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Giovanni Stevanin, Alexis Brice. Spinocerebellar ataxia 17 (SCA17) and Huntington's disease-like 4 (HDL4).. Cerebellum, Springer Verlag (Germany), 2008, 7 (2), pp.170-8. <10.1007/s12311-008-0016-1>. <inserm-00293796>

HAL Id: inserm-00293796

<http://www.hal.inserm.fr/inserm-00293796>

Submitted on 26 Mar 2009

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**SPINOCEREBELLAR ATAXIA 17 (SCA17) AND HUNTINGTON'S DISEASE-LIKE 4
(HDL4)**

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Running title: SCA7 and HDL4

Abstract

Spinocerebellar ataxia 17 (SCA17) or Huntington's disease-like-4 is a neurodegenerative disease caused by the expansion above 44 units of a CAG/CAA repeat in the coding region of the TATA box binding protein (TBP) gene leading to an abnormal expansion of a polyglutamine stretch in the corresponding protein. Alleles with 43 and 44 repeats have been identified in sporadic cases and their pathogenicity remains uncertain. Furthermore, incomplete penetrance of pathological alleles with up to 49 repeats has been suggested. The imperfect nature of the repeat makes intergenerational instability extremely rare and *de novo* mutations are most likely the result of partial duplications. This is one of the rarer forms of autosomal dominant cerebellar ataxia but the associated phenotype is often severe, involving various systems (cerebral cortex, striatum, and cerebellum), with extremely variable age at onset (range: 3-75 years) and clinical presentation. This gene is thought to account for a small proportion of patients with a Huntington's disease-like phenotype and cerebellar signs. Parkinson's disease-like, Creutzfeldt-Jakob disease-like and Alzheimer disease-like phenotypes have also been described with small SCA17 expansions. The abnormal protein is expressed at the same level as its normal counterpart and forms neuronal intranuclear inclusions containing other proteins involved in protein folding or degradation. The increase in the size of the glutamine stretch enhances transcription *in vitro*, probably leading to transcription deregulation. Interestingly, the TBP protein mutated in SCA17 is recruited in the inclusions of other polyglutaminopathies, suggesting its involvement in the transcription down-regulation observed in these diseases.

Key words: *Spinocerebellar ataxias, spinocerebellar degenerations, Huntington's disease, SCA17, HDL4*

Introduction

Autosomal dominant cerebellar ataxias (ADCAs), often referred to as spinocerebellar ataxias (SCA), are a group of neurological disorders that are clinically and genetically highly heterogeneous (1). They are characterized by progressive cerebellar ataxia that results in uncoordinated movements, unsteady gait and dysarthria often associated with other neurological signs such as ophthalmoplegia, pyramidal or extrapyramidal signs, deep sensory loss and dementia. Onset is generally observed during the third or fourth decade but can also occur in childhood or old age. Neuropathologically, prominent atrophy of the cerebellum and brainstem is usually observed, but other structures may also be affected leading to a considerable range of phenotypes.

Fifteen genes and their mutations have been identified. Translated (CAG)_n/polyglutamine repeat expansions are responsible for the disease caused by 7 of these genes, *SCA 1-3* (2-6), *6* (7), *7* (8-10), *17* (11) and dentatorubral-pallidoluyian atrophy (DRPLA) (12,13), and account for the vast majority of all ADCAs with a known genetic basis, although the precise frequency varies with geographical origin. Other genes with such mutations are unlikely to be identified. Two different studies using the Repeat Expansion Detection technique or the 1C2 antibody that recognizes large polyglutamines found no evidence of other disease-causing genes with large CAG repeats or proteins with polyglutamine expansions encoded by codons CAA or CAG (14,15). Indeed, the majority of newly identified forms, which represent only a small proportion of ADCAs, have non-coding repeat expansions or “classical” mutations in other genes. Non-coding repeat expansions have been reported at the *SCA8* (16), *SCA10* (17) and *SCA12* (18) loci. More recently, mutations in the genes encoding fibroblast growth factor 14 [*FGF14/SCA27*, (19,20)], protein kinase C gamma [*PKCG/SCA14*, (21-28)], spectrin beta III [*SPTBN2/SCA5*, (29)] and potassium channel *KCNC3* [*SCA13*, (30)] were also implicated in ADCA cases. In addition, a point mutation in the promoter region of a gene on chromosome 16 encoding

puratrophin-1, a new Rho GTPase protein, was found in 52 Japanese ADCA type III families (31).

