

Chapter 2

Consequences of Centrosome Dysfunction During Brain Development

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Abstract Development requires cell proliferation, differentiation and spatial organization of daughter cells to occur in a highly controlled manner. The mode of cell division, the extent of proliferation and the spatial distribution of mitosis allow the formation of tissues of the right size and with the correct structural organization. All these aspects depend on cell cycle duration, correct chromosome segregation and spindle orientation. The centrosome, which is the main microtubule-organizing centre (MTOC) of animal cells, contributes to all these processes. As one of the most structurally complex organs in our body, the brain is particularly susceptible to centrosome dysfunction. Autosomal recessive primary microcephaly (MCPH), primordial dwarfism disease Seckel syndrome (SCKS) and microcephalic osteodysplastic primordial dwarfism type II (MOPD-II) are often connected to mutations in centrosomal genes. In this chapter, we discuss the consequences of centrosome dysfunction during development and how they can contribute to the etiology of human diseases.

Keywords Centrosome • Microcephaly • Animal models of microcephaly • Autosomal recessive primary microcephaly (MCPH) • Seckel syndrome (SCKS) • Microcephalic osteodysplastic primordial dwarfism type II (MOPD-II)

2.1 The Centrosome Duplication Cycle

The centrosome is a non-membranous organelle composed of a pair of orthogonally organized centrioles, which during mitosis organize the pericentriolar material (PCM) [1]. The two centrioles are composed of nine sets of microtubules (MTs), polarized filaments of tubulin. The PCM surrounds the centrioles to support mitotic

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spindle assembly and consists of a highly organized matrix of more than one hundred proteins [2–5].

The centrosome is the main MT-organizing centre of animal cells: two centrosomes organize the mitotic spindle during mitosis and—most of the time—it is required to build the MT-cytoskeleton in interphase [6, 7]. In addition, in interphase, the centriole functions as basal body to template the assembly of cilia and flagella [8]. MT nucleation from the centrosome depends on the presence of γ -tubulin containing complexes [9]. The minus-ends of MTs are embedded at the centrosome, while the plus-ends extend in the cytoplasm, forming a polarized network that sustains chromosome (or molecular cargoes) movement. MTs possess an intrinsic dynamic instability and are in general built by 13 polar protofilaments, each being composed by heterodimers of α and β -tubulin [10, 11].

At the end of cell division, each daughter cell contains a single centrosome composed of a pair of orthogonally organized centrioles [12]. This allows the assembly an organized MT network in interphase [13]. To form a bipolar spindle at the next mitosis, the centrosome is duplicated only once per cell cycle in a tightly regulated process (Fig. Fig. 2.1) [15]. Centrosome duplication is licensed by centriole disengagement, which occurs during G1 when centrioles lose their orthogonal configuration [15]. Centriole disengagement allows the assembly—during S-phase—of one daughter procentriole next to each mother. In preparation for mitosis, the centrosomes starts recruiting PCM and the two centrosomes separate and nucleate MTs in order to assemble the mitotic spindle. The very last step of cell division, cytokinesis, will then separate the two centrosomes in two distinct cells.

2.1.1 Proteins Required for Centrosome Duplication

Proteins involved in the centrosome duplication cycle have been initially identified through genome wide screens in *C. elegans* and they present functional homologs in the fruit fly *Drosophila melanogaster* (D) and in humans (*Homo sapiens*, Hs). Their recruitment to the centrosome and their activity are sequential [18–20]. Throughout evolution the three major steps required for centriole duplication have been conserved [16, 17] (Fig. Fig. 2.2). They consist of:

1. Recruitment of kinase activity to the centrosome (proteins involved: SPD-2/HsCEP192/DSPD-2 or HsCEP152/DAsI and ZYG-1/HsPLK4/DSak)
2. Formation of a procentriole-primordium (proteins involved: SAS-6/HsSAS6/DSas-6 and SAS-5/HsSTIL/DAna2)
3. Incorporation of MTs at the newly formed procentriole (proteins involved: SAS-4/HsCPAP/DSas4, HsCP110, Hs γ -tubulin, HsCEP135/DBId10). Of note, other members of the tubulin superfamily (zeta-, epsilon- and delta-tubulin) are required to form centrioles in certain cells (for a review, see [25])

For simplicity, throughout this chapter, we will refer to these genes with their Hs name.

