

Animal Models of Human Cerebellar Ataxias: a Cornerstone for the Therapies of the Twenty-First Century

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Published online: 8 August 2009
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Abstract Cerebellar ataxias represent a group of disabling neurological disorders. Our understanding of the pathogenesis of cerebellar ataxias is continuously expanding. A considerable number of laboratory animals with neurological mutations have been reported and numerous relevant animal models mimicking the phenotype of cerebellar ataxias are becoming available. These models greatly help dissecting the numerous mechanisms of cerebellar dysfunction, a major step for the assessment of therapeutics targeting a given deleterious pathway and for the screening of old or newly synthesized chemical compounds. Nevertheless, differences between animal models and human disorders should not be overlooked and difficulties in terms of characterization should not be occulted. The identification of the mutations of many hereditary ataxias, the development of valuable animal models, and the recent identifications of the molecular mechanisms underlying cerebellar disorders represent a combination of key factors for the development of anti-ataxic innovative therapies. It is anticipated that the twenty-first century will be the century of effective therapies in the field of cerebellar ataxias. The animal models are a cornerstone to reach this goal.

Keywords Cerebellum · Ataxias · Animal models · Pathogenesis · Therapies

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Advances in genetic studies, detailed molecular and cellular analyses, recent brain imaging techniques, emergence of behavioral assessments, and reshaping of models of cerebellar function are generating a massive amount of knowledge [1]. Cerebellar ataxias are being growingly recognized worldwide. There is a medical need to develop effective therapies in this group of disabling disorders for which no cure is currently available. For the first time, innovative therapeutics aiming to target deleterious pathways are under development [2]. Major breakthroughs in our understanding of the pathogenesis of cerebellar ataxias have been reached especially with the elaboration of relevant animal models reproducing human brain disorders. These models have contributed to the deciphering of the molecular mechanisms underlying cell loss.

Classification of Cerebellar Ataxias

Cerebellar ataxias represent a heterogeneous group of disorders characterized by a lack of coordination and imbalance [3, 4]. Patients exhibit various combinations of oculomotor deficits, dysarthria, dysmetria, and kinetic tremor. Various forms of learning are impaired [5]. Recently, the association of cerebellar lesions and neuropsychiatric symptoms has been underlined [6–8]. Some ataxic diseases show a marked cognitive dysfunction [9, 10].

Cerebellar disorders can be classified into inherited and sporadic ataxias. Inherited ataxias are related to a genetic deficit and can be divided into four groups: autosomal dominant ataxias, autosomal recessive ataxias, mitochondrial ataxias, and X-linked ataxias [3]. Dominant ataxias include the so-called spinocerebellar ataxias (SCAs) and the episodic ataxias (EAs) [11, 12]. SCAs are a set of genetic and clinically heterogeneous diseases which share the

feature of progressive lack of coordination. SCAs are classified genetically according to a specific mutation or mapped locus and also according to clinical findings [13–15]. The majority of known mutations involve a sequence of CAG trinucleotide repeats within the coding tract in the respective gene [2, 16, 17]. This is the case for SCA1, SCA2, SCA3, SCA6, SCA7, SCA17, and dentatorubral–pallidolusian atrophy (DRPLA). A CTG repeat expansion is found in SCA8 [18, 19]. Trinucleotide repeats are associated with an abnormal polyglutamine accumulation and formation of nuclear aggregates [20]. A pentanucleotide repeat expansion ATTCT is associated with SCA10 [21]. SCA5, SCA13, SCA14, and 16q22-linked autosomal dominant cerebellar ataxia are characterized by point mutations. Episodic ataxias are a group of diseases caused by a monogenic mutation (EA 1–7) and displaying attacks of incoordination and dysarthria. Autosomal recessive ataxias include Friedreich’s ataxia (FRDA) due to a pathological GAA triplet expansion within the first intron of the frataxin gene, ataxia telangiectasia, ataxia with ocular motor apraxia, ataxia with vitamin E deficiency (AVED), ataxia with CoQ10 deficiency, abetalipoproteinemia, early-onset cerebellar ataxia with retained tendon reflexes, infantile onset spinocerebellar ataxia, Marinesco–Sjögren syndrome, Wilson disease, and spastic ataxia of Charlevoix–Saguenay [15, 22]. There are numerous additional types of recessive ataxias worldwide, identified in a few families only. The group of mitochondrial disorders includes diseases due to mutations in mitochondrial genes. Most of these genes are involved in the energy production, essentially in oxidative phosphorylation. Ataxia may be a main symptom, especially in Kearns–Sayre syndrome; May–White syndrome; mitochondrial neurogastrointestinal encephalomyopathy (ophthalmoparesia, peripheral neuropathy, and gastrointestinal symptoms); Leigh syndrome; neuropathy, ataxia, and retinitis pigmentosa; mitochondrial encephalomyopathy, lactic acidosis with stroke-like episodes; and myoclonus epilepsy with ragged red fibers. X-linked ataxias include Fragile-X tremor ataxia syndrome, caused by a CGG mutation on the X chromosome.

Sporadic ataxias can be subdivided in (1) degenerative and (2) acquired ataxias [23]. Degenerative ataxias include multiple system atrophy (MSA) and idiopathic late-onset cerebellar ataxia. MSA is a progressive adult-onset disease, with two main presentations: a cerebellar form (c-MSA) and a parkinsonian form (p-MSA) [24]. Several drugs or toxics can trigger a cerebellar syndrome. The most common cerebellotoxic agent is alcohol [25, 26]. Immune-mediated ataxias include multiple sclerosis, cerebellar ataxia with antiglutamic acid decarboxylase antibodies, gluten ataxia, Miller–Fisher syndrome, systemic lupus erythematosus, Sjögren syndrome, Cogan syndrome, and thyroiditis [27, 28].

Animal Models

In this issue, we have gathered several contributions which highlight the roles of animal models in our understanding of cerebellar disorders. Tables 1, 2, 3, and 4 summarize the animal models and their corresponding human disorder.

Models of Hereditary Ataxias

The number of models of hereditary ataxias in rodents has increased noticeably [99]. The naturally occurring ataxic mutant mice which have been investigated in depth are the Lurcher mouse (gain in malfunction of the *Grid2* gene encodes the *GluRδ2* ionotropic glutamate receptor), the hot-foot mouse (different deletions in the coding sequences of *Grid2*), the staggered mouse (deletion of the *Rora* gene located on chromosome 9), the Purkinje cell degeneration (*pcd*) mouse (mutation of the *Agtpbp1* gene located on chromosome 13; see below), the nervous mouse, the reeler mouse (mutation disrupting the *Reln* gene on chromosome 5), the weaver mouse (involving an inward rectifying potassium channel strongly expressed in cerebellum), and the dystonia musculorum mouse (mutation of the *Dst* gene located on chromosome 6) [100–102]. A substantial number of transgenic mice with induced mutations have also been generated [33].