SCA17/HDL4

Spinocerebellar ataxia 17 (SCA17) or Huntington's disease-like 4 (HDL4) is a rare neurodegenerative disorder (MIM#607136) that belongs to the group commonly referred to as "polyglutaminopathies" that also includes Huntington's disease (HD), spinal and bulbar muscular atrophy and 6 other forms of ADCA (32). In the absence of treatment, they can all lead to dramatic neurological dysfunction and ultimately to death. The number of glutamines observed in the pathological proteins varies from 21 to >400 in the 9 diseases currently identified, but in most cases the phenotype manifests above a repeat number varying between 35 and 40. This class of disorders also shares, with few exceptions, other common clinical, genetic and physiopathological features suggesting common pathological mechanisms: i.e., a negative correlation between the size of the repeat expansion and the age at onset, anticipation with parental sex bias, instability of the repeat on expanded alleles and the formation of intranuclear inclusions in neurons.

SCA17 was first reported in a sporadic case of a complex neurological disorder with cerebellar ataxia, pyramidal signs and severe intellectual impairment. This patient carried 63 trinucleotide repeats in the gene encoding the TATA-box binding protein (TBP) on chromosome 6q27 (11). This new genetic entity was subsequently identified in familial ADCA cases and was shown to differ in several aspects from other polyglutaminopathies (33-35). Pathological expansions were also found in patients with an HD-like phenotype (HDL4) or with clinical features compatible with Alzheimer, Parkinson's or Creutzfeldt-Jakob disease, highlighting the clinical heterogeneity of this genetic entity (36-38).

TATA-box binding protein

TBP is an important and general transcription factor ubiquitously expressed from a single gene on chromosome 6q27 and constitutes an integral component of the transcription initiation complexes of the 3 RNA polymerases (39-41). The TBP protein is the DNA-binding subunit of the RNA polymerase II transcription factor D (TFIID), a protein complex involved in mRNA transcription, and anchors the complex to the TATA box upstream of the first codon. The TBP protein also plays a role in TATA-less promoter genes by correctly positioning the polymerase on the DNA.

Size and structure of the normal repeat in the TBP gene

The N-terminus of the protein that modulates the DNA binding activity of the C-terminus (41), contains a long stretch of glutamines, as in other transcription factors or homeobox proteins (42). This repeat is impure and is encoded by 3 CAG stretches, interrupted by 1 to 3 CAA codons (Table 1). The glutamine stretch is polymorphic in the normal population and large population studies (>5000 control chromosomes) have determined that the normal range is between 25 to 42 residues, most alleles containing 32 to 39 repeats (11,33-35,37,40,43-45). The allelic distribution varies slightly, however, according to the ethnic/geographical origins (43,45). In a more recent Japanese study, alleles with up to 45 repeats were detected in the control population (38).

Behaviour of the pathological expansions: range and incomplete penetrance

Given its high polymorphism and the mean size of the repeat, which is above the pathological threshold of most polyglutamine diseases, the TBP gene was considered a good candidate gene for neurodegenerative and psychiatric diseases in which anticipation was suspected (40,45). An abnormally expanded CAG repeat (63 repeats) was initially described in a 14-year-old child with severe signs of ataxia and cognitive impairment without family history of neurological disorders (11). A series of studies world-wide subsequently reported familial cases with other repeat

expansions in this gene and allowed the pathological range to be defined. The threshold for pathological expansions varies according to the study from 43 to 45 repeats (36,38,46-48). Sporadic patients carrying from 43 to 63 repeats have been identified, while affected members of families with dominant transmission of the disease carry between 45 and 66 CAG/CAA repeats (34-38,47-57).

Oda *et al.* reported a family in which one patient carried 43 repeats while another carried normal alleles, suggesting that this repeat size may not be pathogenic in this family (38). In addition, alleles with a similar number of repeats were reported in patients carrying known ADCA mutations and have been detected in controls, reinforcing the hypothesis that they are not pathogenic (38,48). In the absence of evidence of co-segregation of the allele with 44 repeats (36,38) and because of the overlap between controls' and patients' ranges, caution is needed in diagnosis for such small expansions, which so far have only accounted for sporadic cases.

Determination of the pathological threshold is also complicated by the existence of an incomplete penetrance, which has been suggested for patients carrying 45 to 49 repeats since healthy carriers with 46, 48 and 49 CAG/CAA repeats aged 59, 69 and 76 years, respectively, have been reported (36,52,54).

Instability and origin of the expansions in the TBP gene

Elongation of repeated CAG elements, alone or as the result of the loss of CAA interruptions, is the major mechanism leading to abnormally elongated SCA17 repeats (11,15,33-36,38,47,50-52,54-58). In 3 cases, including 2 *de novo* expansions, the expanded repeat is the result of partial duplication or insertion of repeats into the CAG/CAA stretch (11,57). Koide *et al.* excluded meiotic unequal crossover and suggested either a displacement of the 5' end of the Okazaki fragment generating a flap endonuclease FEN1-resistant hairpin or unequal sister chromatid recombination potentially leading to partial intramolecular duplication (11). In SCA2, SCA6, SCA7 and HD, neomutations occur mostly on large normal paternal alleles which undergo the

expansion of pure repeats to the pathological range (59-66). In the two SCA17 *de novo* cases, expansions also occurred on paternal chromosomes carrying 37 to 39 repeats, although with a different mechanism.

