

Chapter 3

Genetics of Atypical Parkinsonism

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Abstract In this chapter, we discuss the genetics of sporadic atypical parkinsonism, namely, progressive supranuclear palsy (PSP), corticobasal degeneration (CBD), and multiple system atrophy (MSA). Major new knowledge include new susceptibility loci apart from the H1 haplotype in microtubuli-associated protein tau (*MAPT*) gene for PSP, as well as the discovery of mutations in *COQ2* gene causing familial MSA. Furthermore, we discuss atypical features of new and known PARK-related genes, such as *DNAJC6* and *SYNJ1*. Lastly, we discuss the features of atypical parkinsonism in genetic conditions presenting predominantly with other phenotypes such as dementia (*MAPT*, *PGRN*, *C9ORF72*, *DCTN1*), ataxia (SCAs, FXTAS), dystonia (DRD, DYT12, dopamine transporter deficiency syndrome), and others such as mitochondrial and metabolic disorders.

Keywords Progressive supranuclear palsy • Corticobasal degeneration • Multiple system atrophy • Atypical parkinsonism • PARK • Dystonia–parkinsonism • Dementia • Ataxia • Spasticity

Introduction

Atypical parkinsonian syndromes (APs) are defined as syndromes that present with parkinsonism and features atypical for Parkinson’s disease. Classically, the term is used to describe sporadic neurodegenerative conditions of unknown etiology that

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constitute the major differential diagnoses from sporadic Parkinson's disease, namely, progressive supranuclear palsy (PSP), corticobasal degeneration (CBD), and multiple system atrophy (MSA), which are pathological entities distinct from PD.

However, also a number of genetic conditions may cause parkinsonism with clinical features atypical for PD and diverse or yet unknown pathologies, and the term atypical parkinsonism has been used for these disorders as well. Of those, some are identified as causing predominantly parkinsonism and some as causing predominantly other phenotypes that may also include parkinsonism and in rare cases only parkinsonism. Here, we will discuss firstly the genetics of sporadic APs, secondly genes that cause predominantly APs, and thirdly genes that are linked predominantly to other phenotypes that may include atypical parkinsonism.

Genetics of Sporadic Atypical Parkinsonism: PSP, CBD, and MSA

The most common sporadic atypical parkinsonian conditions include progressive supranuclear palsy (PSP), corticobasal degeneration (CBD), and multiple system atrophy (MSA). These are distinct pathological entities.

Genetics of PSP

PSP is a neurodegenerative disease characterized by symmetric parkinsonism, supranuclear palsy of vertical gaze, early postural instability with falls backwards, and subcortical dementia [111]. This typical PSP phenotype is termed Richardson's syndrome (RS), while further phenotypes have been described [161]. The prevalence of PSP is approximately 5 per 100,000, average age at onset is 63, and mean time from symptom onset to death is 7–9 years. PSP is a 4-repeat tauopathy characterized by degeneration of several subcortical structures including the substantia nigra, the subthalamic nucleus, and the midbrain. Neurofibrillary tangles are present in these areas. Tufted astrocytes (Gallyas positive) are the hallmark feature of PSP that differentiates it in pathology from other 4R tauopathies such as CBD [46]. No effective treatments are available [77, 187, 202].

PSP is almost always sporadic. A genome-wide association study has confirmed that the most common risk allele for PSP is the H1 haplotype of the microtubuli-associated tau (*MAPT*) gene, and further risk loci have been identified [78]. The H1 haplotype of the *MAPT* gene (encoding for tau) is found in over 90 % of the patients. It is suggested that the presence of the H1 *MAPT* haplotype affects alternative splicing of exon 10 of the *MAPT* gene, which may result in an increased ratio of the 4R isoform of the tau protein (4R-tau) compared with the 3R isoform (3R-tau). However, the H1 *MAPT* haplotype did not correlate with age of onset,

disease severity, or survival in a study on 63 PSP patients, implying the presence of other modifying factors [110]. Interestingly, Li et al. using genome-wide methylation analysis showed that differential methylation at 17q21.31 correlates with the H1 haplotype in a dose-dependent manner in patients with frontotemporal dementia (FTD) and PSP, pointing for the first time to an epigenetic mediator of neurodegeneration that increases risk for PSP [105].

