Chapter 1
Introduction

1.1 Malformations of cortical Development (MCDs)

The development of the human cerebral cortex is a complex and tightly regulated process that occurs during several gestational weeks and can be divided into three steps: neural stem cell proliferation and cell type differentiation, neuronal migration, and neuronal positioning and development of cortical organization and connectivity (Gleeson et al., 2014). The disruption of any one of these processes may result in a wide range of developmental brain disorders that are designated as malformations of cortical development (MCD) which may be restricted to discrete cortical areas or may, alternatively, be diffuse. These disorders are recognized as a cause of developmental disabilities and epilepsy (Guerrini et al., 2005).
So far, more than 100 genes have been associated with one or more types of MCD. Disrupted pathways include cell-cycle regulation at many steps (especially mitosis and cell division), apoptosis, cell-fate specification, cytoskeletal structure and function, neuronal migration and basement-membrane function, and many inborn errors of metabolism. A subset of MCD genes – especially those associated with megalencephaly – are associated with postzygotic (i.e., mosaic) mutations in genes of the *MTOR* pathway (Lee et al., 2012). Genetic testing needs accurate assessment of imaging features and familial distribution, if any, and can be straightforward in some disorders but requires a complex diagnostic algorithm in others. Because of substantial genotypic and phenotypic heterogeneity, for most MCDs a comprehensive analysis of clinical, imaging, and genetic data is needed to properly define these disorders.

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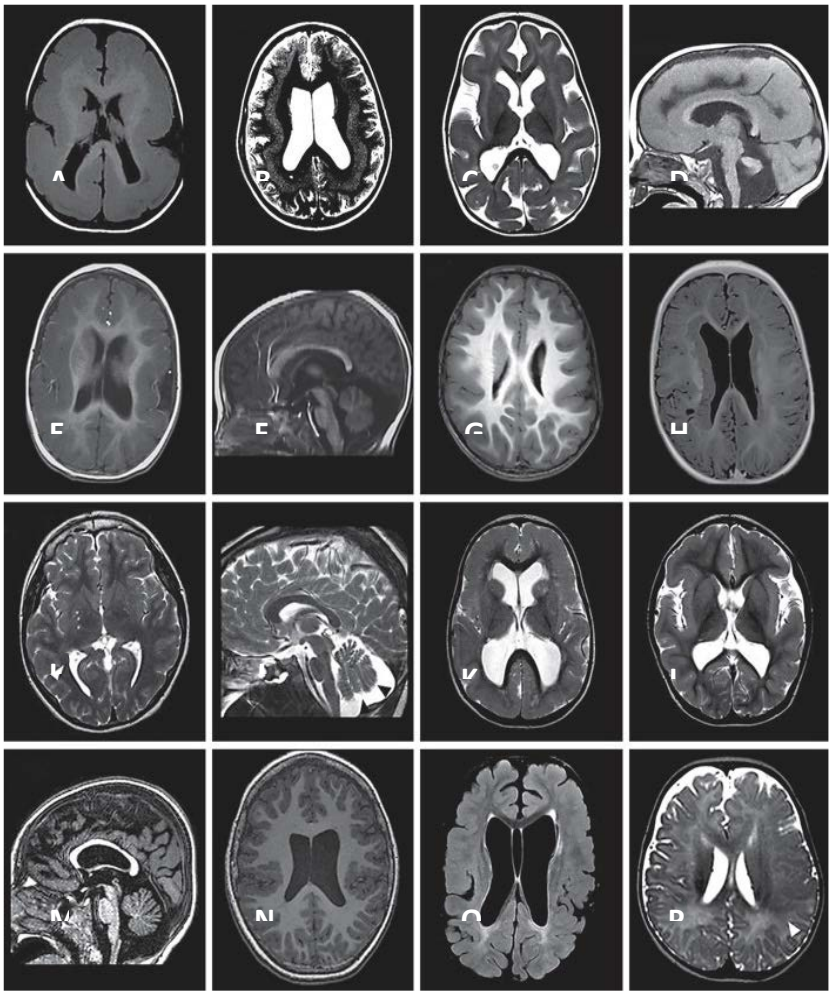
FUP Best Practice in Scholarly Publishing (DOI 10.36253/fup_best_practice)

1.1.1 Lissencephaly and Subcortical Band Heterotopia

Lissencephaly (LIS) or smooth brain and the associated malformation known as subcortical band heterotopia (SBH) are the classic malformations associated with deficient neuronal migration (Dobyns et al., 2012).
LIS is a neuronal migration disorder characterized by absent (agyria) or decreased (pachygyria) convolutions, cortical thickening and a smooth cerebral surface (Barkovich et al., 2012; Guerrini and Dobyns, 2014) (Figure 1, A). Different subtypes of LIS are readily distinguished based on the number of cortical layers affected, and include two-layered, three-layered, and four-layered forms (Forman et al., 2005). The most common, classical LIS (four-layered form), features a very thick cortex (10–20 mm vs. the normal 4mm) and no other major brain malformations. The cytoarchitecture consists of four primitive layers, including an outer marginal layer which contains Cajal-Retzius neurons (layer 1), a superficial cellular layer, which contains numerous large and disorganized pyramidal neurons (layer 2) corresponding to the true cortex, a variable cell sparse layer (layer 3), and a deep cellular layer (composed of medium and small neurons) which extends more than half the width of the mantle (layer 4) (Golden and Harding, 2004).
SBH is a related disorder in which bands of grey matter are interposed in the white matter between the cortex and the lateral ventricles (Guerrini and Parrini et al., 2010) (Figure 1, B). Histopathology demonstrates that heterotopic neurons settle close to the cortex in a pattern suggestive of laminar organization.