The structure of the expanded repeat therefore varies according to i) the number of repeats in internal CAG stretches, particularly the third one in which most expansions occur, ii) the loss of CAA interruptions, which could influence the stability of the region, as well as iii) the presence of internal duplications or insertions (Table 1).

Compared to other polyglutamine diseases, the SCA17 mutation is unusually stable during parent-child transmissions. The discontinuous distribution of repeat size in different populations reflects this stability of the normal repeat (44). This may well result partially from the presence of CAA interruptions, as already observed in SCA1 or SCA2 normal alleles. This would make it unlikely for the multistep gradual expansion to be observed in SCA17. Indeed, the rare cases of intergenerational instability, with increases of +1 to +13, have only been reported in alleles lacking CAA interruptions, resulting in pure CAG stretches over 40 units (Table 1). In these instances, instability is observed both in paternal and maternal transmission (33,52,56).

Epidemiology and relative frequency of SCA17/HDL4

To date, ~55 SCA17 families or cases have been reported world-wide, representing approximately 130 patients. Most families/cases are from Japan (n=17 families) (11,34,38,50,67) and Germany (n=19 families) (33,48,49,52,54,55,68), a distribution reminiscent of SCA6, which is also frequent in both these countries. The remaining families, when the origins have been mentioned, are as follows: 9 from Italy (15,46,53,56,58,69), 3 from Taiwan (37,51), 2 from England (70), 2 from France (36), and one each from Belgium (35), the USA (57) and Portugal (47). The frequency of SCA17 ranges from 0.3 to 3% among studies of ADCA families (11,15,35,38,47,48,67) but represents less than 1% of HD-like patients (36,49). SCA17 was not

found in other series of ADCA or HD-like families (71-73). Its minimal prevalence was estimated to be 0.16/100,000 in the north-east of England (70).

More than ten SCA17 cases had no family history of neurological diseases; two of these cases were proven to result from *de novo* expansions (11,57) while incomplete penetrance was observed in four others (36,38,52,54), which emphasizes the importance of analyzing this gene in isolated cases with a compatible phenotype.

Clinical heterogeneity of SCA17/HDL4

A series of studies have attempted to establish the clinical spectrum of this particular and very heterogeneous form of ADCA (11,11,33-38,47-57,68,74). The clinical and neuropathological spectrum associated with this mutation appears to be broader than previously suspected.

The clinical signs in SCA17 patients reported in the literature are summarized in Table 2. The symptoms at onset, which occur at a mean age of 34.6 +/- 13.2 years (range: 3-75), are predominantly gait instability (15,47,56) or other movement disorders, such as focal dystonia (58,68) or chorea (36,49). Psychiatric disturbances such as behavioural changes, psychosis or depression as well as dementia can also represent the presenting symptoms (11,35,36,49).

At the time patients are examined, the most prevalent abnormality after cerebellar ataxia is dementia (77%). This is particularly important in clinical practice since overt and early dementia is rare in ADCA, with the exception of DRPLA. Psychiatric alterations (35,48,49,56,58) and abnormal movements are frequent, especially chorea, choreoathetosis, and dystonia (34,48,56,58,68,74). Parkinsonism occurs in half of the patients and epilepsy is commonly observed (34,58). Spasticity with brisk reflexes may also be found (11,33,38). The cardinal features of SCA17 are therefore the association of cerebellar ataxia with dementia and other movement disorders. These signs are typically observed in a small proportion of families with an HD-like phenotype, and indeed SCA17 accounts for less than 1% of HD-like cases with cerebellar ataxia (range: 43 to 52 repeats) (36,46,49,50,72). In addition, patients with

schizophrenia, multiple system atrophy, Parkinson's disease with dementia-, Alzheimer disease- or Creutzfeldt-Jakob disease-like phenotypes have been reported to carry expansions in the TBP gene (range: 45 to 55 repeats) (37,51,57,75,76). SCA17 was not, however, found to be a common cause of Parkinson's disease, primary dystonia, epilepsy, bipolar disorder or schizophrenia in large series (11,45,48,77,78).

After short disease durations (2-3 years), MRI findings vary greatly, from normal to moderate global atrophy or a focal atrophy of the cerebellum (33,68). After longer durations, the atrophy is always pronounced in the cerebellum, mild in the brain with relative sparing of the brainstem. Putaminal rim hyperintensities have been reported in one case (79). Dopamine transporter (putamen) and glucose metabolism (putamen cerebellum and caudate nucleus) have been found to be reduced in SCA17 patients (80).