Apart from confirming two independent variants in *MAPT* affecting risk for PSP, this study identified three significant novel signals associated with PSP risk, which may give some insight in the pathophysiology of the disease: EIF2AK3 (eukaryotic translation initiation factor 2- α kinase 3; rs7571971, OR of major allele=0.75, $p=3.2 \times 10^{-13}$), STX6 (syntaxin 6; rs1411478, odds ratio [OR] of major allele=0.79, $p=2.3 \times 10^{-10}$), and MOBP (myelin-associated oligodendrocyte basic protein; rs1768208, OR of major allele =0.72, $p=1.0 \times 10^{-16}$) [78]. EIF2AK3 is a gene that encodes PERK, a component of the endoplasmic reticulum (ER) unfolded protein response (UPR). When excess unfolded proteins accumulate in the ER, PERK is activated and protein synthesis is inhibited allowing the ER to clear mis-folded proteins. However, tau, which is the primary mis-folded protein in PSP, is not expected to traffic through the ER. The second PSP susceptibility gene STX6 encodes syntaxin 6 (Stx6), and genetic variation at STX6 could influence movement of mis-folded proteins from the ER to lysosomes via the endosomal system. Lastly, MOBP encodes a protein (MOBP) that is produced by oligodendrocytes and is present in the major dense line of CNS myelin. MOBP is highly expressed in the white matter of the medulla, pons, cerebellum, and midbrain, regions affected in PSP, suggesting that myelin dysfunction oligodendrocyte misfunction contributes to PSP pathogenesis [78]. Ferrari et al. subsequently identified point mutations in each of these genes in a subset of the PSP cases used in the original GWAS [57]. Although implication of EIF2AK3 and MOBP could not be fully assessed, they showed that the single nucleotide polymorphism rs1411478 (STX6) is a strong expression quantitative trait locus with significantly lower expression of STX6 in white matter in carriers of the risk allele [57]. Further research is needed to identify the functional links between these risk loci and disease pathophysiology.

Genetics of CBD

Corticobasal degeneration (CBD) is a rare neurodegenerative disorder typically characterized by progressive asymmetric levodopa-resistant parkinsonism, dystonia, myoclonus, and further cortical signs (e.g., apraxia, alien limb phenomena, cortical sensory loss) [10, 186]. This typical CBD phenotype is now called corticobasal syndrome (CBS), while further phenotypes have been described [94]. CBD is a 4R tauopathy characterized by widespread deposition of hyperphosphorylated tau protein (specifically 4-repeat tau) in the brain. There is marked neuronal degeneration in the substantia nigra and the frontoparietal cortex. The hallmark feature of

CBD pathology is the characteristic astrocytic plaques that differentiate CBD from other 4R tauopathies such as PSP (tufted astrocytes) [109].

Since CBD is also a tauopathy, several studies have investigated the possible role of *MAPT* variants in the pathogenesis of the disorder. Indeed, the H1 haplotype was also found to be associated with the development of CBD [78, 79]. In a recent study, a systematic sequence analysis of *MAPT* coding and 3' untranslated region (3'UTR) in a large cohort of autopsy-confirmed CBD patients ($N=109$) was performed. This identified a novel *MAPT* mutation in exon 13 (p.N410H) in a case that was neuropathologically indistinguishable from sporadic CBD and represents the first case meeting neuropathologic diagnostic criteria for CBD harboring a *MAPT* mutation. On immunoblot, the p.N410H mutation carrier had the same insoluble tau profile as seen in CBD. Sequence analysis of the complete *MAPT* 3'UTR in autopsy-confirmed CBD cases further identified two rare variants with nominally significant association with CBD. An ATC nucleotide insertion ("MAPTv8") was found in 4.6 % of CBD patients compared to 1.2 % of controls ($p=0.031$, $OR=3.71$) and rs186977284 in 4.6 % CBD patients, but only 0.9 % of controls ($p=0.04$, $OR=3.58$). Rs186977284 was also present in 2.7 % of a large cohort of autopsy-confirmed PSP patients ($N=566$) and only 0.9 % of an additional control series ($p=0.034$, $OR=3.08$), extending the association to PSP [93].

Genetics of MSA

Multiple system atrophy (MSA) is a neurodegenerative disorder characterized by autonomic failure and parkinsonism and/or cerebellar signs. MSA-parkinsonism (MSA-P) is characterized predominantly by parkinsonism and autonomic failure at presentation, whereas in MSA-cerebellar type (MSA-C), cerebellar signs occur with autonomic failure [13, 213]. The prevalence is about 4 per 100,000, typical age at onset is 53–55 [214], and mean survival time is 9 years [214]. MSA is an α -synucleinopathy characterized by abnormal α -synuclein-positive cytoplasmic inclusions in oligodendrocytes, termed glial cytoplasmic inclusions, mainly found in the basal ganglia, cerebellar structures, and motor cortex. Neuropathological examination often reveals gross abnormalities of the striatonigral and/or olivopontocerebellar systems, which upon microscopic examination are associated with severe neuronal loss, gliosis, myelin pallor, and axonal degeneration [4, 47].

SNCA (α -synuclein) gene is encoding for the α -synuclein protein. *SNCA* variants have been studied as risk factors to develop MSA. 10 single nucleotide variants of *SNCA* most associated with risk of developing PD were tested in 413 MSA cases, and 2/10 *SNCA* variants were significantly associated with a risk of developing MSA [176]. These results were confirmed in an independent cohort of 108 MSA patients (rs11931074, $OR=6.2$, $p=5.5 \times 10^{-12}$; rs3857059, $OR=5.9$, $p=2 \times 10^{-10}$) [5, 176]. Al-Chalabi et al. examined 32 *SNCA* variants in 239 MSA cases and found that two of the variants were associated specifically with the MSA-C subtype (rs3822086; rs3775444) [5]. A GWAS in MSA is not available as of now, but is under way.