Figure 1: Brain MRI of patients with different malformations of the cerebral cortex. **A** T1-weighted axial section. Posterior to anterior pachygyria in a boy with *LIS1* mutation. **B** T2-weighted axial section. Diffuse SBH in a girl with *DCX* mutation. **C**, **D** T2-weightedaxial section and T1-weighted sagittal section. Lissencephaly and cerebellar hypoplasia in a girl with *RELN* mutation. **E**, **F** T1-weightedaxial section and T1-weighted sagittal section. Thickened cortex with simplified gyral pattern and cerebellar hypoplasia in a girl with *TUBA1A* mutation. **G** T1-weighted axial section. Diffuse simplified gyral pattern with prominent thickening and infolding of the sylvian fissures in a boy with *TUBB2B* mutation. **H** T1-weighted axial section. Typical, classical bilateral PNH in a girl with an *FLNA* mutation. Bilateral nodules of subependymal heterotopia are contiguous and rather symmetric, extensively lining the ventricular walls. **I**, **J** T2-weighted axial section showing mild colpocephaly with unilateral PNH (white arrowhead) and T2-weighted sagittal section through the midline, showing cerebellar vermis hypoplasia (black arrowhead) with mega cisterna magna in a patient carrying a deletioni n the 6q27 chromosomal region. **K** T2-weighted axial section. Bilateral frontoparietal polymicrogyria in a boy with *GPR56* mutation. **L**, **M** T2-weighted axial section and T1-weighted coronal section. Pachygyria and perisylvian polymicrogyria in a girl with *DYNC1H1* mutation. **N** Axial T1-weighted section in a patient with a mosaic *PIK3R2* mutation. **O**, **P** T1-weighted and T2-weighted axial images form patients carrying mosaic mutations in the *MTOR* gene with different percentages of mosaicism [**O**: p.Thr1977Ile, 20% of mosaicism in blood, **P**: p.Ser2215Phe, 5.5% of mosaicism in dysplastic brain tissue) showing bilateral cortical dysgyria (**O**) and focal cortical dysplasia (**P**, white arrowhead)]. (from Parrini et al., 2016)



Children with the most common types of LIS (or SBH) typically appear normal as newborns. Most affected children come to medical attention during the first year of life due to neurological deficits in the first weeks or months [Barkovich et al., 2012]. The major medical problems encountered are ongoing feeding problems and epilepsy of many different types that are often intractable. Classical LIS is rare; patients with severe LIS have early developmental delay, early diffuse hypotonia, later spastic quadriplegia, and eventual severe or profound mental retardation. Seizures occur in over 90% of LIS children, with onset before 6 months in about 75% of the cases (Guerrini and Filippi et al., 2005). Most LIS children will subsequently continue to have epileptic spasms in association with other seizure types. The EEGs show diffuse, high amplitude, fast rhythms, which are considered highly specific for this malformation. The main clinical manifestations of SBH are mental retardation and epilepsy (Barkovich et al., 1994). Epilepsy is present in almost all patients and is intractable in about 65% of the cases: about 50% of these epilepsy patients have focal seizures, and the remaining 50% have generalized epilepsy (Parrini et al., 2016).

Genetic basis and diagnosis

Lissencephaly, subcortical band heterotopia, and lissencephaly with cerebellar hypoplasia are always genetic. To date, mutations in 12 lissencephaly genes have been identified, which account for roughly 90% of patients. However, two major genes have been associated with classic lissencephaly and SBH. The *LIS1* gene causes the autosomal form of LIS (Reiner et al., 1993), while the *DCX* gene is X-linked (des Portes et al., 1998; Gleeson et al., 1998). Although either gene can result in either LIS or SBH, most cases of classic LIS are due to deletions or mutations of *LIS1* (Mei et al., 2008), whereas most cases of SBH are due to mutations of *DCX* (Matsumoto et al., 2001). *LIS1* encodes a 45 kDa protein (PAFAH1B1), which functions as a regulatory subunit of platelet-activating factor acetylhydrolase (PAF-AH) (Hirotsune et al.,1998). *DCX* encodes a 40 kDa microtubule-associated protein (DCX) that is expressed in migrating neuroblasts (Gleeson et al., 2000). The DCX protein contains two tandem conserved repeats. Each repeat binds to tubulin and both repeats are necessary for microtubule polymerization and stabilization. *LIS1*-related LIS is more severe in the posterior brain regions (p>a gradient), whereas *DCX* related LIS is more severe in the anterior brain (a>p gradient). About 60% of patients with p>a isolated LIS (ILS) carry genomic alterations or mutations involving *LIS1* (Mei et al., 2008). A simplified gyral pattern in the posterior brain, with underlying SBH, has been associated with mosaic mutations of *LIS1* (Sicca et al., 2003). Most *DCX* mutations cause a>p SBH/pachygyria. Mutations of *DCX* have been found in all reported pedigrees and in 80% of sporadic females and 25% of sporadic males with SBH (Matsumoto et al., 2001). Genomic deletions of the *DCX* gene have been identified in females with sporadic SBH and in males with X-linked lissencephaly (Mei et al., 2007). Maternal germline or mosaic *DCX* mutations may occur in about 10% of cases of either SBH or X-linked lissencephaly (Gleeson et al., 2000b). Hemizygous males with *DCX* mutations have classical LIS, but rare boys with