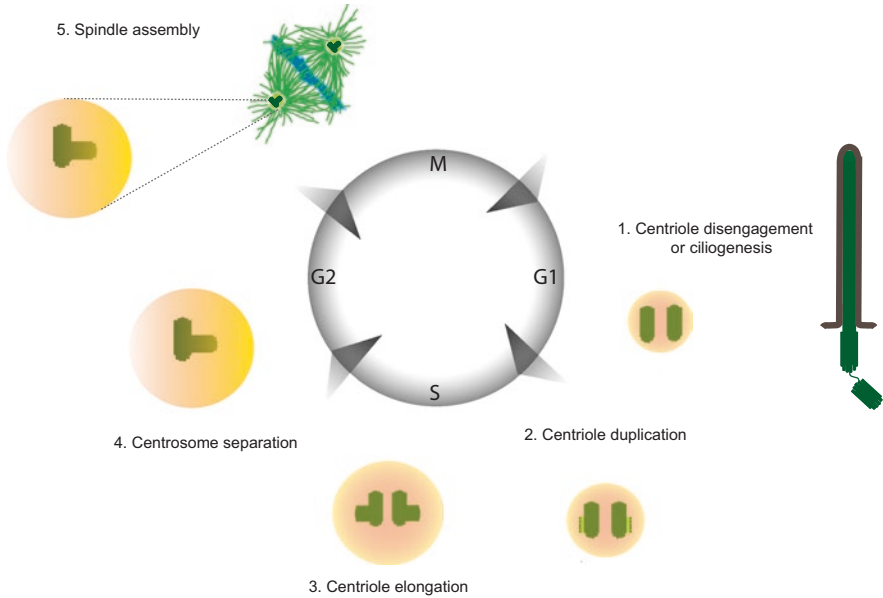


Fig. 2.1 The centrosome duplication cycle. The centrosome is composed of a pair of centrioles (*green cylinders*) [12] surrounded by pericentriolar material (PCM) (*orange*) [14]. It normally duplicates once, in coordination with the cell cycle (composed by sequential G1-, S-, G2- and M-phase) [15]. (1) Centriole disengagement or ciliogenesis. At the end of cell division, each daughter cell contains a single centrosome composed of a pair of orthogonally organized centrioles. This configuration is lost in G1 in a process called “disengagement”, which license the centrosome duplication cycle [15]. Alternatively, the mother centriole can dock at the membrane and form the basal body that templates the assembly of cilia and flagella [8]. (2) Centriole duplication. During S-phase a number of proteins are timely recruited on the disengaged centrioles and trigger the assembly of a new centriole next to each parental one (see Fig. 2.2 for a more detailed description of the process) [18–20]. (3) Centriole elongation. The newly formed centrioles continue to elongate during S-phase and the rest of the cell cycle [21]. From G2 onwards, the centrosomes reinforce the recruitment of PCM material, which will serve to organize the mitotic spindle in M-phase [22]. (4) Centrosome separation. At the beginning of M-Phase, centrosomes separate and migrate at opposite side of the cell [23]. Each centrosome will be composed of two centrioles that organize the PCM: an older, parental centriole and a daughter one. (5) Spindle assembly. In mitosis, the centrosomes nucleate MTs and organize the mitotic spindle, a network that contacts the chromosomes and allows their segregation at opposite pole of the cells [24]

2.2 The Centrosome and the Mitotic Spindle

The mitotic spindle supports chromosome separation during mitosis. It consists of a bipolar, antiparallel array of MTs [11, 26, 27]. In animal cells it is composed by MTs nucleated mainly by the centrosome. Astral MTs are typical of centrosomal-spindles: they emanate from the centrosome into the cytosol and—contacting the cortex—play important roles in spindle orientation [28–31]. The mitotic spindle is composed by different populations of coexisting MTs. These can be distinguished

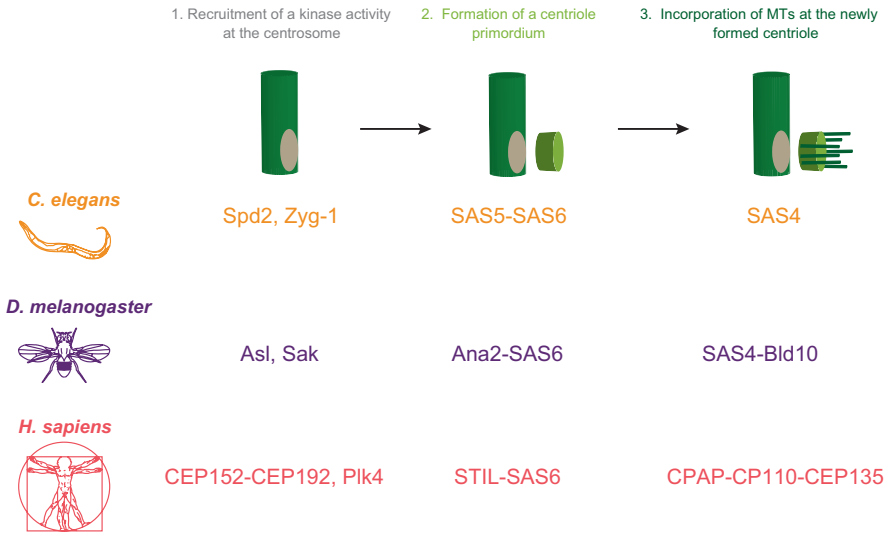


Fig. 2.2 Proteins required for centrosome duplication. The core machinery required for centrosome duplication is well conserved [16, 17]. The proteins sequentially required for centriole duplication in *C. elegans*, *D. melanogaster* and *H. sapiens* are listed. They act timely to induce recruitment of kinase activity to the centrosome (1), formation of a centriole-primordium (2) and incorporation of MTs at the newly formed centriole (3)

based on their orientation, function and stability. Kinetochore MTs connect the chromosomes to the spindle machinery while MTs that emanate from opposite poles and interact in an antiparallel fashion are named interpolar MTs [27] (Fig. 2.1).

MTs can also be assembled by the Augmin complex through branching from pre-existing MTs [32]. Additionally, MTs are nucleated at the level of the chromatin by the establishment of a RanGTP gradient after nuclear envelope breakdown [33–38]. Chromatin-dependent spindle assembly occurs physiologically in different systems. For instance, this occurs frequently during female meiosis, even in human oocytes [39]. However, this process can also support spindle assembly when centrosomes are experimentally removed (e.g. [40–43]).