Recently, a combination of linkage analysis and next-generation genome sequencing identified homozygous and compound heterozygous variants of the gene *COQ2* (coenzyme Q2 4-hydroxybenzoate polyprenyltransferase) as a cause of MSA in familial cases from Japan and as a risk factor to develop sporadic MSA [127]. *COQ2* is important for the biosynthesis of coenzyme Q10, which in turn is an important factor for mitochondrial respiratory chain function. The most common of these mutations, p.V343A, was suggested to increase the risk of MSA through functional impairment of coenzyme Q10, which leads to increased oligodendrocyte apoptosis due to oxidative stress [127, 138].

A heterozygous deletion in *SHC2* (src homology 2 domain containing-transforming protein 2) in monozygotic twins discordant for MSA has also been reported [173]. The authors further observed copy number variation in *SHC2* in 32 % (10 of 31 patients) of MSA patients and in no controls of Japanese descent. However, a more recent study did not find copy number variation of the *SHC2* gene to be a significant genetic factor for non-Japanese MSA patients implying that this may only play a role in MSA pathogenesis in Japanese cohorts [56].

Atypical Parkinsonism in PARK-Related Genes

Mutations in the recessive *ATP13A2/PARK9* gene that encodes a predominantly neuronal lysosomal type 5 P-type ATPase have been detected in patients with the recessively inherited Kufor–Rakeb syndrome. Kufor–Rakeb syndrome is typically characterized by juvenile-onset (12–29 years), levodopa-responsive parkinsonism (with fluctuations and dyskinesias), vertical supranuclear gaze palsy, cognitive dysfunction (dementia and visual hallucinations), and pyramidal signs [128, 218]. Further characteristic features include oculogyric dystonic spasms and facial–facial–finger mini-myoclonus [15, 48, 115, 160]. T2*-weighted MRI imaging may show evidence of brain iron accumulation in some patients, which can be a helpful clue to suspect this disorder [139, 140, 160, 174]. There is no pathology from a patient with Kufor–Rakeb syndrome reported, but recently exome sequencing in a family with pathologically confirmed neuronal ceroid-lipofuscinosis has identified *ATP13A2* mutations that segregated with the affected family members [29].

Mutations in *PLA2G6/PARK14* are identified as one cause of adult-onset parkinsonism with additional dystonia and complicated by pyramidal involvement. *PLA2G6* gene mutations were previously known to cause infantile neuroaxonal dystrophy and are also one cause of neurodegeneration with brain iron accumulation. In adult-onset cases, parkinsonism is characterized by the presence of tremor including a pill-rolling rest component, rigidity, and severe bradykinesia with a good response to levodopa. However, there was early development of dyskinesias [139, 184].

Mutations in the F-box only protein 7 gene (*FBXO7*) cause PARK15, a recessive form of juvenile parkinsonism with pyramidal signs. It was identified in one Iranian kindred with predominant pyramidal signs and later demonstrated by different mutations found in further ethnicities with prominent juvenile parkinsonism with

varying degrees of levodopa response [106, 114, 139, 184, 222]. The brain pathology in patients with PARK15 remains unknown. However, FBXO7 immunoreactivity in the Lewy bodies of typical PD, and in glial cytoplasmic inclusions of multiple system atrophy, is reported, suggesting an involvement of this protein in the pathogenesis of the common forms of synucleinopathies [86, 223].

DNAJC6 and *SYNJ1* (PARK20) have been recently identified as the cause of autosomal recessive, juvenile parkinsonism, using exome sequencing combined with genome-wide homozygosity mapping [39, 53, 82, 92, 97, 136, 147, 153, 172, 194, 211]. The phenotype of *DNAJC6* mutations ranges from juvenile parkinsonism without further signs or with mental retardation, pyramidal signs, and epilepsy, while a case with obesity, epilepsy, and mental retardation but no signs of parkinsonism has been reported [53, 82, 92]. *DNAJC6* encodes the neuronal co-chaperone auxilin. In the case of *SYNJ1*, the same homozygous mutation, p.Arg258Gln, was identified independently in two consanguineous families of Iranian and Italian origins, with parkinsonism, dystonia, and cognitive deterioration. Response to levodopa was poor and limited by side effects [97, 153]. Neuroimaging revealed brain atrophy, nigrostriatal dopaminergic defects, and cerebral hypometabolism [97, 153]. *SYNJ1* encodes synaptojanin 1, which plays a role in the post-endocytic recycling of synaptic vesicles (Table 3.1).

Atypical Parkinsonism in Genetic Disorders Predominantly Presenting with Other Neurologic Features

Traditionally a gene is tied to the recognition of a characteristic phenotype, but once the genetic defect is identified, the phenotypic characterization broadens. Indeed, genes identified in cohorts of patients presenting with diverse predominant features such as dementia, ataxia, chorea, or dystonia are now well recognized to also cause atypical parkinsonism, and in fact, in some cases atypical parkinsonism may be the predominant phenotype. In some cases, the atypical parkinsonism may resemble the classical PSP, CBD, or MSA phenotypes, leading to diagnostic confusion [190]. These genetic conditions are described below and are given in Table 3.1.