missense mutations and anteriorly-predominant SBH and rare females with DCX mutations and normal brain MRI have been described (Guerrini et al.,2003). Autosomal recessive lissencephaly with cerebellar hypoplasia consists of mild frontal predominant lissencephaly, plus severe hippocampal and cerebellar hypoplasia and dysplasia. This pattern has been associated with mutations in *RELN* (Hong et al., 2000) or *VLDLR* (an essential cell-surface receptor for reelin) (Figure 1, C-D) (Boycott et al., 2005). Many patients with *ACTB* and *ACTG1* mutations show pachygyria with a>p severity gradient, similar to that observed in males with *DCX* mutations (Riviere et al.,2012; Verloes et al., 2015). A mutation in the *CDK5* gene has been identified in four individuals with lissencephaly and cerebellar hypoplasia born from a highly consanguineous family (Magen et al., 2015). In patients with classic lissencephaly, cytogenetic and molecular investigations are part of the diagnostic process. When isolated lissencephaly is diagnosed, careful assessment of the antero-posterior gradient of the abnormal cortical pattern will suggest whether to investigate *LIS1* or *DCX*. When lissencephaly is more severe posteriorly, it is worth performing first MLPA to rule out *LIS1* deletions/duplications. If a deletion/duplication is not found, *LIS1* sequencing should then be performed. In boys whose MRI shows more severe pachygyria in the frontal lobes, sequencing of the *DCX* gene is indicated. In patients with SBH direct sequencing of *DCX* should be performed. If a *DCX* mutation is not found, MLPA analysis then should be performed. Direct sequencing is also indicated in the mothers of patients harbouring a *DCX* mutation or other female relatives. Analysis of the *ACTB* and *ACTG1* genes should be performed in patients with frontal predominant pachygyria who are not harbouring *DCX* mutations.
Most reported *LIS1* alterations are *de novo*: given the theoretical risk of germline mosaicism in either parent (which has never been demonstrated for *LIS1*), a couple with a child with lissencephaly is usually given a 1% recurrence risk. However, recently, Mineyko et al. described a male with pachygyria who inherited a novel *LIS1* gene mutation from the mother with somatic mosaicism. (Mineyko et al., 2016) In addition, we identified a mother and son with focal epilepsy, mild cognitive impairment, and pachygyria, carrying a novel constitutional missense variant in the LIS1 gene, segregating in the proband and in his mother.
When a *DCX* mutation is found in a boy with lissencephaly, mutation analysis of *DCX* should be extended to the proband's mother, even if her brain MRI is normal. If the mother is a mutation carrier, the mutation will be transmitted according to Mendelian inheritance. If the mother is not a carrier, there still is a risk of germline mosaicism, which is roughly estimated at around 5%.

1.1.2 Tubulinopathies and Related Disorders

Mutations of tubulin genes were first reported as causing lissencephaly (for *TUBA1A*) (Keayset al., 2007) or polymicrogyria (PMG) (for *TUBB2B*) (Jaglin et al., 2009). However, the cortical malformations seen in most individuals with mutations of tubulin or tubulin motor genes comprise a wide spectrum of morphological abnormalities whose characteristics are at times distinctive but can also overlap with those of lissencephaly and polymicrogyria by brain imaging and

neuropathology (Cushion et al., 2013; Poirier et al., 2013). The full range of these malformations vary from extreme lissencephaly with completely absent gyri, total agenesis of the corpus callosum, and severe cerebellar hypoplasia, to less severe lissencephaly with moderate-to-severe cerebellar hypoplasia, to classic lissencephaly, to an atypical polymicrogyria-like cortical malformation with cerebellar hypoplasia (Cushion et al., 2013;Poirier et al., 2013). Cortical thickness varies and can be mildly thin, normal or mildly thick. Most children with mutations of tubulin genes have severe intellectual disability and intractable seizures.

Genetic basis and diagnosis
Nine genes (*KIF2A, KIF5C, TUBA1A, TUBA8, TUBB, TUBB2B, TUBB3, TUBG1* and *DYNC1H1*) associated with tubulinopathies have been identified so far (Bahi-Buisson et al., 2014). Findings from functional studies suggest that abnormal brain development in tubulinopathies results from a dominant negative effect of heterozygous missense mutations (in the absence of loss-of-function mutations) on the regulation of microtubule-dependent mitotic processes in progenitor cells, and on the trafficking activities of the microtubule-dependent molecular motors KIF2A, KIF5C, and *DYNC1H1* in post-mitotic neuronal cells (Poirier et al., 2013). Heterozygous missense mutations of *TUBA1A* have been found in this syndrome, with *TUBA1A* accounting for ~30% of patients (Kumar et al., 2010; Cushion et al., 2013) (Figure 1, E-F-G). Testing is available for all of the tubulin and tubulin motor genes so far identified. For all but *TUBA8*, only *de novo* heterozygous missense mutations have been found. The phenotype (if any) associated with truncation or deletion mutations of most of the tubulin genes is unknown. Probably, these genes are intolerant to loss of function mutations, as also suggested by the observation that in the ExAC Database (http://exac.broadinstitute.org/), the tubulin genes, with the exception of *TUBA8*, have a probability of loss of function intolerance (pLI) near to 1.00, a value consistent with an almost complete intolerance. A single family with a tubulinopathy phenotype has been reported with a homozygous mutation of *TUBA8* (Abdollahi et al., 2009).