Importantly, while bipolar mitotic spindle assembly can occur in the absence of centrosomes, these organelles are normally required to ensure correct spindle orientation. Spindle orientation determines the position of daughter cells at the end of mitosis and contributes to the differential inheritance of cytoplasmic and cortical factors [40, 44–48].

2.3 The Centrosome and the Cilium

One important role of the centrosome in interphase is to function as a basal body to template the assembly of cilia and flagella. In light of human brain anatomy and function, two kinds of cilia need to be described: motile cilia and primary cilia.

Motile cilia normally present 9 MT doublets plus a central pair of MTs and are required to mediate fluids movement in the human body. In the brain, ependymal cells are responsible for the flux of the cerebrospinal fluid (CSF). These cells are multiciliated: they present hundreds of cilia, which are formed by sequential, multiple non-canonical centriole duplication cycles [49, 50].

Primary cilia slightly differ from motile cilia in their structure, as they lack the central pair of MTs [51]. These cilia, also known as non-motile cilia, mainly function as signalling hubs. In the brain, they are important to sense signalling molecules transported in the CSF, including growth factors, sonic hedgehog (Shh) and Wnt ligands [52–58].

2.4 General Principles Governing the Effects of Centrosome Dysfunction

Centrosomes play important roles in determining the outcome of cell division, both in terms of cell fate and cell survival. We conceive that centrosome defects can impair this process by affecting at least four different mechanisms: orientation of the mitotic spindle [28, 30, 40, 45, 48, 59, 60], correct chromosome segregation [61–64] and assembly of a primary cilium [53]. In addition, centrosome loss can affect cell proliferation: it has been recently shown that centrosome removal triggers p53 activation and arrests vertebrate cell in G1 [65, 66].

The position of the spindle defines where daughter cells will be positioned at the end of mitosis as well as the cortical/cytoplasmic inheritance they will receive. During symmetric cell division, the factors inherited by daughter cells are equivalent and the daughter cells will have similar fates. During asymmetric cell division, daughters are unequal and will differ in fate [46]. In *Drosophila* neural stem cells, cell fate-determinants are anchored to the membrane and directly transmitted to daughter cells by cortical inheritance, while in mammalian NSCs structural elements such as junctions, the apical membrane and the basal lamina are proposed to be responsible for cell fate determination [46, 57, 67–69]. Interestingly, the centrosome itself can be inherited asymmetrically by stem cells and differentiating cells [70–73]. The role of centrosome asymmetry during development or in maintaining tissue integrity is still not understood. A plausible explanation comes from a study performed in vertebrate cells in culture where it has been shown that, after mitosis, primary cilia grow asynchronously in the two daughter cells [74]. The cell that inherits the older centrosome will initiate ciliogenesis earlier than its sister, putting forward the concept that centrosome asymmetry might influence the capacity to sense environmental signals [74].

Centrosome defects can generate abnormal cilia, both in terms of number or structure. For instance, the nucleation of extra primary cilia can impact on the ability of a cell to transduce Sonic Hedgehog (Shh) and Wnt signaling and might lead to alterations in cell fate [53, 58].

In addition, defects in centrosome number (mainly centrosome amplification) and function can impair spindle activity during chromosome segregation. This can lead to alterations in the karyotype of daughter cells, a condition known as aneuploidy [75]. The pathological implications of an abnormal number of chromosomes are extremely broad and can be associated with both over proliferation (e.g. cancer) [76] or defective growth (e.g. microcephaly) [62], which will be further discussed in the following paragraphs.

Aneuploidy *per se* can be at the basis of premature differentiation or cell death [62, 77–80]. Additionally, lengthening of the G1 phase of the cell cycle has been shown to cause exhaustion of proliferative divisions and favour differentiation, probably by allowing the cell extra time to sense differentiation signals [81–83].

2.5 Neocortex Development: Evolutionary Insights

Drosophila is an invertebrate organism commonly used to understand the genetic bases of developmental processes. Brain development in *Drosophila* is quite stereotyped and the deep knowledge of its anatomy and of the cell types composing it render it an ideal model to explore the role of different factors in neurogenesis. During embryonic development, a population of neural stem cells called neuroblasts (NBs) delaminates from the neuroectoderm and give rise to the larval brain, composed by two lobes and a ventral nerve cord [84]. After a period of dormancy, proliferation of the larval NBs resumes. NBs divide in an asymmetric fashion and generate two daughter cells with distinct fates: a new NB, which retains the stem-cell potential, and a ganglion mother cell, which undergoes a single additional division. At the end, each NB gives rise to a reasonably invariant set of neurons and glial cells [85].

The vertebrate brain (including Zebrafish, mouse and human brain) can roughly be subdivided in three parts: the forebrain, the midbrain, and the hindbrain [86].

The mammalian brain is characterized by the development of the neocortex, composed of six layers of neurons. It is the part of cerebral cortex which underwent the biggest and most recent phylogenetic expansion, mainly by growth in the lateral and radial dimension [57, 87, 88]. It originates from the divisions of neuroepithelial cells, which give rise to a set of intermediate progenitors that will undergo additional divisions. Taverna et al. have proposed a classification of these populations based on the localization of progenitor mitosis with respect to the ventricular zone (VZ) (apical—AP, basal—BP and subapical progenitors—SAP), the extent of cell polarity and their proliferative capacity [57].