Atypical parkinsonism in Genes Predominantly Causing Dementia

Microtubule-associated protein tau (*MAPT*) and progranulin (*PGRN*) gene mutations both inherited in a dominant pattern and mainly causing frontotemporal dementias (FTDs) (with 3R/4R and TDP-43 pathology, respectively) can present with atypical parkinsonism and PSP as well as CBS phenotypes [31, 32, 34–36, 64, 125, 142, 149, 164, 165, 167, 168, 192, 208]. Clues to test for *MAPT* mutations would be the earlier age at onset (between the third to fifth decade) [6, 142, 149, 166, 168, 192], a positive family history of parkinsonism or dementia [64, 125, 165], and early and prominent behavioral problems that usually precede the classical PSP or CBS signs.

Table 3.1 An incomplete list of genetic conditions that may cause atypical parkinsonism, along with their respective genes, mode of inheritance, mean age of onset, MRI, and DaTSCAN findings

	Gene	Transmission	Age of onset (years)	Major features in MRI brain	DaTSCAN
<i>PARK-related parkinsonism</i>					
PARK8	<i>LRRK2</i>	AD	~Mean 60–65	From normal to generalized atrophy	Abnormal
PARK9 (Kufor–Rakeb)	<i>ATP13A2</i>	AR	Juvenile	Diffuse moderate cerebral and cerebellar atrophy and in some putaminal and caudate iron accumulation	Abnormal
PARK14	<i>PLA2G6</i>	AR	Juvenile	Cortical and cerebellar atrophy, may show iron in Gpi, may show white matter changes	Abnormal
PARK15	<i>FBXO7</i>	AR	Juvenile	Brain atrophy or maybe normal	
PARK20	<i>SYNJ1</i>	AR	Juvenile to adulthood	Brain atrophy	Abnormal
<i>Genes predominantly causing dementia</i>					
Frontotemporal lobar degeneration	<i>MAPT</i>	AD	~Mean 40	Symmetric frontotemporal atrophy	Abnormal
	<i>PGRN</i>	AD	~Mean 60	Asymmetric fronto-temporo-parietal atrophy	Abnormal
	<i>C9ORF72</i>	AD	~Mean 52	Bilateral frontal atrophy with variable degrees of parietal +/-temporal atrophy; usually no striking asymmetry	Abnormal
Alzheimer's dementia	<i>PSEN1</i>	AD	~Mean 45	Medial temporal atrophy	May be abnormal
Perry syndrome	<i>DCTN1</i>	AD	~Mean 45–50	May show midbrain atrophy	Abnormal

(continued)

Table 3.1 (continued)

Gene	Transmission	Age of onset (years)	Major features in MRI brain	DaTSCAN
<i>Genes predominantly causing ataxia</i>				
Spinocerebellar ataxias				
<i>ATXN2</i>	AD	~Mean 32	Pontocerebellar atrophy 25 % have hot cross bun sign	Abnormal
<i>ATXN3</i>	AD	Range 5–75	Pontocerebellar atrophy	Abnormal
Fragile X tremor-ataxia syndrome	X-linked dominant	~Mean 60	Increased signal in MCP and CCS in T2-weighted images	~47 % Abnormal
<i>Genes predominantly causing dystonia</i>				
DYT3	X-linked dominant	~Main 30	Severe atrophy of the caudate and putamen; hyperintensity with an outer rim in the putamen	Abnormal
DYT5a	AD	~6–10	Usually normal	Normal
DTDS	AR	Infantile to adulthood	Maybe normal, in some white matter changes	Abnormal
DYT12	AR	4–58 years	Usually normal	Abnormal
Wilson's disease	AR	First decade (but up to adulthood)	Can show the “face of the giant panda” midbrain May show hyperintensities in basal ganglia, midbrain, thalami, and pons	Abnormal
Inborn error of manganese metabolism	AR	First decade (but up to adulthood)	Hyperintensities in basal ganglia and cerebellum in T1-weighted images	
NBIAs	Diverse	First decade (but up to adulthood)	Eye of the tiger in PKAN, further see genetics of NBIA's	Maybe normal or abnormal
<i>Genes causing predominantly spasticity</i>				
HSPs	AR	First decade (but up to adulthood)	Atrophy of the corpus callosum	Maybe normal or abnormal

<i>Genes causing predominantly chorea</i>					
Huntington's disease	<i>huntingtin</i>	AD	Wide range from early childhood to late adulthood	Caudate atrophy	Maybe normal or abnormal
Neuroacanthocytosis	<i>VPSI3A</i>	AR	Wide range from early childhood to late adulthood	May show striatal atrophy in particular the head of the caudate	Maybe normal or abnormal
<i>Others</i>					
Cerebrotendinous xanthomatosis	<i>CYP27A1</i>	AR	~Mean 40	Cerebellar atrophy Hyperintensities in dentate in T2-weighted images	Abnormal
Gaucher's disease	<i>GBA</i>	AR	From 3rd to 7th decade	Normal	Abnormal
Niemann-Pick C	<i>NPC</i>	AR	Second to third decade	May show frontal atrophy and hyperintensities in parietal-occipital periventricular white matter	Unknown
Mitochondrial	Various	AR, AD	From juvenile to adulthood	Variable changes	Abnormal
Genetic PRION	<i>PRNP</i>	AD	Wide range from juvenile to seventh decade	Hyperintensities in putamen and caudate in T2, FLAIR, and DWI sequences	Abnormal
Leukoencephalopathy with axonal spheroids	<i>CSF1R</i>	AD	Wide range	Leukoencephalopathy	Abnormal