Diagnosis is established by genetic testing and other laboratory investigations are not necessary. Unfortunately, once the disease has manifested, it is unremittingly progressive, leading to loss of autonomy, with death occurring at a mean age of 39 +/- 20 years, after a mean disease duration of 19 +/- 9 years. Treatment is purely symptomatic.

Phenotype-genotype correlations

The clinical picture and age at onset are variable even among patients of the same family carrying the same number of repeats, suggesting that the size of the repeat has a limited influence on the course of the pathology (35). There is a correlation, although not as strong as in other ADCAs (81), between the age at onset and the size of the repeat (Figure 1). Exponential regression shows that only 64% of the variance in the age at onset is explained by the repeat size. The influence of modifier genes could be crucial to explain the remaining variance and could also account for the wide clinical heterogeneity. Since most of the SCA17 expansions are stable, it is unlikely that somatic mosaicism of the size of the expansion accounts for the inter-individual variability, in contrast to other polyglutaminopathies. Alternatively, the very low correlation could be due to

the difficulty in determining the exact age at onset because of the variability in the presenting sign, which is not always cerebellar ataxia. Interestingly, age at death correlated with the size of the triplet repeat in a small cohort of 16 patients of diverse origins (Figure 1) (34,35,48,56,58,74).

Anticipation does not appear to be a feature of this disease, which is in accordance with the very rare instability of the CAG/CAA repeat. Maltecca *et al.*, however, reported a familial case with a marked anticipation associated with a marked instability of the repeat (56).

Homozygosity has been shown to lower the age at onset in DRPLA, SCA3 and SCA6, but not in HD, which, however, shows increased severity (82-85). Three SCA17 patients homozygous for repeat expansions in the TBP gene were not more severely affected than patients carrying one abnormal copy of the gene, supporting a gain of function hypothesis (38,50,54). This might be due to incomplete penetrance of one of the expanded alleles. Neuropathological alterations did however extend to the hippocampus and brainstem in one homozygous patient (50).

Neuropathology of SCA17/HDL4

While the clinical profile of SCA17 is reminiscent of DRPLA, its neuropathological basis differs. Neuropathological lesions are mild in the brainstem compared to other ADCA entities (35) but are similarly marked in the cerebellum and the cerebral cortex.

Six patients' brains have been investigated neuropathologically and showed similar features (34,35,48,50,58). There was a mild global atrophy of the brain, predominant in the cerebellum because of severe Purkinje cell loss and Bergman's gliosis. Neuronal loss was mild in the dentate nucleus (except in Rolfs *et al.*, ref. 48) and the granular layer. Atrophy was moderate in the cerebral cortex, predominating in the motor cortex and visual areas with abnormal arborisation of neuronal dendrites and spongiosis (35,50,58). In the brainstem, the pontine nuclei were spared but the locus coeruleus and the substantia nigra were mildly affected, with a few deposits of free melanin pigment in the latter (35,58).

There were, however, differences according to the size of the repeat and/or disease duration. Atrophy of the substantia nigra was only observed in patients with the longest disease duration (48). The inferior olivary nuclei were also atrophied in all but one patient, who carried the smallest repeat size (n=46) and had a disease duration of only 10 years (35,48,58). Similarly, the basal ganglia were spared in this patient (35), whereas atrophy was severe in the other patients, particularly in the caudate nucleus (50,58). Finally, the spinal cord was normal except in a patient with a 54-repeat expansion and a 24-year disease duration, who showed a loss of anterior horn cells (48). There were no significant differences at the pathological level between heterozygous and homozygous patients, except additional atrophy of the hippocampus in one of the latter (50).

Physiopathological consequences of the expansion

The SCA17 gene product, TBP, has a well known function and is widely expressed in the central nervous system and other tissues, which contrasts with the selective pattern of degeneration observed in patients.

As in other ADCAs, the pathological hallmarks of this disease are the presence of neuronal intranuclear inclusions (NIIs) containing the pathological proteins, as well as heat shock proteins and ubiquitin (34,35), however with a lower frequency. Staining, using specific antibodies or the 1C2 antibody (14,86), is essentially nuclear, often diffuse and is focal in 0 to 3% of the neurons according to the structure (50,58). NIIs were not detected in visceral organs (50) but have been observed in various structures of the brain. They are found predominantly in the cerebral cortex and the basal ganglia, the mid-brain reticular formation, but also in structures that are spared, such as the pontine nuclei, dentate nucleus, anterior horn and inferior olives (35,50,58). However, they are not detected in Purkinje cells, which severely degenerate (48). In general, except for the cerebral cortex, there is an inverse correlation between the presence of NIIs and the severe lesions in a given structure (35,58): i.e., no NIIs are detected in the Purkinje and granule cell

layers or in the locus coeruleus, all of which degenerate, but they are detected in the putamen, dentate nucleus and pontine nuclei, which are unaffected or only mildly affected (35). Moderate atrophy of the inferior olivary nuclei was, however, reported in one case which had the highest density of NIIs (58). More interestingly, Bruni *et al* observed a link between the density of diffuse nuclear staining and cell loss, suggesting a more toxic effect of the non-aggregated protein (58).