Lee and Jeong report on the Pogo (pogo/pogo) mouse, a naturally occurring neurological mutant from a Korean wild-type mouse *KJR/MsKist* [103]. The pogo mouse is characterized by a loss of balance and motor coordination. Gait is wobbly. The tendency to fall over appears at about 2 weeks of age and continues throughout life. The Pogo mutation is believed to be an allele of P/Q-type calcium channel mutants such as tottering, leaner, and rolling mouse Nagoya (see below). These channels play crucial roles in neuronal signaling and in neurotransmitter release at many central synapses and at the neuromuscular junction. The pogo mutation is inherited as an autosomal recessive trait. The pogo locus has been mapped to a region between *D8Mit67* and *D8Mit240* on mouse chromosome 8 [104]. The tottering and its allele leaner and rolling mouse Nagoya have been mapped to the *D8Mit128/D8Mit231* marker region. These mutants have been studied as models of spinocerebellar ataxia and epilepsy. The mutation responsible for tottering has been mapped to *Cacna1a*, a gene encoding the alpha subunit of a P/Q-type calcium channel [37]. Mutations in *Cacna1a* are responsible in tottering alleles for seizures, cerebellar degeneration, and ataxia [105]. Mutations in the human *CACNA1A* gene have been found in three inherited disorders belonging to the family of channelopathies: familial hemiplegic migraine, episodic ataxia type 2, and spinocerebellar ataxia type 6 [106]. The homozygous pogo/pogo phenotype is similar to that of

Table 1 Animal models of dominant ataxias

Type	Gene mutation	Animal model
SCA1	CAG (35–83)	Mice (<i>CAG82Q</i>), L7 promoter, mice (<i>CAG82Q</i>), L7 conditional promoter; mice knock-in (<i>CAG154Q</i>) [29–33]
SCA2	CAG (34–750)	Mice (<i>CAG58Q</i>), L7 promoter [34]
SCA3	CAG (56–86)	Mice (<i>YAC-MJD1/CAG67–84Q</i>), MJD1 promoter; mice (<i>mjda1a-CAG71Q</i>) [35, 36]
SCA4	–	Mice (<i>tottering</i> , <i>tg</i> and <i>tg-la</i>) mutants, mice (<i>Cacna1a^{R192Q}</i>), mice (<i>Cacna1a-CAG84Q</i>) [37–39]
SCA5	Missense mutations	–
SCA6	CAG (19–33)	Mice (<i>Cacna1a-CAG84Q</i>) [40]
SCA7	CAG (41–306)	Mice (<i>CAG90Q</i>), promoter L7, mice (<i>CAG128</i>) promoter PDGF-B, mice (<i>CAG92</i>), promoter Prp, mice (<i>CAG266Q</i>) [40–42]
SCA8	CTG (80–300)	Mice (<i>CTG116</i>) [43, 44]
SCA10	ATTCT (800–4500)	Mice (<i>Atn10^{-/-}</i>) [21]
SCA11	–	–
SCA12	CAG (66–93)	–
SCA13	–	–
SCA14	Missense mutations	Mice (<i>curly tail</i>) mutant [45]
SCA15	–	Mice (<i>Itp1EXdel¹⁸</i>) [46]
SCA16	–	–
SCA17	CAG/CAA (43–63)	<i>Xenopus</i> (<i>antisense-targeting tbp</i>), mice (<i>Tbp delta-N</i>), mice (<i>tbp^{-/-}</i>) [47–50]
SCA18	–	–
SCA19	–	–
SCA20	–	–
SCA21	–	–
SCA22	–	–
SCA25	–	–
DRPLA	CAG (48–93)	Mice (<i>DRPLA-CAG76Q</i>), mice (<i>full-length humanDRPLA</i>) [51, 52]
FGF14	FGF 14	–

tottering alleles. However, pogo mouse frequent falls backward as a result of hindlimb overextension [107]. The pathological defects are mainly located to the cerebellum [103]. In P/Q-type voltage calcium channel (*Cav2.1*) mutant mice, Purkinje cell loss is not associated with the onset or development of ataxia but rather reflects the degree of the ataxic phenotype [105]. Tyrosine hydroxylase (TH), the rate-limiting enzyme in the biosynthetic pathway of the catecholamines, is expressed transiently during development and is low or absent in the adult mouse [108]. TH is ectopically expressed in Purkinje cells of several ataxic mutant mice including tottering alleles (*tg/tg*, *tg^{la}/tg^{la}*, *tg^{rol}/tg^{rol}*) and dilute-lethal (*d^l/d^l*) mutant mice [109, 110]. Interestingly, ectopic TH expression is conspicuous in a subpopulation of Purkinje cells in the Pogo mouse, and TH immunoreactive Purkinje cells are clustered in an array of parasagittal stripes. Almost all TH immunoreactive Purkinje cells express zebrin II [111].

Plomp et al. discuss the neuromorphological and electrophysiological findings in the rolling Nagoya mouse [112]. This mouse was initially reported by Oda [113]. The mutation was identified in 2000 [114]. The phenotype in

homozygous mice is characterized by a broad-based, severe ataxic gait. Mice exhibit frequent lurching and abnormal cyclic movements of the hind limbs when walking, rolling on their back or side. Symptoms become obvious between postnatal days 10 and 14. Overall, the ataxia is more severe than in tottering but less severe than in leaner mice. Rolling Nagoya mice do not show absence seizures, motor seizures, or paroxysmal dyskinesias, which might be an advantage for testing the anti-ataxic effects of drugs, in the context of human CACNA1A mutation-related cerebellar ataxia [115, 116]. The mutation causes a charge-neutralizing amino acid change from a highly conserved arginine to glycine at position 1262 in the *Cav2.1- α 1* protein [114]. This mutation impairs the characteristic pattern of positively charged amino acids of one of the channel's voltage sensors, reducing the voltage sensitivity of the channel. Firing patterns in Purkinje neurons are aberrant. The R1262G mutation leads to reduced Ca⁺⁺ influx in cerebellar and other neurons that express the channel, leading to aberrant expression of many neuronal proteins and possibly also to the apoptosis of some neurons.