Abbreviations: MCP middle cerebellar peduncles, *CCS* corpus callosum splenium, *MRI* magnetic resonance imaging, *DatSCAN* dopamine transporter imaging, *MAPT* microtubule-associated tau, *PGRN* progranulin, *C9ORF72* chromosome 9 open reading frame 72, *PSEN1* presenilin 1, *DCTN1* dyactin, *LRRK2* leucine-rich repeat kinase 2, *ATXN* ataxin, *FMR1* fragile X mental retardation 1, *GBA* glucocerebrosidase, *NPC* Niemann-Pick C, *PRNP* prion protein, *CSF1R* colony-stimulating factor 1, *SPG11* spastic paraplegia 11, *DTDS* dopamine transporter deficiency syndrome

In contrast, the mean age at onset in *PGRN* mutation carriers is 60 years (range: 35–83 years) [14, 64, 177, 221], and the penetrance reaches that of 90 % at age 70 [26], so a positive family history is not always present. Clinical clues to suspect *PGRN* in a patient with RS or CBS would be a long preceding history of frontal dysfunction [203, 221]; signs of parietal lobe involvement (e.g., dyscalculia, limb apraxia, etc.), which are unusual for sporadic PSP (but usual in CBD); and hallucinations that rarely occur in sporadic PSP and CBD. Different studies report CBS as one of the three most common phenotypes seen in *PGRN* mutation carriers (the other two being bvFTD and PNFA) [14, 17, 18, 24, 35, 36, 49, 66, 87, 141, 157, 164, 185, 209]. A careful language evaluation may help to predict *PGRN* mutations in these patients; PNFA is occasionally the initial manifestation, before the CBS phenotype emerges. MRI imaging shows asymmetric fronto-temporo-parietal atrophy [6], rarely the case in PSP, but similar to findings in CBD [91, 188]. Sequential testing for *MAPT* and *PRGN* in patients with a positive family history is recommended and available [64]. Measurement of progranulin plasma levels may also be helpful if genetic testing is not available [58].

Hexanucleotide expansions in the newly described gene, chromosome 9 open reading frame 72 (*C9ORF72*) (TDP-43 pathology), cause FTD–amyotrophic lateral sclerosis (ALS) overlap syndromes [117, 118, 156], and in 35 % of these patients, atypical parkinsonism may be present [25, 37, 38, 76, 108, 117, 118, 134, 156]. A positive family history, signs of upper or lower motor neuron disease, and the presence of hallucinations are important clues to suspect these mutations [25, 37, 38, 108, 134, 156].

Lastly, Perry syndrome, a rare autosomal dominant disorder due to mutations in the dynactin (*DCTN1*) gene (TDP-43 pathology) may present with atypical parkinsonism and an RS, CBS, as well as MSA phenotype [212, 215]. Clinical clues to suspect these mutations include central hypoventilation, weight loss, and psychiatric symptoms (e.g., apathy, hallucinations) [100, 129, 135, 145, 146, 151, 204]. Response to levodopa varies from no response to significant improvement and development of motor fluctuations and dyskinesias [22, 55, 129, 135, 145, 146, 151, 204, 212, 215, 216].

CBS has been described commonly with Alzheimer’s disease (AD) pathology in sporadic AD patients [7, 23, 50, 61, 73, 83, 104], and earlier age at onset and myoclonus are thought to be more suggestive of AD rather than CBD pathology [50, 83, 99]. Increased saccadic latency has been described in AD and CBD, and thus this feature may not be helpful in the differential diagnosis [27]. Some mutations in presenilin 1 (*PSEN1*) have been described to cause parkinsonism with myoclonus, dystonia, apraxia, and frontal dementia mimicking CBD, although there is usually no striking asymmetry and there may be seizures, which rarely occur in CBD [99]. Mutations in *APP* and *PSEN2* may also present with parkinsonism but mostly mimicking dementia with Lewy bodies (DLB) [155].

Atypical parkinsonism in Genes Predominantly Causing Ataxia

Spinocerebellar ataxias (SCA) represent a clinically and genetically heterogeneous group of neurodegenerative disorders in which progressive degeneration of the cerebellum and spinocerebellar tracts of the spinal cord are associated with a variable

combination of signs of central and peripheral nervous system involvement (see also Chap. 11). Extrapyramidal features, including parkinsonism, have been described in several of these such as SCA2 and SCA3.