The evolution of different types of progenitor cells in the primate and human brain has contributed to the expansion of the cerebral cortex [88]. In particular, a novel type of non-epithelial progenitors has been described in the outer subventricular zone (OSVZ), which are proposed to have contributed to the evolutionary expansion of the human brain [89].

The human brain strongly differs from that of other mammals by its degree of corticalization, which accompanies an increase in cognitive functions [90, 91]. This impressive growth in brain size has been accommodated in the skull thanks to gyri-fication. Interestingly, it has been reported that the formation of gyri in the otherwise unfolded mouse cortex (lissencephalic) can be induced by modifying the expression pattern of a single protein or by forcing the expression of a human gene [92, 93].

2.5.1 Centrosome and Brain Development: Lessons from Drosophila

In order to explain the effects of centrosomal defects on brain development, we will start by presenting two extreme cases: what happen when centrosomes are absent and when they are present in excess (while for others—more specific—models, we address the readers to the corresponding paragraphs). Both scenarios can be obtained by mutating or overexpressing proteins involved in the centrosome duplication cycle. For instance, mutations in Plk4 result in centrosome loss, while Plk4 overexpression causes centrosome amplification [59, 94].

In the absence of centrosomes, mitotic spindles can be assembled from the vicinity of chromatin or from pre-existing MTs [32, 36, 37, 95]. However, centrioles are indispensable to nucleate sensory cilia and sperm flagella [96–98]. Flies without centrioles can develop in viable adults, but they die shortly after eclosion because their sensory neurons lack cilia, affecting vital function such as movement, smell and proprioception [59, 94, 99–101]. Acentrosomal mitoses do not generate aneuploidy in dividing NSCs. However, due to lack of astral MTs, spindle orientation and asymmetric cell division are perturbed, leading to an expansion of the stem cell pool, which is tumorigenic in allogeneic transplantations [40, 44, 47, 102].

When extra centrosomes are present, their efficient clustering at the spindles poles allows the formation of bipolar spindles and ensures correct chromosome segregation. Flies with centrosome amplification do not present gross cilia defects. However, asymmetric cell division is again perturbed, and the brain holds tumorigenic potential [59].

Overall, we think that centrosome defects mostly affect spindle positioning in *Drosophila* and that this is the main route by which cell proliferation is affected. However, the mammalian brain can respond differently to the same kind of perturbations (see paragraph, see below for further details).

Of note, not all tissues have the same way of responding to centrosome loss and amplification. While centrosomes number in the brain is not a variable influencing faithful chromosome segregation, it can generate aneuploidy in the wing disc [63, 103]. These results suggests that, when centrosomes are perturbed, mitotic fidelity will rely on the strength of alternative mechanisms for spindle assembly or on the capacity to achieve centrosome clustering.

2.5.2 *Centrosome and Brain Development: Lessons from Zebrafish*

Small head size phenotypes were obtained by Novorol and colleagues in Zebrafish after knockdown (KD) of four centrosomal genes: *stil*, *aspm*, *wdr62* and *odf2* [104] (see also [105]), generating abnormal centrosome number and localization. In these mutants the microcephalic brain results mainly from mitotic defects - namely pro-metaphase delay [104], while the contribution of p53-dependent apoptosis is minor. In addition, the work from Pfaff, K.L. and colleagues [106], also reported a strong mitotic phenotype with highly disorganized spindles in Zebrafish in the absence of *Stil*. An additional Zebrafish model with non-functional centrosomes was obtained by targeting NEDD1, which is required to recruit γ -tubulin at the centrosome [107]. NEDD1 knockdown (KD) resulted in mitotic arrest and apoptosis. Depending on the intensity of the KD, the phenotype was spanning from embryonic lethality to severe defects in the brain [107].

Depletion of Plk4 causes a strong size reduction in Zebrafish, mainly due to abnormal spindles and mitotic defects, including a substantial delay in mitotic progression [108]. Moreover, the impairment of centriole duplication due to Plk4 knockdown results in a dilution of basal bodies and causes a dose-dependent ciliary phenotype [108]: while a mild reduction in Plk4 levels mainly affect mitosis by reducing the number of centrioles and thus altering the bipolar configuration of the spindle, a stronger KD resulting in complete centriole/basal body loss impairs the ability of cells of growing cilia [108].

The consequences of centrosome amplification in the Zebrafish brain have been studied recently [109]. In this system, extra centrosomes do not cluster and induce the formation of multipolar spindles. Multipolar divisions can lead to the presence of multiple nuclei in one of the daughter cells. When occurring in the neuroepithelial progenitors, this leads to apoptosis, tissue degeneration and death, affecting mostly retinal neuronal layering [109].

2.5.3 *Centrosome and Brain Development: Lessons from Mouse*

Similarly to *Drosophila*, centrosome removal and amplification in mouse can be achieved genetically by manipulating genes involved in the centrosome duplication cycle [62, 110].

Since most vertebrate cells are ciliated, lack of centrioles would be expected to cause lethality due to the absence of cilia. However, CPAP mutant mouse embryos die earlier than mutants lacking cilia. In rodents, centriole presence becomes essential from embryonic day 9 [110–114] and experimental removal of centrosomes causes mitotic delay and p53-dependent cell death in the embryo [110, 115, 116].