The fact that the lack of TBP in TBP knock-out mice is embryonic lethal, whereas homozygosity for SCA7 trinucleotide expansions in humans is not, indicates that the expansion is not responsible for a major loss of TBP function (87). The absence of major differences between heterozygous and homozygous carriers suggests complete dominance, which is compatible with a gain of function mechanism or with a dominant negative effect of the mutation.

In vitro, SCA17 models demonstrated that the increase in the size of the glutamine stretch inside full-length TBP enhances its insolubility and aggregation as well as the transcription of a CRE-mediated luciferase reporter gene (44). Interestingly, TBP is sequestered in other polyQ diseases, suggesting its direct involvement in the transcription deregulation, although this is an early downregulation of transcription (88-90). The exact mechanisms remain unknown but, given the role of TBP in anchoring the transcription machinery to the DNA, it can be postulated that alteration of the tertiary structure of this protein would lead to an alteration of its binding to the DNA and/or activation or binding function of other TFIID components.

Conclusion

SCA17 is a rare neurodegenerative disorder occurring in Asians and Caucasians. The cardinal features are the association of cerebellar ataxia, dementia, psychiatric features and parkinsonism, with frequent occurrence of abnormal movements such as chorea or dystonia. This clinical profile overlaps with those of other neurodegenerative diseases and patients with Alzheimer disease-like, Creutzfeldt-Jakob disease-like or Parkinson's disease-like phenotypes or, more

importantly, with a Huntington's disease-like phenotype (HDL4) have been reported to carry SCA17 mutations.

SCA17 is caused by CAG expansions that can be associated with a loss of CAA interruptions, or partial CAG/CAA repeat duplications in the TBP gene, leading to polyglutamine expansions above 43-44 repeats. Incomplete penetrance concerns repeats between 45 and 49 units and the repeat is stable except in expanded alleles having lost CAA interruptions. The pathogenicity of repeats with 43 and 44 repeats remains unclear. These features have consequences for genetic counselling, particularly the existence of reduced penetrance for presymptomatic testing.

TBP and ubiquitin-positive NIIs are detected in the cerebral cortex, basal ganglia, pons and dentate nucleus but are absent in Purkinje cells, a pattern that does not match perfectly with neuronal loss. Atrophy mainly concerns the cerebellum, with global atrophy of the cortex, dentate nucleus, substantia nigra and locus coeruleus.

TBP, which is also involved in other polyglutamine disorders, probably represents a key element of the pathology in these disorders, all of which are associated with transcription deregulation.

Acknowledgments

The authors' work is financially supported by grants from the European Community (to the EUROSCA network), the Verum Foundation, the association Connaître les Syndromes Cérébelleux (to the SPATAX network) and the Programme Hospitalier de Recherche Clinique.

References

1. Schols L, Bauer P, Schmidt T, Schulte T, Riess O. Autosomal dominant cerebellar ataxias: clinical features, genetics, and pathogenesis. *Lancet Neurol.* 2004;3:291-304.
2. Orr HT, Chung MY, Banfi S, Kwiatkowski TJ, Jr., Servadio A, Beaudet AL et al. Expansion of an unstable trinucleotide CAG repeat in spinocerebellar ataxia type 1. *Nature Genet.* 1993;4:221-226.
3. Pulst SM, Nechiporuk A, Nechiporuk T, Gispert S, Chen XN, Lopes-Cendes I et al. Moderate expansion of a normally biallelic trinucleotide repeat in spinocerebellar ataxia type 2. *Nature Genet.* 1996;14:269-276.
4. Imbert G, Saudou F, Yvert G, Devys D, Trottier Y, Garnier J-M et al. Cloning of the gene for spinocerebellar ataxia 2 reveals a locus with high sensitivity to expanded CAG/glutamine repeats. *Nature Genet.* 1996;14:285-291.
5. Sanpei K, Takano H, Igarashi S, Sato T, Oyake M, Sasaki H et al. Identification of the spinocerebellar ataxia type 2 gene using a direct identification of repeat expansion and cloning technique, DIRECT. *Nature Genet.* 1996;14:277-284.
6. Kawaguchi Y, Okamoto T, Taniwaki M, Aizawa M, Inoue I, Katayama S et al. CAG expansion in a novel gene for Machado-Joseph disease at chromosome 14q32.1. *Nature Genet.* 1994;8:221-227.
7. Zhuchenko O, Bailey J, Bonnen P, Ashizawa T, Stockton DW, Amos C et al. Autosomal dominant cerebellar ataxia (SCA6) associated with small polyglutamine expansions in the α_{1A} -voltage-dependent calcium channel. *Nature Genet.* 1997;15:62-69.