1.1.3 Neuronal Heterotopia

There are three main groups of heterotopia: periventricular (usually nodular: PNH), subcortical and leptomeningeal (glioneuronal heterotopia found over the surface of the brain), of which only the first two can be detected by imaging. PNH is by far the most frequent. SBH is a mild form of LIS and has been dealt with previously.
PNH consists of nodules of grey matter located along the lateral ventricles with a total failure of migration of some neurons (Barkovich et al., 2012; Guerrini and Dobyns, 2014); it ranges from isolated, single, to confluent bilateral nodules (Figure 1, H). The overlying cortex may show an abnormal organization. When the nodules are bilateral and numerous, a genetic basis is probable, and associated brain malformations are often reported (Parrini et al., 2006). Patients with the classic X-linked PNH typically have bilateral contiguous nodules that spare the temporal horns and mild cerebellar vermis hypoplasia with mega cisterna magna (Parrini et al., 2006). Patients with rare autosomal recessive bilateral PNH can have

severe congenital microcephaly and thin overlying cortex with abnormal gyri (Sheen et al., 2004). In the fairly common posterior predominant syndromes, PNH is limited to the trigones, temporal and occipital horns, and can be associated with overlying polymicrogyria, hippocampal and cerebellar hypoplasia, or hydrocephalus (Pisano et al., 2012).
*A*lthough most patients with PNH come to medical attention because they have focal epilepsy of variable severity, there is a wide spectrum of clinical presentations, including several syndromes with intellectual disability and dysmorphic facial features. There is some correlation between the size of PNH and the likelihood of concomitant structural abnormality of the cortex and clinical severity (Parrini et al., 2006), but there seems to be no correlation between the size and number of heterotopic nodules and cognitive outcome or epilepsy severity. Most females with PNH due to *FLNA* mutations have epilepsy, with normal or borderline cognitive level. Age at seizure onset is variable. Most patients have focal seizures, which can be easily controlled or refractory (Parrini et al., 2006). There is no clear relationship between epilepsy severity and the extent of nodular heterotopia.

Genetic Basis and Diagnosis
The most common syndromic form of PNH (X-linked PNH) consists of bilateral contiguous or near contiguous nodules and is most often caused by *FLNA* mutations. All other PNH syndromes are rare.
X-linked PNH is a clinically and genetically heterogeneous disorder occurring most frequently in women, associated with high rates of prenatal lethality in male foetuses, and a 50% recurrence risk in the female offspring. Almost 100% of the families and 26% of sporadic patients harbor mutations in the *FLNA* gene (Parrini et al., 2006), which also causes cardiovascular abnormalities in some patients of both sexes and gut malformations in boys. Only a few male patients with PNH owing to *FLNA* mutations have been reported (Guerrini et al., 2004). *FLNA* encodes a large actin-binding phosphoprotein that stabilizes the cytoskeleton and contributes to the formation of focal adhesions along the ventricular epithelium [Fox et al., 1998]. *FLNA* may be required for the initial attachment of neurons onto the radial glial scaffolding before migration from the ventricular zone (Lu et al., 2006). Failure of migrating neurons to attach to radial glia is one likely mechanism leading to the formation of heterotopia. A rare recessive form of PNH owing to mutations of the *ARFGEF2* gene was described in two consanguineous pedigrees (Sheen et al., 2004) in which affected children had microcephaly, severe cognitive delay, and early-onset seizures. Other genetic forms of PNH have been associated with chromosomal rearrangements, in particular 6q27deletion (Figure 1, I-J) including *C6orf70* (also known as *ERMARD*) mapping in 6q27, and a few additional putative causal genes (*EML1, FAT4* and *DCHS1)* (Cappello et al., 2013; Conti et al., 2013; Kielar et al.,2014).
FLNA mutation analysis should be performed in patients with 'classical' bilateral PNH. When PNH is associated with microcephaly, the autosomal recessive form caused by *ARFGEF2* mutations should be ruled out. Patients with PNH associated with other brain malformations or extra neurological defects, should be studied with array-CGH. Classical PNH is much more frequent in women and likely to be

caused by *FLNA* mutations. Among carrier women, about half have *de novo FLNA* mutations, whereas the remaining have inherited mutations. Although maternal transmission is much more likely, father-to-daughter transmission is possible. Given that germline mosaicism of *FLNA* has never been reported, the recurrence risk (for other children) seems to be very low when a mutation is found in the proband but neither parent is a carrier. Counselling is very difficult when PNH is not related to either *FLNA* or *ARFGEF2,* and array-CGH study is advised. Familial PNH unrelated to these genes is exceptionally low.