Bitoun and Davies review the characterization of a novel model of autosomal dominant cerebellar ataxia in mouse

Table 2 Models of recessive ataxias

Type of ataxia	Locus	Model
FRDA	9q13	Mice (<i>MCK</i>), promoter muscle creatine kinase, mouse (<i>NSE</i>), promoter neuronal enolase, mice (<i>Cre-ER^T</i>), promoter Prp, mice (<i>KIKO^{GAA230/-}</i>), mice (<i>KIKI^{GAA230/230}</i>), mice (<i>humanGAA/FXN-YAC</i>), <i>C. elegans</i> mutants (<i>frh-1</i>), <i>Drosophila</i> mutants (<i>dfh</i>) [53–59]
Familial coenzyme Q10(CoQ10) deficiency	CoQ10	Mice (<i>clkI^{-/-}</i>), mice (<i>coq7^{-/-}</i>), <i>C. elegans</i> (<i>clk-I^{-/-}</i>), <i>Saccharomyces cerevisiae</i> (<i>coq1-coq8</i>) mutants, diet depletion models [60–63]
Autosomal-recessive spastic ataxia of Charlevoix–Saguenay	13q12	Mice (<i>tumbler</i>) mutant [64]
Early onset cerebellar ataxia with retained tendon reflexes	13q11–12	–
Mitochondrial recessive ataxic syndrome		Mice (<i>PolgA</i> , <i>D257A</i>) [65]
Marinesco–Sjögren syndrome	5q32	Mice (<i>woozy</i>) mutants; mice (<i>tumbler</i>) mutant, [66–68]
Joubert syndrome	9q34	–
JBTS1		–
JBTS2	11p12–p13.3	
JBTS3	JBTS3 6q23	
JBTS4	JBTS4 2q13	
JBTS5		
Cayman ataxia	12q21.32	Jittery mice (<i>AtcayBI^{insEX4}</i>), [68, 69]
Ataxia with isolated vitamin E deficiency	8q13	Mice (α - <i>TTP^{-/-}</i>), diet restriction rat, [70, 71]
Abetalipoproteinemia (Bassen–Komzeweig syndrome)	4q22–q24	<i>Suncus murinus</i> (<i>suncus</i>); mouse (<i>apobEX26stop^{N1785}</i>), (<i>Apob83</i>) mutant [72, 73]
Hereditary motor and sensory neuropathy type IV, Refsum disease	10pter-p11.2	Mice (<i>Phyh^{-/-}</i>) [74]
Cerebrotendinous xanthomatosis	2q33-qter	Mice (<i>Cyp27^{-/-}</i>) [75]
Metachromatic leucodystrophy	22q13	Mice (<i>ASA^{-/-}</i>), (<i>ASA^{-/-CGT}</i>) (<i>ASA^{-/-CST}</i>) [76–78]
Niemann–Pick type C	18q11–121	Mice (<i>BALB/c npc^{nth}</i>), <i>Caenorhabditis elegans</i> (<i>npc-1</i> , <i>npc-2</i>) mutants [79, 80]
GM1 gangliosidosis GM2-gangliosidosis (Tay–Sachs disease)	3p21.33 15q23–24	Cats, cattle ,dogs ,sheep (GM1) mutants, cats (GM2) mutants, mice (<i>Hexa^{-/-}</i>), mice (<i>Hexb^{-/-}</i>), porcine (GM2) mutants [81, 82]
Chorea acanthocytosis	9q21	Mice (<i>CHACdel^{EX}</i>) [60, 61]
Wilson’s disease	13q14–21	Mice (<i>atp7b^{-/-}</i>), mouse toxic milk (<i>tx</i>), LEC rats, bedlington terriers mutants, West Highland White Terrier mutants dogs [83]
Aceruloplasminaemia	3q23–q24	Mice (<i>Cp^{-/-}</i>), [84]
Ataxia telangiectasia	11q22.3	Mice (<i>atm^{-/-}</i>), Mice (<i>Atm y/y</i>) [85, 86]
Ataxia telangiectasia-like disorder	11q21	–
Spinocerebellar ataxia with axonal neuropathy 1	14q31	–
Ataxia with oculomotor apraxia	9p13	–
Ataxia with oculomotor apraxia 2	9q34	–

with growth retardation from 2 to 3 weeks of age and adult-onset region-specific Purkinje cell loss, as well as cataracts and defects in early T cell maturation [117]. Robotic animals display an unusual jerky gait, first apparent from 3 to 4 weeks [118]. The mice show a progressive decrease in size of the molecular layer, resulting in significant atrophy of the cerebellum from 6 months [119]. The mutation involves AF4, a member of the AF4/LAF4/

FMR2 (ALF) family of transcription cofactors. In the cerebellum, the expression of AF4 gene is restricted to the Purkinje cell layer, with markedly reduced levels in lobe X. The onset of degeneration coincides with the completion of dendritic development and acquisition of mature Purkinje neuron electrophysiological properties [120]. AF4 is involved in lymphopoiesis and leukemogenesis. The Af4 knockout mouse shows severe impairment in B and T cell

Table 3 Models of X-linked ataxias

Disorder	Animal model
Fragile X tremor ataxia syndrome	Mice (<i>fmr1</i> ^{-/-}), <i>Drosophila</i> (<i>Dfxr</i>) mutants, mice (<i>fmr1</i> -CGG102/110), <i>Drosophila</i> (<i>humanFMR1</i> -CGG90) [87–90]
Arts syndrome	–
X-linked adrenoleukodystrophy	Mice (<i>Abcd2</i> ^{-/-}), <i>Drosophila</i> (<i>bubblegum</i>) [91, 92]
Congenital ataxias	–
Rett syndrome	Mice (<i>mecp2</i> ^{-/-}), mice (<i>mecp2EX^{3/4mut}</i>) [93, 94]
Ataxia–dementia (SCAX4)	–

development, especially in early stages during proliferation and recruitment of cell precursors [121]. The ALF proteins are transcriptional regulators [122, 123]. The ALF family member FMR2 has been linked to a neurological disorder in human. Loss of FMR2 gene expression via expansion of CCG trinucleotide repeats in the 5'-untranslated region has been shown to cause FRAXE, an X-linked form of mild mental retardation associated with learning deficits [124]. The phenotype of the *Fmr2* KO mouse is reminiscent of the human phenotype with impaired learning and memory performance [125].