8. David G, Abbas N, Stevanin G, Dürr A, Yvert G, Cancel G et al. Cloning of the SCA7 gene reveals a highly unstable CAG repeat expansion. *Nature Genet.* 1997;17:65-70.
9. Koob MD, Benzow KA, Bird TD, Day JW, Moseley ML, Ranum LPW. Rapid cloning of expanded trinucleotide repeat sequences from genomic DNA. *Nature Genet.* 1998;18:72-75.
10. Del-Favero J, Krols L, Michalik A, Theuns J, Löfgren A, Goossens D et al. Molecular genetic analysis of autosomal dominant cerebellar ataxia with retinal degeneration (ADCA type II) caused by CAG triplet repeat expansion. *Hum Mol Genet.* 1998;7:177-186.
11. Koide R, Kobayashi S, Shimohata T, Ikeuchi T, Maruyama M, Saito M et al. A neurological disease caused by an expanded CAG trinucleotide repeat in the TATA-binding protein gene: a new polyglutamine disease? *Hum Mol Genet.* 1999;8:2047-2053.
12. Koide R, Ikeuchi T, Onodera O, Tanaka H, Igarashi S, Endo K et al. Unstable expansion of CAG repeat in hereditary dentatorubral-pallidolusian atrophy (DRPLA). *Nat Genet.* 1994;6:9-13.
13. Nagafuchi S, Yanagisawa H, Sato K, Shirayama T, Ohsaki E, Bundo M et al. Dentatorubral and pallidolusian atrophy expansion of an unstable CAG trinucleotide on chromosome 12p. *Nat Genet.* 1994;6:14-18.
14. Stevanin G, Trottier Y, Cancel G, Dürr A, David G, Didierjean O et al. Screening for proteins with polyglutamine expansions in autosomal dominant cerebellar ataxias. *Hum Mol Genet.* 1996;5:1887-1892.
15. Brusco A, Gellera C, Cagnoli C, Saluto A, Castucci A, Michielotto C et al. Molecular genetics of hereditary spinocerebellar ataxia: mutation analysis of spinocerebellar ataxia genes and CAG/CTG repeat expansion detection in 225 Italian families. *Arch Neurol.* 2004;61:727-733.

16. Koob MD, Moseley ML, Schut LJ, Benzow KA, Bird TD, Day JW et al. An untranslated CTG expansion causes a novel form of spinocerebellar ataxia (SCA8). *Nature Genet.* 1999;21:379-384.
17. Matsuura T, Yamagata T, Burgess DL, Rasmussen A, Grewal RP, Watase K et al. Large expansion of the ATTCT pentanucleotide repeat in spinocerebellar ataxia type 10. *Nat Genet.* 2000;26:191-194.
18. Holmes SE, O'Hearn EE, McInnis MG, Gorelick-Feldman DA, Kleiderlein JJ, Callahan C et al. Expansion of a novel CAG trinucleotide repeat in the 5' region of PPP2R2B is associated with SCA12. *Nat Genet.* 1999;23:391-392.
19. van Swieten JC, Brusse E, de Graaf BM, Krieger E, van de GR, de K, I et al. A mutation in the fibroblast growth factor 14 gene is associated with autosomal dominant cerebellar ataxia [corrected]. *Am J Hum Genet.* 2003;72:191-199.
20. Dalski A, Atici J, Kreuz FR, Hellenbroich Y, Schwinger E, Zuhlke C. Mutation analysis in the fibroblast growth factor 14 gene: frameshift mutation and polymorphisms in patients with inherited ataxias. *Eur J Hum Genet.* 2005;13:118-120.
21. Chen DH, Brkanac Z, Verlinde CL, Tan XJ, Bylenok L, Nochlin D et al. Missense mutations in the regulatory domain of PKC gamma: a new mechanism for dominant nonepisodic cerebellar ataxia. *Am J Hum Genet.* 2003;72:839-849.
22. Stevanin G, Hahn V, Lohmann E, Bouslam N, Gouttard M, Soumphonphakdy C et al. Mutation in the catalytic domain of protein kinase C gamma and extension of the phenotype associated with spinocerebellar ataxia type 14. *Arch Neurol.* 2004;61:1242-1248.