1.1.4 Polymicrogyria

The term polymicrogyria defines an excessive number of abnormally small gyri that produce an irregular cortical surface with a lumpy aspect (Bielschowsky, 1916). Polymicrogyria can be limited to a single gyrus, involving a portion of one hemisphere, be bilateral and asymmetrical, bilateral and symmetrical, or diffuse. Sometimes, it is associated with deep clefts that may extend through the entire cerebral mantle to communicate with the lateral ventricle (schizencephaly) (Barkovich and Kjos et al., 1992). Macroscopically, polymicrogyria appears as an irregular or pebbled cortical surface. The perisylvian cortex is the most frequently affected. The cortex often appears thickened to 8–12 mm, but when viewed microscopically, it is overfolded and not necessarily thick. While polymicrogyria most often occurs as an isolated malformation, it can occur with several other brain malformations, including microcephaly, megalencephaly, grey matter heterotopia, ventriculomegaly as well as abnormalities of the septum pellucidum, corpus callosum, brainstem and cerebellum. When schizencephaly is present, the cortex edges can seem to fuse (closed lips) or stay at distance (open lips). The clefts of schizencephaly can be unilateral or bilateral. An area of polymicrogyria can occur in the cortex contralateral to a unilateral cleft (Yakovlev and Wadsworth, 1946).
Using CT and low-field strength MRI, polymicrogyria is difficult to discern and may only appear as a mildly thickened, irregular cortex. For this reason, polymicrogyria is frequently misdiagnosed as pachygyria or LIS. The imaging appearance of polymicrogyria varies with the patient's age. In newborns and young infants, the malformed cortex is very thin with multiple, very small undulations. After myelination, polymicrogyria appears as thickened cortex (usually 6–10 mm) with irregular cortex-white matter junction. In schizencephaly, the grey matter lining the cleft has the imaging appearance of polymicrogyria with an irregular surface, deep infolding (the cleft), mildly thick cortex, and stippling of the interface between grey and white matter. Schizencephaly is often bilateral but frequently asymmetrical; the contralateral hemisphere should be closely assessed for milder clefts or polymicrogyria without cleft (Barkovich and Kjos, 1992). Polymicrogyria has been described in a number of topographic patterns. Most of these are bilateral and symmetrical, the most common of which is bilateral perisylvian polymicrogyria, although the perisylvian form maybe asymmetric or unilateral. Other bilateral symmetric forms are generalized, bilateral frontal, and parasagittal parieto-occipital polymicrogyria (Guerrini et al., 1997; Barkovich et al., 1999;

Leventer et al., 2010), although little or no neuropathological data is available to support the classification.
The clinical manifestations of polymicrogyria vary widely and depend on several factors. The most severe outcomes occur in children with severe microcephaly (–3 SD or smaller), abnormal neurological examination, widespread anatomic abnormality, and additional brain malformations such as heterotopia or cerebellar hypoplasia. The best outcomes are in individuals who have localized unilateral polymicrogyria without other malformations. Polymicrogyria can affect eloquent cortical areas representing language or primary motor functions, yet these functions can be retained with little or no disability (Guerrini and Barba, 2010). Bilateral perisylvian polymicrogyria is associated with mild to moderate intellectual disability, epilepsy, and impaired or motor skills. More severely affected patient shave minimal or no expressive speech. The frequency of epilepsy in these patients is 60–85%, although seizure onset may not occur until the second decade, usually between 4 and 12 years of age (Kuzniecky et al., 1993; Barkovichet al., 1999).
Patients with closed-lip schizencephaly typically present with hemiparesis or motor delay, whereas patients with open-lip schizencephaly typically present with hydrocephalus, seizures and intellectual disability, which can be severe (Packard et al., 1997). Seizure types include infantile spasms, complex partial seizures as well as tonic, atonic, and tonic-clonic seizures, although these are less common.

Genetic Basis and Diagnosis
Numerous causes, both genetic and non genetic, have been associated with polymicrogyria. Non genetic causes other than hypoxia or hypoperfusion relate mainly to congenital infections, primarily cytomegalovirus (Evrard et al., 1989; Barkovich and Lindan et al, 1994). Polymicrogyria is associated with a wide number of patterns and syndromes as well as mutations in several genes: various types of single-gene inheritance have been hypothesized for polymicrogyria, based on observations of families with X-linked (Guerreiro et al., 2000; Villard et al., 2002; Santos et al., 2008), autosomal dominant (Guerreiro et al., 2000; Chang et al., 2006), and autosomal recessive forms (Hilburger et al., 1993; Guerreiro et al., 2000). Bilateral frontoparietal polymicrogyria, (fig. 1 K) has been associated with mutations in the *GPR56* gene in families with recessive pedigrees (Piao et al., 2004). Polymicrogyria occurs with a few types of severe congenital microcephaly, such as autosomal recessive syndromes associated with mutations in the *WDR62* (Bilgüvar et al., 2010), *NDE1 (*Alkuraya et al., 2011), or *KATNB1* (Mishra-Gorur et al., 2014) genes. Polymicrogyria with microcephaly or normal head size has been reported with several tubulin and tubulin motor genes, especially *TUBB2B* (Figure 1, G) (Jaglin et al., 2009; Guerrini et al., 2012) and *DYNC1H1* (Figure 1, L, M) (Poirier et al., 2013). Autosomal recessive forms of polymicrogyria have been linked to mutations of *RTTN* (Kheradmand Kia et al., 2012). Also, polymicrogyria has now been reported in several megalencephaly syndromes. Recently, it has been demonstrated that mutations in *PIK3R2*, a pivotal gene of the PI3K-AKT-mTOR pathway, may account for up to 15% of all patients with bilateral perisylvian polymicrogyria with or without megalencephaly (Figure 1, N) (Mirzaa et al., 2015).