Bazzi and Anderson recently showed that a null mutation in CPAP results in embryonic lethality at midgestation. They also observed a prometaphase delay and demonstrated its involvement in p53 activation and p53-dependent apoptosis [110].

When progressive loss of centrioles is taking place in the neuronal precursors, mice develop microcephaly [45, 110]. p53 removal rescues cell death and the reduced brain size phenotype. However, it does not rescue the defects in tissue architecture due to abnormal spindle orientation that leads to misplacement of neural progenitors [45]. Very recently it has been shown that—in addition to randomizing spindle orientation—CPAP silencing in post-mitotic neurons leads to abnormal morphology and slower neuronal migration [117]. The defective neuronal migration described here is ascribable to the function that CPAP exert on interphase rather than mitotic MTs, and open new possible roles for centrosomal genes in contributing to growth disorders. Supporting this view, Gabriel, E. and colleagues have shown that CPAP promotes neural progenitors fate by promoting cilia disassembly, rather than by a centrosomal function [118].

As centrosome loss, centrosome amplification in the mouse central nervous system causes microcephaly [62]. Compared to *Drosophila*, mouse neural stem cells have less efficient clustering mechanisms. Multipolar spindles cause errors in chromosome segregation that leads to aneuploidy and p53-dependent cell death. Interestingly, p53 inhibition rescues cell death, but prompts premature differentiation of progenitor cells, mirroring results obtained in *Drosophila* aneuploid brains [119]. However, while in flies premature differentiation is a primary response to aneuploidy, in mouse it is probably a secondary mechanism taking over only when the p53 primary response is not efficient. These observations seem paradoxical, since aneuploidy has long been regarded uniquely as conferring proliferative advantage. However, recent studies showing a negative effect of aneuploidy on proliferation put forward the novel concept that chromosome imbalance mostly hinders proliferation, and only specific gain or losses might favor malignant transformation (which might not occur through proliferative advantage—e.g. see [120–122]).

2.6 The Centrosome and Its Role in Primordial Microcephalic Disorders

Primordial microcephalic disorders include a spectrum of diseases characterized by severe growth retardation. Autosomal recessive primary microcephaly (MCPH) (2.6.1), microcephalic osteodysplastic primordial dwarfism type II (MOPD-II) (2.6.2) and primordial dwarfism disease Seckel syndrome (SCKS) (2.6.3) are all primordial microcephalic disorders that share phenotypic and genetic traits. In the following paragraphs, we will present a summary of clinical description and molecular insights for each of these syndromes. These disorders can be linked to premature exhaustion of proliferative division of stem cells, due to premature differentiation or cell death. The causes underlying cell death/differentiation can be

multiple and include defects in spindle robustness [123], in spindle positioning/orientation [124], in cell cycle progression or DNA damage repair [125] or in chromosome segregation [62].

2.6.1 Autosomal Recessive Primary Microcephaly (MCPH: Microcephaly Primary Hereditary)

MCPH is characterized by a reduction of the occipito-frontal circumference, which can be nearly normal at birth (−2) but is inevitably worsen in the first year of life (−3) [126]. It is a rare genetic disease, found in about 100 families [127]. Brain size reduction is proportionate, albeit affecting particularly the cerebral cortex [128]. Other clinical features are mental retardation, mild seizures and particular neuronal migration defects [126–129].

MCPH causal mutations are found in a large number of genes and can all cause premature differentiation, cell death and displacement of neural progenitors. Thirteen MCPH loci (1–13) have so far been identified in human patients, encoding for 13 different genes. MCPH genes can be grouped in 3 (partially overlapping) categories:

1. genes with a role in centrosome and spindle function (CEP152, CEP63, SAS-6, STIL, CPAP/CENPJ, CEP135, CDK5RAP2, CDK6, ASPM, WDR62 and STIL; see next paragraphs for a detailed description);
2. genes with a role in chromosome dynamics. This include the kinetochore gene CASC5, encoding for KNL1 [130] and CENPE. CENPE is encoded in an MCPH locus, but generates a more severe phenotype, similar to MOPD-II [131];
3. genes with a role in DNA-damage related pathways. In this category we can include Microcephalin, PHC1, ZNF335 [132–135]. Of note, CDK6, ASPM, STIL are involved in both cell cycle regulation and centrosome function.

In light of recent results an additional, fourth class of genes involved in cell cycle regulation (Microcephalin and ASPM), should be considered [81, 133].

For the purposes of this chapter, we will focus on the genes with a role in centrosome and spindle function (category 1) and we will describe their identification in MCPH, MOPD-II and SCKS. For the other genes, we address the reader to [127, 136, 137]. However, a small digression should be made on Microcephalin (Mcp1). Microcephalin is mostly known for its role in DNA-related processes (DNA damage response, chromosome condensation) [129, 138, 139] but was also involved in the etiology of microcephaly through its role in coupling the centrosome cycle with mitosis [140]. Indeed, mutations in *Drosophila* MCPH1 are early embryonic lethal. Mutant embryos exhibit asynchronous nuclear and centrosome cycle, abnormal centrosomes and spindles, chromatin bridging due to premature chromosome condensation and mitotic arrest [141, 142].

