TPM, CLB, STP treatment did not influence on epilepsy course; mild improvement was achieved after high levetiracetam (LEV) doses introduction, but was observed during one month only. Very rapid development regression was observed at the second years of life; autism with severe mental impairment and ataxia was confirmed when she was 3 years old.

Brain MRI was normal. Generalized series of delta waves, paroxysms of spikes and spike wave complexes (3 – 4 Hz) with slow background activity and focal sharp waves and sharp wave slow wave complexes in the right frontal-temporal region were observed in EEG.

Proband’s mother shows intellectual impairment with epilepsy history, but epileptic syndrome has not been precisely diagnosed. She was treated with clonazepam (CLN) and VPA at the age of 1 – 15 years. She is a heterozygous p.Arg1245* mutation carrier in the SCN1A gene.

**Case 4: WS with atypical course (SCN1A p.Thr1174Ser and ARX c.449-43_1448del)**

Proband, 21-year-old male (Table 1, Figure Fam4 II-1) is with negative family history for migraine or epilepsy, but his mother (I-2), who was a ARX c.449-43_1448del mutation carrier suffered from affective disorders. There was no information on any neurological disorders of his father, a heterozygous SCN1A p.Trp1174Ser mutation carrier. At the age of 3 months, the day after DTP+Polio vaccination he experienced short loss of consciousness, with flaccidity and paleness, without seizures. PB treatment was introduced. Patient development had been normal till the age of 7 months, when infantile spasms (IS) occurred with subsequent tonic seizures. Head USG was normal, and hysparrythmia was observed in EEG. After VPA introduction seizure decrease was observed. Cognitive development and speech regression has been observed since then. Sporadic IS were accompanied by daily hemiconic seizures (usually in clusters) at the age of 2 years; appearing on both sides alternatively, frequently related to high fever / infection. Generalized paroxysms of spikes and spike wave complexes (3–4 Hz) were observed in EEG. VGB added to existing antiepileptic treatment caused tonic-clonic status epilepticus. TPM and LTG induced myoclonic seizures. VPA was withdrawn due to pancreatitis. Partial seizure remission was achieved by nitrazepam (NT) introduction at the age of 4 years. Episode of acute encephalopathy, lasting for a week, occurred at the age of 6 years. He was comatose, seizures were not observed. Demyelination process was detected in MRI and generalized background slowing was found in EEG. He was treated with steroids. Laboratory results (including blood tests, cerebrospinal fluid tests) were negative for viral infection and metabolic disorders. Patient general functional status deteriorated – severe mental impairment was diagnosed with subsequent tetraparesis. Full seizure remission was achieved after LEV introduction at the age of 12 years.

The male patient was finally diagnosed with atypical WS.

**Case 5: EFMR (SCN1A p.Thr1174Ser and PCDH19 p.Asp155Tyr)**

10-year-old girl (Table 1; Figure 1, Fam5 III-2), developed acute encephalopathy at the age of 7 months, preceded by tonic-clonic seizures. She was comatose for 23 days. Pneumonia and viral encephalitis (her brother was suffering from chickenpox during this period) was diagnosed, even cerebrospinal fluid and blood test (general and viral) were negative. Bacterial infection, borreliosis and the most common metabolic disorders were excluded. MRI showed cortico-subcortical atrophy, moderate ventricular enlargement, and hypertensity on T2-weighted images within the white matter suggesting encephalitis. VPA and PB treatment was introduced; seizures were not observed. Finally, she fully recovered. The next episode of tonic seizures clusters with long-lasting apnoea was observed when she was at the age of 17 months. EEG was normal, intellectual development equalled 83 points, based on Brunet-Lezine scale. TPM was added to previous antiepileptic treatment. Focal seizures clusters lasting several minutes to dozens of hours were observed during the next years (between 23 months of age and 8 years of age). Generalized tonic-seizures were very rare. Antiepileptic and steroids treatment were not effective, LTG and VGB provoked seizures intensity up to status epilepticus. EEG showed focal changes in temporo-parieto-occipital region predominantly in right hemisphere, or generalized, in the form of sharp waves, sharp wave slow wave complexes, and rarely spikes and spike wave complexes. Seizures appearance was not always related to infections, but during high fever with or without seizures her general status was very severe, like in acute encephalopathy. Antiepileptic treatment was modified at 8 year of age – STP was added to VPA and CLB, achieving seizure remission. Patient suffers currently from mild intellectual impairment, which is accompanied by severe ataxia. Mild cerebral atrophy is seen in MRI and EEG findings are within normal range.