Chen and colleagues underline the consequences of the mutations of the SCN8A gene, one of the sodium channel α -subunit genes [126]. The SCN8A gene is primarily expressed in neurons and glia. In the cerebellum, the SCN8A gene is expressed in many types of neurons, including Purkinje cells, granule cells, and neurons in cerebellar nuclei [127]. A patient with cerebellar atrophy, ataxia, and mental retardation with a protein truncation mutation of sodium channel *Scn8a* has been reported [128].

Several mutant alleles of *Scn8a* have been characterized, showing various combinations of ataxia, dystonia, and muscle weakness [129–131]. Various deficits in Purkinje cell function have been found in *Scn8a* mutant mice, although no major loss of Purkinje cells, as reported in many other types of mutant mice, has been described except in older *Scn8amedJo* mice. There is a decreased density of gamma-aminobutyric acid (GABA) immunolabeling in somata of Purkinje cells in mutant mice as compared to control mice, suggesting that the decreased Purkinje cell activity in the mutant mice might be due to a downregulation of GABA metabolism [132]. Glutamine and taurine concentrations are higher in almost all brain regions of *Scn8amedJ* mice as compared to controls. Glutamine is involved in glutamate synthesis and taurine participates in osmoregulation [133]. Changes in glutamine and taurine suggest an upregulation of glial amino acid metabolism.

The clinical and genetic characterization of dominant SCAs has made a jump. About 30 SCAs are now described in details. Corresponding animal models of polyglutamine-related neurodegeneration have been generated. Vig et al. [134] show that vacuoles appearing early in SCA1 Purkinje cells could develop through an autophagic mechanism. The degeneration of the interface between Bergmann glia and Purkinje cells results in the formation of these vacuoles. These latter cells appear earlier as compared to intranuclear inclusions and onset of behavioral abnormalities [135]. Besides transgenic mouse models, *Drosophila* models overexpressing the mutant protein have been generated, having analogies with the human disorder such as nuclear inclusion formation and late-onset cell degeneration [136, 137]. The gain of toxic function resulting from the protein mutation can be investigated in details. It is also of interest to compare the data obtained from cultured cerebellar cells and from in vivo studies. For instance, the mutant protein associated with SCA7 (*ataxin7*) activates the apoptotic

Table 4 Models of acquired ataxias

Disorder	Animal model
Stroke	Vascular occlusion Ischemia–reperfusion model
Intoxication	See text
Tremor	Administration of harmaline [95]
Immune-mediated	EAE [96]
Infectious/para-infectious	Direct infection
Traumatic	Cerebellar trauma [97]
Paraneoplastic	Administration of antibodies Modification of the immune reaction
Endocrine	Reviewed in [98]
Developmental	Mutant studies in mouse—investigations of the foliation patterns

pathway, whereas in vivo models of SCA7 show ataxia and Purkinje dendrite degeneration in absence of Purkinje cell apoptosis [42, 138, 139]. Transgenic mice expressing polyQ-expanded TBP (TATA-box binding protein) have allowed the unraveling of the effects of the polyQ domain of TBP in transcriptional regulation, improving our understanding of SCA17 whose presentation is highly heterogeneous [48, 140]. Although high expression of mutant proteins in mice results in the successful generation of polyglutamine-related changes in the brain, there are still some discrepancies in terms of lesion distribution or cell types that are affected [141]. In addition, no model has yet successfully reproduced the specific neuronal loss observed in humans. The impact of neuroimaging on the appraisal of the neurodegenerative process occurring in the human cerebellum is noticeable and advanced imaging techniques are now being applied in animals with great hope [142, 143]. Quantitative methods allow an accurate estimation of components of the cerebellum, from childhood to the elderly [144]. Applications for ataxic disorders are straightforward.

A few mutant hamsters have been reported [145]. They are used as models for movement disorders such as dystonia or parkinsonism [146, 147]. Akita and Arai report on a spontaneous model of Purkinje cell loss in hamster [148]. The major clinical sign of the mutant hamsters is a moderate ataxia of gait, with trembling of the head, unsteady walking, or stumbling. This ataxia is associated with a rapid loss of the cerebellar Purkinje cell population after the third postnatal week [148]. The expression of *Nna1*, the gene of the *pcd* mutation in mice [149, 150], is almost completely suppressed in the brain of mutant hamsters. The *pcd* mouse has been considered as an important model for understanding of cerebellar degeneration and for the evaluation of new therapies such as grafting or administration of insulin-like growth factor 1 (IGF-1) [151–153]. This latter strategy is supported by the observation that IGF-1 mRNA expression drops in cerebellar Purkinje cells of *pcd* mouse as neurons undergo apoptosis [154]. At least ten independent phenotypic alleles of *pcd* have been identified so far, most studies having been performed with the *pcd*^{1J}, *pcd*^{3J}, and *pcd*^{5J} mice. The *pcd*^{1J} mice show an almost complete loss of cerebellar Purkinje cells and an indirect degeneration of granule cells [155]. Loss of Purkinje neurons occurs abruptly after the second postnatal week. Selected populations of thalamic neurons begin to degenerate at 7 weeks of age [156]. Transneuronal degeneration occurs in the inferior olivary complex and the deep cerebellar nuclei in old mutants [157]. *Nna1* encodes a putative zinc carboxypeptidase containing nuclear localization signals and an ATP/GTP binding motif. *Nna1* has been mapped to mouse chromosome 13 [151]. In adult wild-type mice, a 4-kb *Nna1* transcript is expressed mainly in the

brain, testis, and heart [158]. *Nna1* expression levels in the brain of homozygous mutants are undetectable in *pcd*^{1J} and *pcd*^{2J} or significantly lower in *pcd*^{3J} as compared to the wild-type control. The *Nna1* transgene introduced into the *pcd*^{3J} mice under regulation of the Purkinje cell-specific L7/*pcp2* promoter rescues the neuronal cell loss as well as the ataxia, confirming that the loss of function of *Nna1* is responsible for the *pcd* phenotype [138]. Both the ataxic hamsters and the *pcd* mice exhibit an autosomal recessive trait, and mutant hamsters have a normal life span under conventional breeding conditions similar to the *pcd* mutant mice. Differences between the ataxic hamster and the *pcd* mouse include the moderate reduction of granule cell density in the ataxic hamster, as well as the subtle involvement of the cerebellar nuclei, inferior olivary complex, and thalamic neurons, highlighting a distinct profile of late-onset degeneration in these two animal models. Therefore, the ataxic hamster could be used to investigate cerebellar disorders characterized by relatively low levels of secondary degeneration.