SCA2 (due to expansion of a glutamine tract in the ataxin-2 gene) typically presents with ataxia, slowed horizontal saccades, and peripheral neuropathy; however, phenotypes with a parkinsonism-predominant profile or purely parkinsonism, early postural instability, and vertical supranuclear gaze palsy (SGP) have been described [59, 69, 144, 167, 180, 181, 198], mostly in patients of Asian origin, with later age at onset and shorter repeat expansion [59, 69, 112, 144, 198]. SCA3 (Machado–Joseph disease) is the most frequent cause of autosomal dominantly inherited cerebellar ataxia in Europe, Japan, and the United States and is caused by an expanded polyglutamine CAG repeat size of >44 [162]. Age at onset varies from 5 to 75 years and inversely correlates with CAG repeat length. The parkinsonian variant of SCA3 is associated with lower range repeat expansions and a later age at onset, similar to SCA2 [42, 162, 175]. Cerebellar ataxia, parkinsonism, and only mild cognitive dysfunction [89, 107, 207] in addition to cardiovascular and sympathetic sweating dysautonomia (in up to 45 %) can clinically be mistaken for MSA, particularly when family history is negative [96, 197]. Further SCAs, such as SCA8, SCA17, and SCA6, more rarely present with parkinsonism [2].

Fragile X tremor-ataxia syndrome (FXTAS) is a late-onset (>50 years) neurodegenerative disorder, occurring in carriers of a premutation CGG repeat expansion (55–200 repeats) in the fragile X mental retardation 1 (*FMRI*) gene. The penetrance of FXTAS in male carriers over 50 years is ~40 %, and recently it has been postulated that female carriers develop FXTAS more often than previously suggested [199]. Autopsy reveals intranuclear inclusions in neurons and astrocytes and dystrophic white matter [12, 19, 65, 199]. The typical phenotype consists of the combination of intention tremor and ataxia, but parkinsonism, autonomic dysfunction, cognitive decline, psychiatric features, and neuropathy have been described, and tremor is not always present [12]. A family history of mental retardation or premature ovarian failure provides important clues [19]. However, in a recent series 43 % of the FXTAS patients had no family history of fragile X syndrome [9]. Additional features include autonomic dysfunction presenting, as in MSA, with impotence, orthostatic hypotension, urinary frequency, and urinary incontinence [9, 70]. However, MSA is rarely misdiagnosed as FXTAS – among 426 clinically diagnosed MSA cases, only four were found to have FXTAS in a study [84]. Dopamine transporter imaging (DaTSCAN) in few cases may be normal, and in which case, it is helpful in the differential diagnosis with MSA [116].

Atypical parkinsonism in Genes Predominantly Causing Dystonia or Dystonia–Parkinsonism

X-Linked Recessive Dystonia–Parkinsonism (DYT3; XDP; “Lubag”)

DYT3 dystonia, which clusters in Filipinos, is an X-linked recessive disorder. Although this disorder typically affects males, rarely, females may also be affected, possibly due to severe X-inactivation or based on homozygosity for the mutation [103]. DYT3

reaches complete penetrance by the end of the fifth decade in males and later in females (up to 75 years) and is associated with specific sequence changes in the TAF1 gene [126, 183]. Usually symptoms start in adulthood as focal dystonia, tend to progress, and generalize. Parkinsonism is often present (up to 36 %) and in some cases may precede the onset of dystonia or can be the predominant or sole feature throughout the disease course [54, 75, 103]. Parkinsonism may improve with levodopa in the early stages but becomes less responsive or unresponsive over the course of the disease. Investigations in XPD patients show an abnormal DaTSCAN and a clearly abnormal IBZM SPECT, implying decreased dopamine D2 receptor expression. On positron emission tomography (PET), striatal glucose metabolism is selectively reduced. Fluorodopa uptake is normal, suggesting that the origin of the extrapyramidal symptoms is localized rather postsynaptically to the nigrostriatal pathway (see also Chap. 7) [196].

Dopa-Responsive Dystonias (DYT5; Segawa's Disease)

DYT5 was initially described by Segawa et al. in 1976 [178] and later by Nygaard and colleagues as dopa-responsive dystonia (DRD) because of the dramatic and sustained response to low dose of levodopa [132]. The disease is inherited as an autosomal dominant trait with reduced penetrance that appears to be gender dependent with females more frequently expressing symptoms. It is caused by mutations in the *GTPCHI* (GTP cyclohydrolase 1) gene [80]. *GTPCHI* is the rate-limiting enzyme in the synthesis of tetrahydrobiopterin, an essential cofactor for tyrosine hydroxylase (TH) which in turn is needed to synthesize dopamine, explaining the remarkable therapeutic effect of levodopa substitution. The typical phenotype includes childhood (average 6 years) limb-onset dystonia with diurnal variation (e.g., worsening of the symptoms as the day progresses), improvement after sleep, and dramatic response to levodopa [60, 193]. Later in the course of the disease, parkinsonian features occur frequently, and patients may also show typical, late-onset isolated parkinsonism, which responds well to levodopa therapy, but, unlike in idiopathic PD, patients usually do not develop motor fluctuations and dyskinesias [133], although this is not exclusive [41, 102]. Early-onset parkinsonism due to mutations in one of the recessive PARK genes (mostly Parkin) has to be considered in the differential diagnosis of a young patient presenting with prominent leg dystonia that is responsive to levodopa therapy. Early-onset DRD patients show normal DaTSCAN in contrast to patients with young-onset Parkinson's disease [28]. The latter concept has been recently challenged, by demonstrating that later-onset DRD cases presenting with PD may have abnormal DaTSCANs; thus, *GTPCHI* mutations may be risk factors to develop classic PD (see also Chap. 7) [123].