The family medical records revealed the migraine history of proband’s father (II-1) and grandfather (I-1), both heterozygous SCN1A p.Trp1174Ser mutation carriers. Father’s sister also suffered from migraine, but was not available for molecular testing.

**Discussion**

Most epilepsies / epilepsy syndromes are characterized by explicit clinical and aetiology heterogeneity. A genetic contribution to epilepsy has been well established through the twin and family studies indicating its mono- and, mainly polygenic / multifactorial character. Recently conducted analysis using the massive parallel sequencing technologies showed, that rare monogenic epilepsies include both...
familial and, in the severe cases like epileptic encephalopathies, "sporadic" forms caused by de novo mutations in particular genes. Inter- and intrainfamilial heterogeneity of monogenic forms of epilepsy caused by the same mutation indicates other factors involvement – genetic and environmental [21]. The role of such factors in the disease pathogenesis may vary in each patient, what is observed in clinical variability of GEFS+ (GEFS2P) families with SCN1A mutations [22]. Genotype–phenotype correlation determination is particularly difficult in cases with different genetic defects coexistence, in which symptoms can be overlapped or endured. The picture is complicated by the fact, that standard diagnostic tests do not detect mutations modifying the main disease course [23]. Such mutations, of small additive effect, may be localized in the same, as a main pathogenic mutation, gene or in the other ones. Such situations seem to be more common than expected since the whole genomic / exomic sequencing (WGS/WES) has been employed in identification of neurogenetic disorders molecular background. The good examples are homozygous / biallelic mutations identification in the SCN1B [24,25] and SCN1A [26] genes. In the first case patients developed DS, although heterozygous mutations in the \textit{SCN1A} are mainly related to GEFS+ (GEFS1P). Homozygous missense mutations identified in consanguineous families by Brunklaus et al. caused DS and GEFS2P, while heterozygous carriers remained unaffected [26]. Pathological mutations in the \textit{SCN1A} gene were also described as co-morbid with the POLG gene mutation [27] and electron transport chain defects [28] resulting in expression of both, mitochondrial disease and DS. This data suggest that multiple gene mutations could alter phenotype in some patients. Many additional factors such as epileptic activity and interictal epileptiform discharges, and antiepileptic treatment, and others environmental factors apart from DNA changes may have impact on phenotypical variability [29]. For example, the significant impact of improper treatment on cognitive development outcome in patient #2 is considered.

Here, we present a group of probands, the p.Trp1174Ser substitution in the \textit{SCN1A} gene carriers, which might be a causative factor of familial GEFS+ syndrome, but also acts as a factor potentially changing the phenotypes of the epileptic encephalopathies caused by other mutations in the \textit{SCN1A}, ARX and \textit{PCDH19} genes.

The p.Trp1174Ser mutation caused the GEFS+ in Fam.1 – possible migraine in mother (I-2) and mild epilepsy phenotypes in two children (II-3,II-4). No epilepsy symptoms are observed in boy (II-2), also a mutation carrier, what indicates variable penetrance of this substitution. Intellectual impairment was observed in three subjects of this family, too – mutation's carriers (I-2,II-2) and non-carrier (II-1). That is why it seems this feature should be considered independently from epilepsy symptoms. In two families (Fam.2 and 3) substitution coexisted with truncating \textit{SCN1A} mutations. In the Fam.2 p.Trp1174Ser substitution alone probably caused migraine in proband's mother and grandmother (I-2, II-2). In proband (III-1) it was localised on maternal chromosome 3’ in cis to main pathogenic mutation p.Arg712’, and probably had no influence on the final phenotype. The severe disease course of this patient was rather related to improper treatment before the molecular diagnosis. Different situation was observed in Fam.3. Mutations p.Trp1174Ser and p.Arg1245’ were biallelic. The truncating mutation was heritable, but in proband's mother (I-2) caused less severe phenotype. Proband's clinical picture indicates that missense substitution presence had got significant impact on the disease course. Patient showed acute and severe development regression in the second year of life and very early autism onset. In children with typical DS such symptoms are developed gradually [21] and significant IQ decrease is observed in longer period of time, usually between the 4 to 6 years of life [30]. This patient showed extreme treatment resistance. During the 11 years of treatment no remission was observed. This might be related to the presence of two trans \textit{SCN1A} mutations of course, although we cannot exclude partial consequence of antiepileptic drugs use contraindicated in DS patients.