23. van de Warrenburg BP, Verbeek DS, Piersma SJ, Hennekam FA, Pearson PL, Knoers NV et al. Identification of a novel SCA14 mutation in a Dutch autosomal dominant cerebellar ataxia family. *Neurology*. 2003;61:1760-1765.
24. Yabe I, Sasaki H, Chen DH, Raskind WH, Bird TD, Yamashita I et al. Spinocerebellar ataxia type 14 caused by a mutation in protein kinase C gamma. *Arch Neurol*. 2003;60:1749-1751.
25. Verbeek DS, Knight MA, Harmison GG, Fischbeck KH, Howell BW. Protein kinase C gamma mutations in spinocerebellar ataxia 14 increase kinase activity and alter membrane targeting. *Brain*. 2005;128:436-442.
26. Chen DH, Cimino PJ, Ranum LP, Zoghbi HY, Yabe I, Schut L et al. The clinical and genetic spectrum of spinocerebellar ataxia 14. *Neurology*. 2005;64:1258-1260.
27. Klebe S, Durr A, Rentschler A, Hahn-Barma V, Abele M, Bouslam N et al. New mutations of Protein Kinase C α associated with Spinocerebellar Ataxia Type 14 (SCA14). *Ann Neurol*. 2005;
28. Seki T, Adachi N, Ono Y, Mochizuki H, Hiramoto K, Amano T et al. Mutant protein kinase C gamma found in spinocerebellar ataxia type 14 is susceptible to aggregate and cause cell death. *J Biol Chem*. 2005;
29. Ikeda Y, Dick KA, Weatherspoon MR, Gincel D, Armbrust KR, Dalton JC et al. Spectrin mutations cause spinocerebellar ataxia type 5. *Nature Genet*. 2006;38:184-190.
30. Waters MF, Minassian NA, Stevanin G, Figueroa KP, Bannister JP, Nolte D et al. Mutations in voltage-gated potassium channel KCNC3 cause degenerative and developmental central nervous system phenotypes. *Nature Genet*. 2006;38:447-451.

31. Ishikawa K, Toru S, Tsunemi T, Li M, Kobayashi K, Yokota T et al. An autosomal dominant cerebellar ataxia linked to chromosome 16q22.1 is associated with a single-nucleotide substitution in the 5' untranslated region of the gene encoding a protein with spectrin repeat and rho Guanine-nucleotide exchange-factor domains. *Am J Hum Genet.* 2005;77:280-296.
32. Zoghbi HY, Orr HT. Glutamine repeats and neurodegeneration. *Annu Rev Neurosci.* 2000;23:217-247.
33. Zuhlke C, Hellenbroich Y, Dalski A, Kononowa N, Hagenah J, Vieregge P et al. Different types of repeat expansion in the TATA-binding protein gene are associated with a new form of inherited ataxia. *Eur J Hum Genet.* 2001;9:160-164.
34. Nakamura K, Jeong SY, Uchihara T, Anno M, Nagashima K, Nagashima T et al. SCA17, a novel autosomal dominant cerebellar ataxia caused by an expanded polyglutamine in TATA-binding protein. *Hum Mol Genet.* 2001;10:1441-1448.
35. Fujigasaki H, Martin JJ, De Deyn PP, Camuzat A, Deffond D, Stevanin G et al. CAG repeat expansion in the TATA box-binding protein gene causes autosomal dominant cerebellar ataxia. *Brain.* 2001;124:1939-1947.
36. Stevanin G, Fujigasaki H, Lebre AS, Camuzat A, Jeannequin C, Dode C et al. Huntington's disease-like phenotype due to trinucleotide repeat expansions in the TBP and JPH3 genes. *Brain.* 2003;126:1599-1603.
37. Wu YR, Fung HC, Lee-Chen GJ, Gwinn-Hardy K, Ro LS, Chen ST et al. Analysis of polyglutamine-coding repeats in the TATA-binding protein in different neurodegenerative diseases. *J Neural Transm.* 2005;112:539-546.