Some copy-number variants have been associated with polymicrogyria, but only deletions in 1p36.3 and 22q11.2 are common (Robin et al., 2006; Dobyns et al., 2008). Indeed, when these 2 loci are excluded, copy number variants seem to be rare. A causal gene has not been identified for any of these loci.

1.1.5 Megalencephaly, Hemimegalencephaly and Focal Cortical Dysplasia

The term megalencephaly refers to an abnormally large brain that exceeds the mean for age and gender by 2SD (De Myer, 1986). Megalencephaly has most often been classified simply as a disorder of brain size, but recent studies have shown that megalencephaly with normal cortex by imaging, megalencephaly with polymicrogyria, and dysplastic megalencephaly (including classic hemimegalencephaly) as well as FCD can all result from mutations in genes in the PI3K-AKT-mTOR pathway (Lee et al., 2012; Poduri et al., 2012; Rivière et al., 2012). Hemimegalencephaly and FCD constitute a spectrum of malformations of cortical development with shared neuropathological features. The former is primarily defined by macroscopic enlargement of (more or less) one hemisphere, while FCD is primarily defined by histopathology. As currently classified (Blümcke et al., 2011), FCD encompasses a wide spectrum of cortical malformations with variable features, including microscopic neuronal heterotopia, dyslamination, and abnormal cell types. FCD has been divided into 3 major types and 9 subtypes based on histopathological features (Blümcke and Spreafico, 2011; Blümcke et al., 2011). Type 1 FCD is characterized by abnormal cortical lamination, type 2 FCD includes cortical dyslamination with dysmorphic neurons (2a) and balloon cells (2b), type 3 FCD occurs in combination with other brain lesions (e.g., tumors) (Blümcke et al., 2011). The histological changes in hemimegalencephaly, which can be considered as an extreme hemispheric form of FCD, are similar, if not identical, to FCD type 2, with cortical dyslamination and dysmorphic neurons, without (type 2a) or with (type 2b) balloon cells, blurred junctions between grey and white matter, and increased heterotopic neurons in white matter (De Rosa et al.,1992; Blümcke et al., 2011; Guerrini et al., 2015).
The most common cortical malformation in megalencephaly is perisylvian polymicrogyria that looks very similar to perisylvian polymicrogyria in patients with normal or small head size. The cortical changes in hemimegalencephaly are severe and consist of an enlargement of part or a complete hemisphere (or less often bilateral asymmetrical involvement) with no consistent preference for which lobes of the brain are enlarged (Salamon et al., 2006).
The developmental and health complications of megalencephaly differ widely. The most common problems include developmental delay, intellectual disability, and seizures that can start early in life and be intractable. Children with diffuse symmetrical or mildly asymmetrical megalencephaly, with or without associated polymicrogyria, have a large head size at birth that soon exceeds +3 SD (Mirzaa et al., 2012). Their early development is delayed, and later cognitive development varies from normal to severe intellectual disability. Seizures can begin at any time in childhood. Epilepsy usually begins in the first weeks or months of life and can include infantile spasms and other epileptic encephalopathies. The most common

clinical sequelae of FCD are seizures. Developmental delay, cognitive disability, and focal neurological deficits are only observed with extensive dysplasias. Early seizure onset has been associated with infantile spasms with asymmetrical or focal features (Guerrini and Filippi, 2005).

Genetic Basis and Diagnosis

Megalencephaly without cortical malformations occurs in benign autosomal dominant macrocephaly, a poorly defined disorder. Megalencephaly with polymicrogyria occurs in megalencephaly-capillary malformation syndrome (with mutations of *PIK3CA*) and megalencephaly-polymicrogyria polydactyly-hydrocephalus syndrome (with mutations of *PIK3R2* or *AKT3*) (Mirzaa et al., 2012). Hemimegalencephaly most often occurs without syndromic features, and has recently been associated with mosaic mutations of *PIK3CA*, *AKT3*, and *MTOR* (Figure 1, O-P). (Lee et al., 2012) Hemimegalencephaly has also been associated with tuberous sclerosis (D'Agostino et al., 2004; Tinkle et al., 2005). The highly focal and variable nature of FCD type 2b, and the pathological resemblance to tubers in tuberous sclerosis, led to the hypothesis that somatic mosaic mutations of genes that encode proteins in the PI3K-AKT-mTOR pathway, which includes the tuberous sclerosis associated genes *TSC1* and *TSC2,* were implicated in FCD (Crino, 2009). This hypothesis has been in part confirmed by studies documenting pathogenic germline and mosaic mutations in the *mTOR* gene or in other genes belonging to the PI3K-AKT-mTOR pathway (i.e., *A KT3*, *DEPDC5* and *NPRL3*) in the dysplastic tissue of FCD type 2a and 2b (D'Gama et al., 2015; Lim et al., 2015; Sim et al., 2015). In addition, somatic duplications in the 1q chromosomal region compassing the *AKT3* gene have been
associated with megalencephaly, hemimegalencephaly, and FCD type1b (Poduri et al., 2012; Wang et al.,
2013; Conti et al., 2015). When performing genetic testing for disorders possibly caused by mosaic mutations, the screening of multiple tissues (e.g., blood, saliva, and skin fibroblasts) is advisable. Indeed, although testing DNA extracted from blood is the gold standard for identifying de novo constitutive mutations, the analysis of different tissues may help in identifying mutations that are only present in a subset of somatic cells (Nellist et al., 2015).