From clinical point of view, we found cases 4 (Fam.4 II-1) and 5 (Fam.5 II-1) the most interesting among presented group of patients. Probands were diagnosed with epileptic encephalopathies due to mutations in the other genes - ARX and \textit{PCDH19}. However, both of them presented symptoms typical of mutations in \textit{SCN1A} gene, too. The patient with DS developed the first event after vaccination, what is rather typical for children with \textit{SCN1A} mutations [31]. Subsequent infantile spasms and tonic seizures appeared after several months. At the age of 2 years gradual DS remission was observed, but the hemiconcious seizures triggered by high fever / infections started. The presence of such seizures, as well as adverse or no effect to the usually used in WS treatment, may also indicate the significant role of the \textit{SCN1A} mutation on final phenotype expression. The case of female patient harboring both \textit{PCDH19} and \textit{SCN1A} mutations is in fact very complex one. Her phenotype shares symptoms of both EFMR and DS. Probably, that is why she was twice independently referred for genetic diagnosis (once as DS, and the other time as a suspicion of having \textit{PCDH19}). Her epilepsy course with clusters of focal seizures could have suggested the EFMR phenotype, as focal seizures clusters are less characteristic for Dravet syndrome, whilst severe ataxia she developed later on is rather related to DS phenotype [32].

Additionally, WS and EFMR probands suffered from the acute encephalopathy episodes. Its occurrence in children carrying the \textit{SCN1A} mutations has already been reported [33,34]. It may be a very significant complication in DS, but has been also described in previously healthy children, as well as in patients diagnosed with partial epilepsy or febrile seizures, who were carriers of such mutations [32,34-36]. The presence of the p.Trh1174Ser substitution in the \textit{SCN1A} might contribute to acute encephalopathy occurrence in described patients, although in different pathomechanism in each of them, what has been confirmed by the various MRI data (demyelination in WS vs. cortico-subcortical atrophy in EFMR). Various clinical outcomes might be dependent on main mutation type or other factor not known for us, yet.

Migraine was recognized in six relatives of our three patients. It is worth to add that the link between migraine (or broadly meaning 'headaches') and epilepsy is very complicated and beyond the role of \textit{SCN1A}. There are three types of headache-related seizures according to the current ICHD-2 so far: (1) migraine-triggered seizure (migralepsy), (2) hemiconcious epileptica and (3) post-ictal headache. Parisi et al. [37] has shown a new view on this topic. According to these Authors, a new entity should be introduced into forthcoming ICHD-3 classification i.e. ictal epileptic headache, where a headache might be a sole manifestation of epileptic seizure or even non-convulsive status epilepticus. So, we could only speculate if some of them being mutation carriers may have epileptic seizures recognized as migraine.

Our data confirm possible involvement of more than one genetic factor as a molecular background in observed phenotype, beside the reduced penetrance or specific mutations variable expressivity. In epileptic encephalopathies cases with atypical or "plus" course the possible involvement of other genetic factors should always be considered. How complex may be influence of molecular factors on
phenotype shows growing evidence that the role of SCN1A is beyond the spectrum of GEFS/DS. As Kasperaviciute et al. [38] showed in the GWAS study with 1018 patients, SCN1A was associated with mesial temporal lobe epilepsy with hippocampal sclerosis with febrile seizures. More recently, meta-analysis of combined genome-wide association data from 12 cohorts of individuals with epilepsy and controls made by ILAE Consortium on Complex Epilepsies suggests that specific loci can act pleiotropically, raising risk for epilepsy broadly, or can have effects limited to a specific epilepsy subtype which would be the subject of further investigation [39].

Taking this into account, it would be worth considering how wide the genetic diagnosis should be performed in patients whose clinical picture is beyond established epilepsy criteria? Genetic analysis widening should also be considered in families with variable phenotypes, in cases of unexpected antiepileptic drug treatment response and in cases with acute encephalopathies. Additional modifiers identification may influence on clinical prognosis, patient management and genetic counselling. The implications for the latter in patients with ‘additional genetic hits’ are really complex and this should be considered in the incoming ‘NGS era’.

Conflicts of interest
The authors have no conflicts of Interest.

Acknowledgement
This work was supported by grants from the MSHE/NSC NN407054439 and 800/N-ESFEuroEPINOMICS/10/2011/0.

References