In a minority of cases, DRDs can also be inherited as an autosomal recessive disorder with mutations in the genes coding for other enzymes involved in dopamine synthesis including tyrosine hydroxylase (TH) [60, 113], sepiapterin reductase (SR), and aromatic L-amino acid decarboxylase (AADC) deficiency [3]. The clinical manifestations are often more severe and can include mental retardation, oculogyria, hypotonia, severe bradykinesia, drooling, ptosis, and seizures [189]. Recently it has been shown that TH patients may develop dyskinesias [148].

Hereditary Dopamine Transporter Deficiency Syndrome (DTDS)

Hereditary dopamine transporter deficiency syndrome (DTDS) is the first biogenic amine “transportopathy” to be described. It is an autosomal recessive condition leading to infantile parkinsonism–dystonia caused by pathogenic mutations in the *SLC6A3* gene encoding the dopamine transporter (DAT) [98], which mediates the active reuptake of dopamine and regulates the amplitude and duration of dopamine neurotransmission [98]. All children present with irritability, axial hypotonia, and feeding difficulties in infancy, with a hyperkinetic movement disorder that evolves into hypokinetic parkinsonism–dystonia. Ocular abnormalities included eye flutter, saccade initiation failure, slow saccadic eye movements, eyelid myoclonus, and oculogyric crises [98, 130, 131]. However, the phenotypic spectrum of this condition is expanding, with the first adults diagnosed with DTDS now recognized, and the condition is now considered as a differential for juvenile and early-onset parkinsonism [131]. Diagnosis can be based on CSF studies that show a raised ratio of HVA:5-HIAA >5 (normal range 1.3–4.0), a key finding in DTDS diagnosis [98]. The majority of patients are unresponsive to nearly all available therapeutic agents, including levodopa, anticholinergics, benzodiazepines, and deep brain stimulation [98, 120, 130].

Rapid-Onset Dystonia–Parkinsonism (DYT12)

Rapid-onset dystonia–parkinsonism is inherited as an autosomal dominant trait with reduced penetrance. Six heterozygous missense mutations have been identified in the Na⁺, K⁺-ATPase *ATPIA3* (alpha 3 subunit) gene, and all are shown to impair cell viability in cell culture experiments [30, 40, 101]. The disease phenotype designated rapid-onset dystonia–parkinsonism because of key clinical features including abrupt onset, within hours to weeks, of dystonia with signs of parkinsonism usually triggered by physical or emotional stress (fever, childbirth, running, alcohol binging). The age of onset varies from 4 to 58 years but typically presents in the teens or early twenties, and the distribution follows a rostrocaudal (face > arm > leg) gradient with prominent bulbar involvement. A presentation that could be more easily confused with PD has been recently described in a genetically proven patient with gradual onset at age 38 years of unilateral bradykinesia and rigidity, however, without improvement on levodopa therapy. This was followed by overnight onset of oromandibular dystonia 3.5 years after his first clinical presentation with parkinsonism (see also Chap. 7) [85].

Wilson’s Disease

Wilson’s disease (WD) is an autosomal recessive disorder with reduced biliary excretion of copper and impaired formation of ceruloplasmin, leading to copper accumulation in the liver, brain, kidney, and cornea. WD is caused by mutations in the *ATP7B* gene and usually manifests in the first decade of life, although late

presentations have also been described [72, 74, 119]. Clinical manifestations include liver damage, psychiatric symptoms, and neurologic features. Juvenile and adult-onset parkinsonism are common features, which do not respond to levodopa, but respond well to specific WD treatment [33]. Evaluation should include serum and 24-h urine copper, serum ceruloplasmin, slit lamp examination looking for Kayser-Fleischer rings, free copper estimation, and if necessary, a liver biopsy [119]. Mutational analysis is labor intensive and is thus not used for screening purposes but confirms the exact mutation in patients with suspected Wilson's disease (see also Chap. 14).

Inborn Error of Manganese Metabolism

A recessive inborn error of manganese metabolism [205] due to mutations in the *SLC30A10* (solute carrier family 30, member 10) gene, encoding a manganese transporter, results in manganese accumulation mainly in the basal ganglia and cerebellum, and the liver, and causes a syndrome of early-onset generalized dystonia, cirrhosis, polycythemia, and hypermanganesemia [152, 205, 206]. Patients with parkinsonism–dystonia have also been described [44, 45, 152]. The metabolic signature of this disorder is the extreme hypermanganesemia with polycythemia and depleted iron stores (e.g., low ferritin, increased total iron-binding capacity), while laboratory findings reflecting hepatic dysfunction vary even between members of the same family [152, 205]. Manganese induces erythropoietin gene expression, and this could be the mechanism leading to polycythemia [52]. T1-weighted MRI images show hyperintensities in the basal ganglia and cerebellum [152, 191, 205]. As in Wilson's disease, manganese chelation treatment is helpful for both neurologic and systemic features (see also Chap. 14) [191].