Murine models of FRDA have provided insights into the early effects of frataxin deficiency. Homozygous frataxin deletion is lethal at embryonic day 6.5 [53]. Heterozygous mutant mice are totally asymptomatic (50% residual frataxin). FRDA conditional animal models are viable [54]. The first expresses a recombinase under the muscle creatine kinase (MCK), the second under a neuron-specific enolase (NSE) promoter. In summary, these models show heart and striated muscle- or neuron-restricted deletion of frataxin [54]. Both models reproduce cardiac hypertrophy, large sensory neuron dysfunction without alteration of small sensory and motor neurons, and deficits in complexes I, III of the respiratory chain as well as aconitase activities as observed in FRDA patients. There is no skeletal muscle involvement. No increased oxidative stress is detectable in the conditional mouse models [55]. The NSE model develops progressive movement disorders characterized by gait abnormalities and loss of proprioception [54]. Electrophysiological studies reveal a specific large sensory nerve conduction defect with normal motor nerve conduction. These features mimic the abnormalities observed in patients. Another attractive murine model exhibiting the neurological features of FRDA in humans is the tamoxifen-inducible recombinase (Cre-ER^T) under control of the mouse prion protein (*Prp*) promoter. The course is slowly progressive, with cerebellar and sensory ataxia in absence of motor involvement [56]. Histological lesions include posterior columns degeneration and severe lesions of Clarke's columns neurons. To study the influence of the *GAA* repeat, the FRDA knock-in–knockout (KIKO) mouse has been generated, expressing 35–40% of wild-type residual frataxin. However, these mice do not develop phenotypic abnormalities similar to FRDA patients. Mice

homozygous for the knock-in allele containing the (*GAA*)₂₃₀ repeat (KIKI) have become a valuable tool for evaluating epigenetic changes associated with *GAA* expansion and correlating them with frataxin expression. Several *Caenorhabditis elegans* models with knockdown have been created to study the role of the frataxin homolog *fih-1*. These animals have extended life span despite a small body size, reduced fertility, and altered response to oxidative stress [57]. The frataxin knockdown animals present a consistent pleiotropic phenotype (slow growth, egg-laying defects, abnormal pharyngeal pumping, and defecation defects) associated with an increased sensitivity to oxidative stress [58]. The UAS-GAL4 transgene-based RNAi method has also been used to impose downregulation of the *Drosophila* frataxin homolog (*dfh*). This model mimics FRDA phenotype. The function of *dfh* is essential during development [59]. Flies exhibit a markedly reduced life span and a slight decline in climbing ability [159].

The neurological symptoms and pathological findings observed in α -tocopherol knockout mice (α -TTP^{-/-}) closely resemble those of AVED in human [72]. Mice are normal until the age of 1 year. Deficient mice on normal or deficient α -tocopherol diet show shaking of the head and mild ataxia while walking. Abnormalities worsened gradually and, at the age of 18 months, mice develop tremor and become clearly ataxic and paretic in the hind limbs. Dystonia is also observed. Wild-type mice fed on α -tocopherol-deficient diet do not differ significantly from wild-type mice on a normal diet [71].

Clk-1 gene encodes a demethoxyubiquinone hydroxylase catalyzing the production of coenzyme Q (CoQ) in mitochondria [60]. *Clk-1* mutants of yeasts, nematodes, and mice cannot synthesize CoQ, but instead accumulate DMQ [60, 62, 63]. *Clk-1*-deficient mice lacking CoQ fail to survive beyond the embryonic day 10.5. Mouse *coq7* gene is homologous to *Saccharomyces cerevisiae coq7/cat5* and is necessary for biosynthesis of CoQ. COQ7-deficient mouse shows a small-size body and delayed embryogenesis. Morphological studies reveal a failure in the radial arrangement in the developing cerebral wall. Dietary CoQ tests in *Drosophila melanogaster* does not increase life span or decrease age-dependent decline in cytochrome c oxidase activity.

A mutant *BALB/c* mouse strain represents an interesting model for Niemann–Pick disease (NPC). This model displays a biochemical phenotype similar to patients with NPC1 disease, including neurodegeneration [79], irregular dendritic trees and spines [160], and progressive tauopathy [161, 162]. The amount of cholesterol within mitochondria membranes is significantly elevated in NPC1 mouse brains and neural cells. In addition, the mitochondrial membrane potential, the activity of ATP synthase, and the level of ATP are markedly decreased in NPC1 mouse brains and

neurons. NPC1 neurons show an impaired neurite outgrowth, which can be rescued by exogenous ATP. Two *C. elegans* homologs of the human NPC1 gene, designated *npc-1* and *npc-2*, have been generated to assess mechanisms underlying Niemann–Pick disease [80]. Mutant animals for *npc-1* develop slowly, laid eggs prematurely, and are hypersensitive to cholesterol deprivation. These phenotypes in *C. elegans* provide a model system for both genetic and chemical suppressor screening that could identify promising drugs.

The *Phyh* knockout mouse has been generated to study Refsum's disease. Toxicity of high phytanic acid levels has been confirmed in different tissues of this model. *Phyh*^{-/-} mice under a 0.25% phytol diet show liver steatosis and hepatocytes degeneration. Phytol causes an increase in plasma levels of alanine-amino transferase and amylase, indicative of liver and pancreas damage [74]. Phenotypically the *Phyh*^{-/-} mice show an abnormal gait when supplements of phytol are administered. The toe spread, paw print area, and base of support of the hindpaws are decreased, leading to an unsteady gait, explained in particular by a denervation of intrinsic foot muscles and a peripheral neuropathy. Histochemical analysis in the cerebellum reveals a loss of Purkinje cells. Furthermore, astrocytosis in the inferior colliculus, thalamus, and cerebellum are observed.

Jittery is a spontaneous autosomal recessive mouse mutation which arose around 1935 during the process of maintaining the mouse strain Bagg albino [163], which later became BALB/c [68]. Mice homozygous for the jittery mutation exhibit severe trunk and limb ataxia. They die of dehydration and starvation by 3–4 weeks of age [164]. Jittery is caused by a mutagenic B1 insertion into exon 4 of the *Atcay* gene [69]. The locus on 19p13.3 associated with Cayman ataxia might be homologous to the locus on mouse chromosome 10 associated with the recessive ataxic mouse jittery [69].