Genes with a role in centrosome and spindle function that are at the origin of MCPH were previously classified in centriole duplication genes, genes encoding PCM proteins and genes that encode spindle-pole associated proteins [143].

2.6.1.1 Centriole Duplication Genes: CEP152, STIL, CEP135, CEP63, SAS-6 and CPAP/CENPJ

CEP152 underwent positive selection in humans [144]. A non-conservative amino acid change in CEP152 has been identified by SNP genotyping in three MCPH families. Only one of the cases reported was heterozygous for the missense mutation, with the second allele characterized by a premature stop codon [144].

Mutations in STIL that results in truncation of the protein has been reported in 4 MCPH families [145]. In 2014, Arquint and Nigg [146] described two truncating mutations in STIL found in MCPH patients which perturbs its ubiquitination, thus compromising its degradation and causing centrosome amplification.

MCPH mutations in CPAP/CENPJ have first been described by Bond and colleagues, [147]. The authors found a homozygous single-base deletion and a substitution resulting in an amino acid change in a very conserved residue of the protein.

A truncated form of the protein encoded by CEP135 has been described in MCPH patients by Hussain et al. [148] and Farooq et al. [149]. So far, reported MCPH mutations in CEP135 are a single base deletion in exon 8 and a splice site mutation leading to complete skipping of exon 11 with loss of the C-terminus domain of CEP135 necessary for the interaction with SAS-6 [149].

The protein encoded by CEP63 interacts with CEP152 and plays an important role in regulating centrosome number. Homozygous mutations in this gene generating a premature stop codon have been found to cause MCPH [150]. Further analysis demonstrated that the protein is normally localized in a discrete ring around the parental centriole and that this localization is lost in patient-derived cells. Centrosome maturation and separation were not found to be perturbed, however, the presence of abnormal spindles—probably due to delayed procentriole assembly and erroneous centriole engagement—highlighted possible defects in centrosome duplication [150]. Surprisingly, the mitotic phenotype observed in CEP63KD cells was rescued by exogenous targeting of CEP152 to the centrosome, suggesting that the microcephalic phenotype could be ascribed to the role of CEP63 in recruiting CEP152 in rapidly proliferating cells. Interestingly, CEP63 deficient mice recapitulate SCKS. In this model, mitotic errors due to centrosomal defects cause p53-dependent cell death, resulting in a reduced brain size. In addition, CEP63 loss impairs male meiotic recombination [151].

A missense mutation within a highly conserved region of SAS-6 has been found by homozygosity mapping in individuals from a Pakistani consanguineous family. Tissue culture analysis of the Ile62Thr SAS-6 mutant revealed that this form of the protein is less efficient in sustaining centriole formation. Further analysis by protein KD revealed the presence of monopolar spindles [152].

2.6.1.2 Genes Encoding PCM Proteins: CDK5RAP2 and CDK6

The formation of a functional mitotic centrosome requires the expansion of PCM around the centrioles, in a process known as centrosome maturation [153, 154].

CDK5RAP2 is a pericentriolar protein required for γ -tubulin recruitment and MT nucleation at the centrosome [155, 156]. It is a MCPH protein highly expressed in the neuronal progenitor pool. Its loss causes depletion of apical progenitors due to cell cycle exit and premature differentiation [157]. CDK5RAP2 mutations were initially identified in two MCPH families. The mutations found were in coding and non-coding regions of the gene respectively, causing an amino acid substitution in the first case and aberrant splicing (generating a truncated protein) in the second [147]. Strikingly, mutations in CDK5RAP2 gene in mice (153) or in human pluripotent stem cell-derived 3D organoid culture system (cerebral organoids) can recapitulate microcephaly, probably due to premature neurogenic non-proliferative divisions [159]. Interestingly, CDK5RAP2 mutations most likely contribute to MCPH onset through defects in several processes. Characterization of a Hertwig's anemia mutant mouse model revealed the presence of multipolar spindles, spindle mispositioning and increased apoptosis due to an inversion in CDK5RAP2 [158]. Cerebral organoids derived from reprogramming of patient skin fibroblasts, mainly displayed misoriented spindles [159]. Finally, in the avian B cell line DT40, CDK5RAP2 function has been linked to the cohesion between centrioles and has been shown to promote cell cycle arrest in cells that underwent DNA-damage [160]. In flies, CDK5RAP2 plays several roles: for instance, it is required for centrosome maturation [161], it regulates centrosome size [162], establishes centrosome asymmetry [163] and represses dendrite branching [164], sustaining the view that mutations in this gene might contribute to MCPH in different ways.

CDK6 is a cyclin dependent kinase required for cell cycle progression and it was found to be mutated in a Pakistani family with MCPH [165]. The mutation—Alanine to Threonine conversion—occurs at the level of a very conserved residue. In the same study, the protein was found to localize at the mitotic centrosomes, but this localization was lost in patient primary fibroblast, leading to the conclusion that CDK6 could play a role in organizing centrosomal-MTs and in centrosome positioning.