Table 1: Most common gene involved in MCDs. ACC = agenesis of the corpus callosum; CBLH = diffuse cerebellar hypoplasia; DMEG = dysplastic megalencephaly; ILS = isolated LIS; MCAP = megalencephaly-capillary malformation syndrome; MDS = Miller-Dieker syndrome; MPPH = megalencephaly-polymicrogyria-polydactyly-hydrocephalus syndrome; PMG = polymicrogyria.

Megalencephaly-polymicrogyria and dysplastic megalencephaly	***Gene***
MPPH, DMEG	*AKT3*
Weaver syndrome	*EZH2*
MCAP	*PIK3CA*
MPPH	*PIK3R2*
FCD Somatic	*MTOR*
FCD	*DEPDC5*
FCD Somatic	*AKT3*
FCD	*NPRL3*
Polymicrogyria (PMG)	***Gene***
Bilateral frontoparietal PMG	*GPR56*
Asymmetric PMG	*TUBB2B*
PMG and rolandic seizures, oromotor dyspraxia	*SRPX2*
PMG and agenesis of the corpus callosum (ACC), microcephaly	*TBR2*
PMG and aniridia	*PAX6*
PMG and microcephaly	*NDE1*
PMG and microcephaly	*WDR62*
PMG fumaric aciduria	*FH*
PMG and ”band-like calcfications”	*OCLN*
Perysilvian PMG and CHARGE syndrome	*CHD7*
PMG and Warburg Micro syndrome	*RAB3GAP1*
PMG and Warburg Micro syndrome	*RAB3GAP2*
PMG and Warburg Micro syndrome	*RAB18*
PMG-like, microcephaly, ACC	*DYNC1H1*
PMG-like, microcephaly, ACC, CBLH	*TUBA1A*
PMG-like, microcephaly, ACC, CBLH	*TUBA8*
PMG-like, microcephaly, ACC, CBLH	*TUBB3*
PMG-like, microcephaly, ACC, CBLH	*TUBB*
PMG-like, microcephaly, ACC	*EOMES*
PMG and Goldberg-Shprintzen syndrome	*KIAA1279*
PMG and CK syndrome	*NSDHL*

PMG and CEDNIK syndrome	*SNAP29*
PMG and Knobloch syndrome	*COL18A1*
Bilateral Perysilvian PMG	*PIK3R2*
Bilateral temporooccipital PMG	*FIG4*
PMG and microcephaly	*RTTN*

Lissencephaly (LIS)	***Gene***
MDS	*LIS1*
ILS or SBH	*LIS1*
ILS or SBH X-linked	*DCX*
Pachygyria and Baraitser-Winter	*ACTB*
Pachygyria and Baraitser-Winter	*ACTG1*
ILS or SBH	*TUBA1A*
XLAG X-linked	*ARX*
LIS cerebellar hypoplasia	*RELN*
LIS cerebellar hypoplasia	*VLDR*
LIS cerebellar hypoplasia	*CDK5*
Posterior predominant pachygyria	*DYNC1H1*
Posterior predominant agyria/pachygyria	*KIF2A*
ILS	*TUBA1A*
ILS	*TUBB2B*
Posterior predominant pachygyria	*TUBG1*
Classic LIS with variable gradient (p>a or a>p)	*KIF5C*
Periventricular nodular heterotopia (PNH)	***Gene***
Classical bilateral PNH	*FLNA*
Ehlers-Danlos syndrome and PNH	*FLNA*
Facial dysmorphisms, severe constipation and PNH	*FLNA*
Fragile-X syndrome and PNH	*FMR1*
Microcephaly and PNH	*ARFGEF2*
Agenesis of the corpus callosum, polymicrogyria and PNH	*ERMARD*
PNH and Van Maldergem syndrome type 2	*FAT4*
PNH and Van Maldergem syndrome type 1	*DCHS1*
Donnai-Barrow syndrome and PNH	*LRP2*

1.2 MCDs molecular diagnosis

The massive parallel sequencing technology, also known as next-generation sequencing (NGS), has revolutionized the field of molecular biology allowing simultaneous screening for mutations in hundreds of loci. In NGS, fragmented DNA is amplified and sequenced in parallel, then aligned to the reference genome and evaluated for nucleotide changes and small insertions/deletions by bioinformatics software. The advent of NGS has considerably accelerated the identification of MCDs causing genes, greatly increasing their number and related knowledge (Fernández-Marmiesse et al., 2018) Accordingly, the scenario of genetic diagnostic testing has significantly changed with the application of NGS, including whole-exome sequencing (WES) and genes panels sequencing. Genes panels replace a single-gene approach with a panel of genes or gene regions that have known or suspected associations with the disease or the phenotype under study. They can be purchased with preselected or custom designed content to include genomic regions of interest (Di Resta et al., 2018). WES, instead, is not limited to selected genes but includes the exons of almost all the known human protein coding genes (about 20,000) (Bahareh Rabbani et al., 2014). The screening of multiple genes in the same experiment has the invaluable advantage of boosting new genotype-phenotype correlations and possibly identifying genetic causes of MCD for which molecular diagnosis is still missing.
However, although a broader clinical use of WES would be desirable, limitations remain that hamper its use and prefer the use of the gene panel approach due to technical reasons: by reducing the number of regions to be examined, much deeper coverage can be achieved, increasing the chances of detecting Copy Number Variations (CNVs) that involve targeted genes and detecting somatic mosaic mutation. For these reasons, the use of gene panels remains effective particularly in malformation with a focal origin.