A neurologic disorder with clinical, morphologic, biochemical, and genetic similarities to human GM1 gangliosidosis has been discovered in two families of Siamese cats and in one isolated case of a short-hair domestic cat [81]. Affected kittens develop progressive tremors of head and pelvic limbs, generalized dysmetria, which advances to spastic quadriplegia. Additional symptoms are exaggerated acousticomotor responses, impaired vision, and grand mal seizures. This model is of interest in testing potential therapeutic strategies. GM1 gangliosidosis has also been identified in cattle [82], dogs [164, 165], and sheep [166]. Animals are clinically similar to the juvenile (type 2) form of the disease in humans [167]. Interestingly, the GM1 English Springer Spaniel (ESS) and Portuguese Water Dog, unlike other animal models for GM1 gangliosidosis, are characterized by skeletal lesions [168]. The two models

have similar age of onset, organ involvement, bone dysplasia, residual enzyme activity, and lymphocyte vacuolation, but they differ in the visceral storage of glycoproteins containing polylectosaminoglycans [169], as well as in the presence of coarse facial features, noted only in the ESS model [170]. The urine of both dog models contains a protein activator that stimulates the conversion of GM1 ganglioside to GM2 [171]. A mouse model lacking a functional beta-galactosidase gene has been generated by homologous recombination and embryonic stem cell technology. Tissues are deficient in beta-galactosidase mRNA and GM1 ganglioside-hydrolyzing capacity. The feline Korat model for GM2 gangliosidosis is deficient in hexosaminidase A and B activity. Korat cats show a phenotype analogous to human Sandhoff's disease. Post-mortem studies show hepatomegaly and typical storage vacuoles. A murine model of Tay–Sachs disease, the prototype of the GM2 gangliosidoses, has been produced through the targeted disruption of the *Hexa* gene encoding the subunit of alpha-hexosaminidase A (*Hexa*^{-/-}) mice. The mice accumulate GM2 gangliosides in the CNS and membranous cytoplasmic bodies are also found in the brain. The difference in the distribution of storage neurons suggests a distinct metabolism of gangliosides between humans and mice. Similar to the *Hexa*^{-/-} mice, the *Gm2a*^{-/-} mice demonstrate storage in restricted regions of the brain. However, they show abnormal storage in the cerebellum and develop deficits in balance and motor coordination.

Wilson's disease is a severe human disorder of copper homeostasis. The disease is associated with various mutations in the *ATP7B* gene that encodes a copper-transporting ATPase. The *LEC* rat is a mutant inbred strain, which was established from a closed colony of randomly bred Long–Evans rats [82]. This mutant has a deletion in the copper-transporting ATPase gene (*Atp7b*) [172]. *LEC* rats show elevated copper levels in liver, defective incorporation of copper into ceruloplasmin, and reduced biliary excretion of copper [173]. They also show similarities to Wilson's disease in many clinical and biochemical features [174]. They develop intravascular hemolysis secondary to the release of large amounts of nonceruloplasmin copper into the bloodstream [175]. They are also highly susceptible to the development of hepatocellular carcinoma [176]. Another model is the *toxic milk* (tx) mouse, associated with an autosomal recessive mutation impairing copper homeostasis [177]. Offspring of mutant females are born copper-deficient and since their mother's milk is also low in copper, babies die. They present liver nodular fibrosis, bile duct hyperplasia, and portal lymphocytic inflammatory cell infiltration [178]. Toxic milk mice share several biochemical abnormalities with Wilson's disease. The *atp7b*^{-/-} mice also display a gradual accumulation of hepatic copper. Progeny of the homozygous

mutant females demonstrate neurological abnormalities and growth retardation suggestive of copper deficiency.

The heterozygous mutant *Apob* allele mouse (*Apob83*) in which apoB100 amino acid 3798 has been changed to a stop codon shows a phenotype strikingly similar to the familial abetalipoproteinemia. In both human and mouse “apoB83 heterozygotes”, plasma concentrations of apoB83 are extremely low. The apoB83 in the plasma is confined to the most buoyant very low density lipoprotein particles. When compared with a wild-type *Apob* allele, the *Apob83* allele is associated with low levels of the apoB mRNA. ApoB synthesis and secretion are defective. Furthermore, apoB83 is cleared from the plasma extremely rapidly [72, 73].

A homozygous knock-in mouse expressing a proofreading-deficient version of PolgA (*D257A mice*), the nucleus-encoded catalytic subunit of mtDNA polymerase, has been generated to study mitochondrial disorders [65, 178, 179]. The knock-in mice develop a mtDNA mutator phenotype with an increase in the levels of point mutations, as well as increased amounts of deleted mtDNA. This increase is associated with reduced life span, weight loss, reduced subcutaneous fat, alopecia, kyphosis, osteoporosis, anemia, reduced fertility, and heart enlargement. Another model of these disorders is the transgenic mouse, in which mutant POLG is expressed in a neuron-specific manner. The mice show forebrain-specific defects of mtDNA and have altered monoaminergic functions in the brain. They exhibit a distorted day–night rhythm and a robust periodic activity pattern associated with estrous cycle [180].

To establish a direct in vivo link between endoplasmic reticulum (ER) dysfunction and neurodegeneration, a homozygous mouse with respect to the *woozy* (*wz*) mutation was created. The model develops adult-onset ataxia with cerebellar Purkinje cell loss. Interestingly, the *wz* mutation disrupts the gene *Sill* that encodes an adenine nucleotide exchange factor of BiP, a crucial ER chaperone. These findings provide evidence that a perturbation of ER chaperone function in terminally differentiated neurons leads to protein accumulation, ER stress, and subsequent neurodegeneration [64]. A recessive mouse mutation, *tumbler* (*tb*), was previously mapped to chromosome 1 by linkage [67]. *Tb* mice show ataxia, walking in a crab-like fashion and falling. Engert et al. have speculated that these mice harbored a mutation in *Sacs* gene [66].

Accordingly to the biochemical deficit in human, neuronal storage of SGalCer has been observed in arylsulfatase A (*ASA*^{-/-}) mice [77, 78]. These mice accumulate sulfolipids not only in neurons, microglia, and other glial cells but also in nonneural tissues, including kidney and gallbladder [181, 182]. However, the mice accumulate less sulfatides than in humans and do not show

demyelination. The mild phenotype of these mice offers the opportunity to investigate the consequences of lipid storage in particular cell types. The transgenic *ASA*^{-/-} mice are related to the enzymes catalyzing the synthesis of SGalCer in neurons: (1) uridine diphosphate-galactose/ceramide galactosyltransferase (*CGT*) [183] and (2) the 3'-phosphoadenosine-5'-phosphosulfate/cerebroside sulfotransferase (*CST*) [76]. The phenotype presents with accumulation of SGalCer, ataxia, and nerve fiber degeneration in the spinal cord.