2.6.1.3 Genes Encoding Spindle-Pole Associated Proteins: ASPM and WDR62

ASPM is a protein required for spindle integrity, as it plays a role in focusing the poles of the mitotic spindle [166]. It is normally down regulated during the switch from proliferative to neurogenic division of neural progenitors and is required to maintain spindle orientation [167]. Mutations in ASPM are the most common cause of MCPH [168] and strong evidence favor a role for ASPM in neurogenesis: Pulvers and colleagues [169] showed that in mice, ASPM mutations similar to those causing microcephaly in humans, cause abnormal protein localization during mitosis. They

also report the appearance of mild microcephaly that can be rescued by the human transgene. A very recent paper proposed a role for ASPM in the etiology of MCPH by regulating cell cycle progression through G1 instead of spindle orientation. Capecchi and Pozner [81] generated a new mouse model and demonstrated that ASPM can tune cyclin E ubiquitination and—thus—mitotic progression through G1. Interestingly, mutations in the *Drosophila* functional homolog of ASPM can also cause severe defects in brain size and neuroepithelium morphogenesis. The absence of ASPM results in abnormal mitosis and increased apoptosis. In addition, ASPM mutants present abnormal spindle positioning and abnormal interkinetic nuclear migration, which compromises tissue architecture [170].

Missense and frame-shifting mutations in WDR62 have been identified in seven MCPH families, making this gene the second most commonly mutated in MCPH after ASPM. WDR62 is specifically expressed in neuronal precursors undergoing mitosis and, similarly to what has been observed for CDK6, the centrosomal localization of the protein is lost in the mutant form [171]. More recently, the study of a WDR62 mouse model established that mutant progenitor cells show spindle instability (including multipolar spindle formation) leading to mitotic arrest, cell death and microcephaly [172]. Interestingly, mutations in the *Drosophila* functional homolog of WDR62 affect the asymmetry that normally characterizes apical and basal MTOCs during interphase. This is due to a lack of Plk1/Polo recruitment on the apical centrosome, which mediates MTOC activity [173].

2.6.2 *Majewski/Microcephalic Osteodysplastic Primordial Dwarfism Type II (MOPD-II)*

MOPD-II patients are characterized by severe pre-natal and postnatal growth failure with proportionate microcephaly at birth, that evolves in disproportionate microcephaly [174–176]. MOPD can be clinically distinguished from Seckel syndrome mainly from the radiologic finding of skeletal dysplasia [175], as well as by less severe mental retardation but more pronounced growth defects [177]. Mutations in the PCNT gene (encoding a PCM protein) were described to be at the origin of both SCKS and MOPD-II, with the diagnosis often revised when evidence of skeletal dysplasia appear [178]. Absence of PCNT causes defects in spindle structure, which leads to chromosome missegregation [179]. In [177] MOPDII was defined as a “genetically homogeneous condition due to loss of function of pericentrin”. Analyzing the current knowledge, Delaval A. and Doxsey J. proposed three mechanisms to explain the implication of pericentrin in a phenotype of reduced growth: (1) through its role as a DNA-damage checkpoint protein, (2) because of its function in MT nucleation and (3) in light of its role in spindle orientation and organization [180].

1. Role of pericentrin as a checkpoint protein. Mutations in PCNT were reported in individuals with SCKS and cells from these patients displayed defects in the ATR-dependent checkpoint signaling for DNA damage [181]. In addition, peri-

centrin plays a role in anchoring Chk1 at the centrosome, thus regulating the activation of centrosomal cyclin B-Cdk1. Its mutation would then be responsible for premature mitotic entry, even in the presence of DNA damage [182]

2. Function of pericentrin in MT nucleation. Localization of Pericentrin at the centrosome is required to sustain MT nucleation during mitosis [183] and thus to ensure mitotic spindle organization [123]. Interestingly, pericentrin loss phenocopies CDK5RAP2 loss in mice and causes a reduced recruitment of CDK5RAP2 at the centrosome [157].
3. Role of pericentrin in spindle organization. PCNT depletion in human cells causes γ -tubulin loss at the centrosome and disrupts astral MT nucleation, [123], spindle positioning [184] and organization, impairing chromosome segregation [210].

Of note, mutations in mouse PCNT and in the *Drosophila* functional homolog cause ciliary phenotypes. A mouse model with hypomorphic PCNT mutation displayed malformed cilia in the olfactory chemosensory neurons [185]. Similarly, adult flies present defects in sensory neuron cilia and sperm flagella function. However, in this system, PCNT is dispensable for mitosis and spindle formation [101].

2.6.3 Seckel Syndrome (SCKS)

Seckel syndrome was described by Seckel in 1960 as a severe form of dwarfism accompanied by microcephaly, a distinctive *facies* and mental retardation [186]. It is a rare and heterogeneous type of primordial dwarfism, very similar to MOPD and firstly distinguished from it by Majewski and Goecke [175]. Mutated genes identified so far in SCKS play a role in centriole duplication and are CPAP/CENPJ and CEP152 [144, 187–189], initially associated with MCPH (see MCPH section for further details on CEP152), and PCNT (see MOPD-II section for further details). Interestingly, in mouse, a hypomorphic allele of CPAP/CENPJ recapitulates several features of Seckel syndrome. Those arise from defective spindle formation and genetic defects such as polyploidy, aneuploidy and apoptosis [190].

2.7 Centrosomal Genes and Other Growth Syndromes

Genes with a role in centrosome and spindle function that are at the origin of other forms of primordial microcephalic disorders other than MCPH, SKCS and MOPD-II include CPAP, CEP152, PCNT (see previous sections for detailed descriptions), the centriole duplication gene PLK4 and the PCM gene TUBGCP4.