1.3 Possible treatments for MCDs

Currently, there are no treatments for diffuse MCDs, while for FCD and HME the treatment of choice is epilepsy surgery, which is however only applicable to a subset of patients (Korman et al., 2013). Recently, a series of clinical trials on patients and in vivo and in vitro studies in cellular and animal models have demonstrated that pharmacological rescue of mTOR pathway dysregulation represents a novel promising treatment option for FCD/HME.
The serine/threonine kinase mTOR is at the center of signaling pathways that are critical for the regulation of cellular metabolism, growth, and proliferation (Ma XM et al., 2009). mTOR participates to the formation of two separate protein complexes: mTORC1 and mTORC2. mTORC1 is composed by mTOR, raptor, mLST8, Pras40, and Deptor (Peterson et al., 2009; Hara et al., 2002). Some of the mTORC1 components (mTOR, mLST8 and Deptor) are also present in mTORC2, which, in addition, contains several unique subunits, including Rictor, mSIN1 and PRR5 (Sarbassov et al., 2004). The best-known downstream substrates of mTORC1 are S6 kinases (S6K1 and S6K2) and 4E-BP1 (eukaryotic initiation factor 4E-binding protein-1), which are involved in protein translation (Ma XM et

al, 2009). To coordinate cell growth and proliferation, mTORC1 responds not only to growth factors but also to energy, amino acids and oxygen levels (Robert A. et al., 2017). Activation of mTORC1 leads to the phosphorylation of S6K1, which in turn phosphorylates ribosomal S6 protein (RPS6) a component of the 40S ribosomal subunit (Choo et al., 2008). For this reason, the expression of Phospho-RPS6 (P-RPS6) is often used to monitor mTOR activity.

In patients carrying mutations in mTOR pathway genes, the use of mTOR inhibitors might represent an example of personalized treatment based on the knowledge of the etiological cause of the disease. Rapamycin and its analogs (rapalogs) are recognized as the first generation mTOR inhibitors and inhibit the activity of mTORC1 via binding to FKBP-12 and forming a ternary complex with mTOR itself. Rapalogs have the same molecular scaffold of rapamycin but different physicochemical properties. Clinical trials with different rapalogs are ongoing in a wide range of human malignancies. Temsirolimus and everolimus have been approved by the FDA for the treatment of patients with advanced renal cell carcinoma (Hudes G et al. 2007; Motzer RJ et al. 2008) Everolimus has also been approved as monotherapy or a component of combination therapy for pediatric and adult patients with subependymal giant cell astrocytoma (SEGA) and SEGA associated with tuberous sclerosis (TSC). Additional clinical trials to examine the effects of rapamycin on neurocognitive functions, autistic phenotypes, and epilepsy are underway (Ehninger et al., 2013). In vitro studies have demonstrated the efficacy of mTOR inhibitors in the treatment of various neurological disorders. In 2015, Lim and collaborators proved that focal cortical expression of mutant MTOR by in utero electroporation in mice was sufficient to disrupt neuronal migration and cause spontaneous seizures and the occurrence of cytomegalic neurons. Inhibition of mTOR with rapamycin suppressed epileptic seizures and reverted neuronal cytomegalic phenotype. In 2016, Mirzaa and collaborators demonstrated that increased cell size in cultured rodent neurons expressing mutant *MTOR* constructs could be reversed by 7 days of mTOR inhibition with the rapalog everolimus (Mirzaa et al. 2016).

Although the use of rapalogs in various clinical trials have validated the concept that targeting PI3K/AKT/mTOR has a potential therapeutic effect, patients need treatment reduction or discontinuation due to severe adverse events. Since rapalogs suppress the immune system, patients may experience bacterial and viral infection. In addition, their use is also very frequently associated with dermatological adverse events (edema, aphthous ulcers) (Lamming et al. 2013). Rapamycin treatment may also lead to metabolic changes, including hyperlipidemia, decreased insulin sensitivity, glucose intolerance, and an increased incidence of new-onset diabetes (Gyurus et al., 2011).

Metformin, a drug widely used to treat type 2 diabetes, has been recently shown to activate the AMP-activated protein kinase (AMPK), a downstream component of a protein kinase cascade that acts as a sensor of cellular energy charge. (Winder WW et al., 1999)

Activating the AMPK pathway, metformin eventually inhibits the mTOR pathway and causes a reduction in protein synthesis and cellular proliferation (Zhou G et al., 2001). Recently, Kim and collaborators demonstrated that early

treatment with metformin prevented seizure onset and late treatment suppressed seizure frequency in FCD mice electroporated *in utero* with MTOR mutations identified in FCD patients (Kim et al., 2019.). With proven long-term safety and tolerability, metformin appears to be a promising alternative drug for the treatment of MCDs related to mTOR pathway dysregulation.