Neurodegeneration with Brain Iron Accumulation (NBIA) Disorders

NBIA disorders cause complex dystonia–parkinsonism phenotypes and are discussed further in Chap. 13.

Atypical parkinsonism in Genes Predominantly Causing Chorea

Huntington's Disease

Huntington's disease (HD), an autosomal dominant disorder due to a trinucleotide CAG repeat expansion in the huntingtin gene (normal: 15–30 repeats; disease associated: >40 repeats), usually begins in adulthood and is characterized by cognitive decline and psychiatric, oculomotor, and motor abnormalities, usually with chorea as the most prominent feature [51, 88, 154]. The Westphal variant of HD is a distinct

presentation characterized by a rigid-hypokinetic syndrome and is usually associated with young-onset age (<20 years) and accounts for 5–10 % of all HD cases. Juvenile HD is predominantly paternally inherited and associated with larger trinucleotide expansions in the range of 60–100 repeats, but may be as long as 250 trinucleotides [51, 170]. Clinically, juvenile HD often presents as an akinetic rigid disorder and may occur without concomitant choreic movements, and there may be supranuclear gaze palsy. Caudate volume loss on neuroimaging can be seen in both adult-onset and juvenile HD [154].

Neuroacanthocytosis

Neuroacanthocytosis may also present with parkinsonism (Table 3.1) (see also Chap. 8).

Other Genetic Disorders Causing Atypical Parkinsonism

Mitochondrial Disorders

Mitochondrial disorders may present with atypical parkinsonism and can be associated with specific point mutations, microdeletions, and also multiple mtDNA deletions due to, for example, polymerase gamma (*POLG*) mutations, which can be inherited in dominant or recessive mode [137]. PSP-like patients who presented in their sixties with parkinsonism, vertical SGP, and early cognitive dysfunction have been reported [68, 71]; associated features in these patients were deafness, ataxia, and lower motor neuron signs, which are absent in PSP [68, 71]. Of note, *POLG*-related parkinsonism can show an excellent response to levodopa, in contrast to sporadic PSP (see also Chap. 20) [137, 217].

Neurometabolic Disorders

In particular the adult-onset Niemann–Pick C (NPC1 and NPC2 gene mutations), an autosomal recessive lysosomal lipid storage disorder [81, 179], presents with vertical SGP, cerebellar ataxia, dysarthria, dysphagia, cognitive dysfunction, and psychiatric symptoms and should be thought in the differential of patients with a PSP-like phenotype [179]. Biochemical diagnosis of Niemann–Pick C is made by filipin staining of cultured skin fibroblasts, with subsequent confirmation of the diagnosis made by mutation analysis of the *NPC1* (the majority) and *NPC2* genes [1, 219]. Miglustat is the only approved treatment for the neurologic manifestations of the disease, and patients who begin treatment early respond better, highlighting the need for early diagnosis [1, 143, 219, 220].

In the adult-onset form of Gaucher’s disease, patients usually have slow *horizontal* saccades and increased latency launching horizontal saccades [16], which is

usual in CBD [162], but not in PSP [11], in which the saccadic latency is normal and vertical saccades are more and earlier affected than horizontal, particularly downwards. However, some Gaucher's disease patients with prominent slowness of vertical saccades and cognitive dysfunction, mimicking PSP, have been reported [62, 63, 122, 200, 201, 210]. Other neurologic features such as head thrusting (55 %), ataxia (20 %), seizures (16 %), and spasticity (15 %), which are not seen in PSP, provide important clues [8, 43, 67, 200, 201, 210]. Systemic associated features such as splenomegaly, hepatomegaly, bone crisis, bone pain, anemia, and thrombocytopenia are helpful diagnostic clues [200, 201, 210].

Prion Disease

Genetic Creutzfeldt–Jakob disease (gCJD) has been linked to a variety of mutations within the prion protein gene (*PRNP*). Patients with disease onset between their fifth and seventh decade, vertical SGP, “worried facial appearance,” postural instability, axial rigidity, and frontal dementia mimicking PSP have been described in gCJD, mostly with the E200K but rarely also with further mutations and in sporadic CJD [20, 21, 95, 121, 171, 182]. These patients often have cerebellar and pyramidal signs as well as myoclonus, and the rapidity of evolution is helpful to suspect the disorder.

Atypical Parkinsonism with White Matter Changes

The combination of parkinsonism with leukoencephalopathy should prompt to test for colony-stimulating factor 1 (*CSF1R*) mutations, causing leukoencephalopathy with axonal spheroids [90, 124, 150, 158, 195]. Also in CADASIL due to *NOTCH3* mutations, atypical parkinsonism has been described [159]. Mitochondrial disorders may also present with white matter changes in MRI.

Conclusion

The advent in genetics has changed the field of atypical parkinsonism. With regard to the sporadic conditions, PSP, CBD, and MSA, genetic susceptibility loci and rare mutations in relevant genes causing familial forms may provide important clues for the pathophysiology of these disorders. On the other hand, the list of genetic disorders causing young-onset atypical parkinsonism with various features is growing, and syndromic associations are important to suspect these. In some cases, this is quite important due to treatment implications.

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