To elucidate the role of ceruloplasmin in iron homeostasis, an animal model of aceruloplasminemia has been generated by disrupting the homolog murine *Cp* gene [83]. Although normal at birth, *Cp*^{-/-} mice demonstrate progressive accumulation of iron. Histologic analysis show abundant iron stores within reticuloendothelial cells and hepatocytes. Ferrokinetic studies reveal normal iron absorption and plasma iron turnover, suggesting that iron accumulation results from altered compartmentalization within the iron cycle. Accordingly, *Cp*^{-/-} mice show a striking impairment in the movement of iron out of reticuloendothelial cells and hepatocytes. Retinas studies have shown that mice deficient in both *Cp* and *Heph* have a striking age-dependent increase in iron. The iron storage protein ferritin is also increased in the doubly null retinas [184].

A murine model of ataxia telangiectasia by disrupting the *Atm* [*atm*^{-/-}] locus via gene targeting is available [85]. Homozygous mice display growth retardation, neurologic dysfunction, absence of mature gametes, infertility, defects in T lymphocyte maturation, and extreme sensitivity to gamma-irradiation. Animals develop malignant thymic lymphomas. *Atm*-disrupted mice recapitulate the ataxia telangiectasia phenotype in humans. In contrast to other *Atm* mutant mice, the *Atm* y/y mice show a lower incidence of thymic lymphoma and survive beyond a few months of age. They exhibit deficits in motor learning indicative of cerebellar dysfunction. No cerebellar degeneration is observed [84].

Models of X-Linked Ataxias

The knockout mice lacking normal FMR1 (*fmr1*^{-/-}) protein show macroorchidism, learning deficits, and hyperactivity. The mice do not show the specific brain structures abnormalities observed in human [86]. Presumably, the dendritic spines fail to assume a normal mature size and shape. Normal dendritic regression is also impaired [185]. However, unlike in human, the knockout mice do not show statistically significant dendritic spine density [186]. Amount of dense granules are low and metabotropic GluR5 (GRM5)-induced translation is increased [87]. Animals have deficits in classic delay eyeblink conditioning and

cerebellar Purkinje cells showed elongated irregular dendritic spines, with enhanced long-term depression induction at the parallel fiber synapses that innervate these spines [187]. The yeast artificial chromosome (YAC) transgenic mice have been created to determine whether the *fmr1*^{-/-} mouse phenotype could be rescued. The YAC transgene is expressed in cell- and tissue-specific manner [188]. A *Drosophila* model using loss-of-function mutants and overexpression of the FMR1 homolog, *dfxr* (*Drosophila* fragile X-related gene), has also been developed [189]. *Dfxr* nulls display enlarged synaptic terminals, whereas neuronal overexpression result in fewer and larger synaptic boutons. Synaptic structural defects are accompanied by impaired neurotransmission.

The transgenic mouse with an expanded CGG repeat (102/110 repeats) in human FMR1 has elevated *fmr1* mRNA levels and intranuclear inclusions with ubiquitin, Hsp40, and the 20S catalytic core complex of the proteasome as constituents. Both the number and the size of the inclusions are increased during the course of life, which correlate with the progressive character of the cerebellar tremor/ataxia syndrome in humans [88]. Human FMR1 premutated allele of 90 CGG repeats has been expressed in *Drosophila* [89]. The expanded RNA induces neuron-specific degeneration. Microarray analysis detects an altered expression of CASP8, CYFIP1, NTS, and UBE3A.

A mouse model of adrenoleukodystrophy (ALD) by targeted disruption has been generated [90]. Older *Aldp*-deficient mice exhibit an abnormal neurologic and behavioral phenotype, starting at around 15 months of age. This is correlated with slower nerve conduction and with myelin/axonal anomalies detectable in the spinal cord and sciatic nerve, but not in brain [190, 191]. Axonal damage is the first pathologic event in the *Abcd1*^{-/-} mice. Interestingly, overexpression of *Abcd2* prevents both very long chain fatty acids (VLCFA) accumulation and neurodegenerative features, whereas *Abcd1/Abcd2* double mutants exhibit an earlier onset of symptoms and a more severe disease [192]. The *Drosophila* recessive mutant *bubblegum* (*bgm*) shows adult neurodegeneration, with marked dilation of photoreceptor axons. This mutant has elevated levels of VLCFAs, as seen in ALD [91].

MECP2 mutation in Rett syndrome fits with the *mecp2* deficiency in mice [92]. *Mecp2* mice (*mecp2*^{-/-}) phenotypic manifestations include nervousness, body trembling, piloerection, and occasional hard respiration. At late stages, mutants become hypoactive. Heterozygous mutant females show symptoms at a late age: weight gain, reduced activity, and ataxic gait. A substantial reduction in both brain weight and neuronal cell size can be observed [93]. A model with replaced exons 3 and 4 of MECP2 is also available. Mice are viable and fertile. Mice overexpressing wild-type

human MECP2 [193] display enhanced motor/contextual learning and enhanced synaptic plasticity in the hippocampus. After 20 weeks of age, mice developed seizures, hypoactivity, and spasticity.

Models of Sporadic Ataxias

Sporadic cerebellar ataxias are also the cause of a substantial degree of morbidity worldwide. A typical example is the disability resulting from traumatic brain injury (TBI) [194]. Neurological deficits may result from a direct or indirect cerebellar injury. Limb or trunk ataxia, tremor, speech difficulties, and cognitive deficits are common in patients with TBI [195, 196]. Cerebellar deficits may be delayed [197]. Cerebellum is often affected even when the initial injury does not directly involve its components [198]. In this issue, Potts and colleagues discuss the mechanisms of TBI. We have gained insights into the understanding of cerebellar damage thanks to experimental models of TBI, namely fluid percussion injury (FPI), controlled cortical impact injury (CCI), weight drop impact acceleration injury, and rotational acceleration injury. In FPI, a pendulum strikes a fluid-filled piston which transmits a fluid pulse to the surface of the brain. This generates both a focal and diffuse injury, including a cerebral contusion and subarachnoid hemorrhage at the site of impact as well as more diffuse neuronal loss within the ipsilateral hippocampus, thalamus, striatum, amygdala, and medial septum [199]. In CCI, the injury is generated when an electronically controlled piston hits the surface of the brain. The severity of the injury is determined by the height from which the pendulum is dropped. Interestingly, the pathology of injury in the cerebellum after CCI is similar to that resulting from FPI, including Purkinje cell loss and microglial activation [96]. Several studies based on those models have shown that the cerebellar vermis is particularly sensitive to trauma. The weight drop impact acceleration injury induces a more diffuse TBI by delivering a force to the intact skull as opposed to the exposed brain [200]. A rotational component is produced when the head is displaced upon impact. A decreased expression of nitric oxide metabolites has been reported a few minutes after injury, suggesting a relationship to decreased blood flow after TBI [201]. Rotational acceleration injury mimics a rotational force against the brain and is characterized by diffuse subarachnoid hemorrhage, cortical hemorrhages, and astrogliosis [202]. Brain edema and an excitotoxic cascade result in extensive delayed neuronal cell death by apoptotic necrosis in several regions including the cerebellum [203]. Other authors have used a direct cerebellar trauma. FPI applied over the posterior fossa has been associated with impaired excitability of mossy fibers and parallel fibers, contributing to Purkinje cell death [204].