Plk4 PLK4 is the master regulator of centriole duplication [94, 191]. In 2014, two different groups identified mutation in the Plk4 genes in individuals with microcephalic primordial dwarfism [108, 192]. Martin and colleagues analyzed a Zebrafish model for Plk4 loss of function and found that centriole biogenesis is compromised,

causing both longer, abnormal mitosis—which lead to impaired growth—and ciliary phenotypes. Interestingly, the growth and ciliary phenotypes were dependent on Plk4 dosage. Indeed, cilia loss correlates with complete absence of basal bodies, while mitosis can proceed and being perturbed even when centrioles are present, but their number is reduced. This suggests that—in this system—mitosis is more sensitive to centriole depletion than ciliogenesis [108].

TUBGCP4 TUBGCP4 (tubulin gamma complex associated protein 4) is a component of the γ -tubulin ring complex. Compound heterozygous mutations in TUBGCP4 have recently been reported in individuals with autosomal recessive microcephaly and patient-derived fibroblasts presented abnormal MT organization and aneuploidy [193]. Moreover, striking nuclear defects were reported: enlarged nuclei of abnormal shapes, chromatin bridges and multinucleation were detected in patient-derived fibroblasts [193].

In addition, mutations in POC1 centriolar protein A (POC1A) have been reported in patients affected by primordial dwarfism. Patient's fibroblasts displayed abnormal spindles and impaired ciliogenesis [194] and have been shown to contain centrosome amplification [195].

2.8 Other Centrosome-Related Developmental Syndromes

Oral-Facial-Digital Syndrome Type I (OFD1) OFD1 is a complex syndrome, characterized by polycystic kidney disease and malformations of the mouth, face, brain and digits. It represents an interesting case related to defective primary cilium signaling, although it results from mutations in a basal body gene rather than a ciliary gene. The syndrome is mainly caused by mutations in the CXORF5/OFD1 [196], which colocalizes with γ -tubulin, suggesting an association not only with the cilium—but also with the centrosome [197]. Mutations in CXORF5/OFD1 cause dysfunctions of the primary cilium, abnormal proliferation, abnormal Hedgehog and Wnt signalling and defects in planar cell polarity [198]. In normal human embryos, the gene product localizes in the organs affected by the syndrome, including the brain.

Meier Gorlin Syndrome Meier-Gorlin syndrome is a form of microcephalic primordial dwarfism often due to mutations in DNA-replication proteins, like Orc1 [199]. Orc1 depletion in Zebrafish was proposed to cause reduced body size due to an impairment of replication licensing and cell cycle lengthening [199]. However, in addition to controlling DNA replication by interacting with Cyclin A–CDK2, a different domain of Orc1 controls Cyclin E–CDK2-dependent centriole and centrosome copy number [200, 201]. Analysis of Meier-Gorlin causing mutations in Orc1, revealed that they can cause centrosome amplification [201], putting forward the idea that extra centrosomes might contribute to the growth-defective phenotype observed.

2.9 Concluding Remarks and Current Opinions on Microcephaly

The genetic background of animal models used to study human diseases can dramatically influence the phenotypes observed. A representative example can be found in CDK5RAP2 mouse models. While the one used in [158] could recapitulate microcephaly, the system used in [202] did not reveal significant defects in brain size. The high degree of human brain corticalization, its complexity and the presence of specific progenitor cell populations are unique features, difficult to recapitulate with rodent model systems. Thus, the introduction of cerebral organoids represents a great opportunity to study the etiology of human diseases.

Centrosome defects are very often at the origin of microcephaly and reduced growth. However, other genetic or environmental phenomena can generate similar effects. This is for example the case of fetal alcohol syndrome [203]. In addition, a recent outbreak of microcephaly in Brazil with the number of cases increased of 20-fold in the last months [204, 205], indeed suggests that the developing human brain is more vulnerable in terms of size than other organs. Why does the Zika virus, a flavivirus that in adults causes relatively mild syndromes and is transmitted by mosquitoes [206], affects specifically the developing brain remains to be understood.

Zika tropism to the brain was reported in two studies in 1952 and 1971 [207, 208], but only recently it was shown to infect human neural progenitor cells, causing cell death and cell-cycle alterations [209] and providing a possible explanation for the role of Zika in establishing brain size reduction.

Based on the current knowledge, we propose that the main mechanisms by which abnormal centrosomal components can induce defective brain growth are aneuploidy and alteration of cell cycle length. These can cause cell cycle exit or cell death, leading to a premature exhaustion of neural progenitors. The recent Zika outbreak raised awareness on microcephaly, which is normally a rare condition. Despite great advances in elucidating its causes, the reasons why the development of a normal-sized, well-organized brain is more susceptible to centrosome defects than the rest of the body in vertebrates and mammals remains to be understood.

Importantly, the zygotic centrosome mutations found in MCPH mostly generate architecturally normal but smaller brains, without affecting body size. Why is the brain so vulnerable to centrosome mutations is an important question that remains unanswered. One possibility is that neural progenitors are particularly susceptible to centrosome mutations when compared to other progenitors in the body. Alternatively, establishment of brain size might rely more than other organs on cell divisions that occur during developmental stages. However, other possibilities should not be discarded and this remains—in our view—the major open question in the field.

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