Information provided by these models are complementary to those gained from experiments based on axotomy or stab injury [205, 206]. These last models have provided interesting information regarding the discrepancies between Purkinje neurons and climbing fibers in terms of capacity of regeneration in an appropriate environment [207, 208].

Remote damage is not uncommon in cerebellar ataxias. Several factors contribute to the severity of remote cell death, mainly the type and extent of the primary insult, the characteristics of the connectivity, and the intrinsic vulnerability of the circuits [209]. Targeting the mechanisms of remote lesions has become a therapeutic strategy per se. Viscomi et al. have analyzed the degenerative mechanisms in the inferior olive and pontine nuclei after focal cerebellar lesion [210]. The authors have investigated the schedule of neuronal death in olivary and pontine neurons following hemicerebellectomy [211]. Time course of neuronal loss is distinct in the two populations. After hemicerebellectomy, precerebellar nuclei show a significant astrocytic and microglial activation [211]. Glial activation reaches a peak about 3 weeks after ablation of the hemicerebellum. Glial reaction is accompanied by a strong induction of the cytokine interleukin (IL)-1 β , a mediator which is known to enhance neuronal damage [212]. High doses of methylprednisolone improve neuronal survival in precerebellar nuclei and decrease the levels of IL-1 β . Although minocycline—which modulates microgliosis and inhibits caspase protease expression—inhibits microglial activation, there is no beneficial effect in terms of neuronal survival in the precerebellar nuclei. Other groups have reached similar conclusions [213].

There are numerous studies focusing on the vulnerability of the cerebellum to toxic agents [214, 215]. Cerebellar ataxia is classically observed in acute or chronic intoxication to ethanol [25]. Cerebellar degeneration contributes to motor and neuropsychological deficits in chronic alcoholics and in children with prenatal ethanol exposure. The mechanisms underlying these ethanol-induced alterations include excitotoxicity, dietary factors—especially thiamine depletion—glial dysfunction, changes in growth factors, apoptotic mechanisms, and various degrees of oxidative stress. Most of these mechanisms have been unraveled thanks to animal studies based on ethanol exposure, in addition to cell cultures [216, 217]. One model of cerebellotoxicity addresses the acute demyelination induced by cuprizone [218]. The model of cuprizone-induced toxicity reproduces several features of cerebellar deep gray matter observed in demyelinating disorders like multiple sclerosis (MS), a common disorder which affects the cerebellum frequently. Because ataxic deficits in MS significantly contribute to disability and are relatively refractory to therapy, there is a need to extend research beyond the classical models experimental such as autoim-

immune encephalomyelitis (EAE) [219]. Cuprizone is especially toxic for oligodendrocytes [220, 221]. The superior cerebellar peduncle is a main target [222]. Groebe and colleagues show that cerebellar nuclei show an intense demyelination. The white matter of the cerebellar cortex presents a swelling of myelin sheath. The authors also show that cuprizone induces an astroglial proliferation and migration toward the injured area. Astrocytes secrete several cytokines such as tumor necrosis factor- α or interleukin 1- β as well as proinflammatory prostaglandins, which likely participate in oligodendrocyte damage [223, 224]. Other neurotoxins widely used to reproduce human disorders include harmaline and other beta-carboline alkaloids for the investigation of tremor [94, 225, 226] and exposure to heavy metals which are known the target the cerebellar circuits among others [227, 228].

Appealing data on the roles of hormones in cerebellar development have been published recently [229, 230]. The importance of hormonal signaling on the numerous cerebellar functions has been highlighted [231, 232]. Animal models such as congenital hypothyroid animals due to thyroid gland dysgenesis or thyroid dysmorphogenesis, thyroid hormone receptor (TR) gene-mutated animals, and thyroid hormone transport or metabolism-modified animals are representative [97, 233, 234]. The brain itself has the capability of forming steroids *de novo* from cholesterol [235, 236]. Studies on mammals and nonmammals indicate that this neurosteroidogenesis is a conserved property of vertebrates [237]. In mammals, Purkinje cells differentiate just after birth and the formation of cerebellar neuronal circuit becomes complete in the neonate, when the formation of progesterone and estradiol are high. These hormones promote dendritic growth, spinogenesis, and synaptogenesis [237]. Discoveries of hormonal receptors are providing a possible explanation for the link between hormonal defects and ataxias such as Boucher–Neuhauser syndrome or Holmes syndrome [238, 239].

As man embarks on space exploration with the objective of space habitation, the need to understand the impact of gravity is obvious [240]. Many symptoms observed in astronauts are indicative of a vestibular dysfunction. Animal studies support the idea of an effect of altered gravity on CNS functions. However, our knowledge of the consequences of altered gravity on the vestibulocerebellar system is just starting to grow. Developmental sensitivity of the vestibuloocular reflex to hypergravity has been studied in amphibians; fish and insects (lacking a vestibular system) are an example of the complexity of the interactions between altered gravity and timing of vulnerability [241, 242].

In conclusion, a survey of the literature of these last two decades highlights the increasing number of animal models of cerebellar ataxias. In particular, genetically engineered

animals and animals with spontaneous mutations have entered in the routine analysis in many laboratories. These investigations are complementary to the studies carried in human disorders and speed up the discovery of the physiology of the cerebellum [243], the mechanisms of diseases as well as the search for effective therapies. The question of the characterization and relevance of these models should not be underestimated. Morphological differences across species may be marked or subtle and probably meaningless [244, 245]. Future therapies such as application of viral vectors to rescue genes in knockout mice will benefit from a detailed evaluation of the models considered [246, 247]

Acknowledgments M.M. is supported by the FNRS-Belgium; D.M. is supported by the Fonds Erasme-Belgium.

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