38. Oda M, Maruyama H, Komure O, Morino H, Terasawa H, Izumi Y et al. Possible reduced penetrance of expansion of 44 to 47 CAG/CAA repeats in the TATA-binding protein gene in spinocerebellar ataxia type 17. *Arch Neurol.* 2004;61:209-212.
39. Rigby PW. Three in one and one in three: it all depends on TBP. *Cell.* 1993;72:7-10.
40. Imbert G, Trottier Y, Beckmann J, Mandel JL. The gene for the TATA binding protein (TBP) that contains a highly polymorphic protein coding CAG repeat maps to 6q27. *Genomics.* 1994;21:667-668.
41. Lescure A, Lutz Y, Eberhard D, Jacq X, Krol A, Grummt I et al. The N-terminal domain of the human TATA-binding protein plays a role in transcription from TATA-containing RNA polymerase II and III promoters. *EMBO J.* 1994;13:1166-1175.
42. Gerber HP, Seipel K, Georgiev O, Hofferer M, Hug M, Rusconi S et al. Transcriptional activation modulated by homopolymeric glutamine and proline stretches. *Science.* 1994;263:808-811.
43. Gostout B, Liu Q, Sommer SS. "Cryptic" repeating triplets of purines and pyrimidines (cRRY(i)) are frequent and polymorphic: analysis of coding cRRY(i) in the proopiomelanocortin (POMC) and TATA-binding protein (TBP) genes. *Am J Hum Genet.* 1993;52:1182-1190.
44. Reid SJ, Rees MI, Roon-Mom WM, Jones AL, MacDonald ME, Sutherland G et al. Molecular investigation of TBP allele length: a SCA17 cellular model and population study. *Neurobiol Dis.* 2003;13:37-45.
45. Rubinsztein DC, Leggo J, Crow TJ, DeLisi LE, Walsh C, Jain S et al. Analysis of polyglutamine-coding repeats in the TATA-binding protein in different human populations

- and in patients with schizophrenia and bipolar affective disorder. *Am J Med Genet.* 1996;67:495-498.
46. Cellini E, Forleo P, Nacmias B, Tedde A, Bagnoli S, Piacentini S et al. Spinocerebellar ataxia type 17 repeat in patients with Huntington's disease-like and ataxia. *Ann Neurol.* 2004;56:163-164.
47. Silveira I, Miranda C, Guimaraes L, Moreira MC, Alonso I, Mendonca P et al. Trinucleotide repeats in 202 families with ataxia: a small expanded (CAG)_n allele at the SCA17 locus. *Arch Neurol.* 2002;59:623-629.
48. Rolfs A, Koeppen AH, Bauer I, Bauer P, Buhlmann S, Topka H et al. Clinical features and neuropathology of autosomal dominant spinocerebellar ataxia (SCA17). *Ann Neurol.* 2003;54:367-375.
49. Bauer P, Laccone F, Rolfs A, Wullner U, Bosch S, Peters H et al. Trinucleotide repeat expansion in SCA17/TBP in white patients with Huntington's disease-like phenotype. *J Med Genet.* 2004;41:230-232.
50. Toyoshima Y, Yamada M, Onodera O, Shimohata M, Inenaga C, Fujita N et al. SCA17 homozygote showing Huntington's disease-like phenotype. *Ann Neurol.* 2004;55:281-286.
51. Wu YR, Lin HY, Chen CM, Gwinn-Hardy K, Ro LS, Wang YC et al. Genetic testing in spinocerebellar ataxia in Taiwan: expansions of trinucleotide repeats in SCA8 and SCA17 are associated with typical Parkinson's disease. *Clin Genet.* 2004;65:209-214.
52. Zuhlke C, Dalski A, Schwinger E, Finckh U. Spinocerebellar ataxia type 17: report of a family with reduced penetrance of an unstable Gln49 TBP allele, haplotype analysis supporting a founder effect for unstable alleles and comparative analysis of SCA17 genotypes. *BMC Med Genet.* 2005;6:27

53. De Michele G, Maltecca F, Carella M, Volpe G, Orio M, De Falco A et al. Dementia, ataxia, extrapyramidal features, and epilepsy: phenotype spectrum in two Italian families with spinocerebellar ataxia type 17. *Neurol Sci.* 2003;24:166-167.
54. Zuhlke C, Gehlken U, Hellenbroich Y, Schwinger E, Burk K. Phenotypical variability of expanded alleles in the TATA-binding protein gene. Reduced penetrance in SCA17? *J Neurol.* 2003;250:161-163.
55. Zuhlke CH, Spranger M, Spranger S, Voigt R, Lanz M, Gehlken U et al. SCA17 caused by homozygous repeat expansion in TBP due to partial isodisomy 6. *Eur J Hum Genet.* 2003;11:629-632.
56. Maltecca F, Filla A, Castaldo I, Coppola G, Fragassi NA, Carella M et al. Intergenerational instability and marked anticipation in SCA-17. *Neurology.* 2003;61:1441-1443.
57. Shatunov A, Fridman EA, Pagan FI, Leib J, Singleton A, Hallett M et al. Small de novo duplication in the repeat region of the TATA-box-binding protein gene manifest with a phenotype similar to variant Creutzfeldt-Jakob disease. *Clin Genet.* 2004;66:496-501.
58. Bruni AC, Takahashi-Fujigasaki J, Maltecca F, Foncin JF, Servadio A, Casari G et al. Behavioral disorder, dementia, ataxia, and rigidity in a large family with TATA box-binding protein mutation. *Arch Neurol.* 2004;61:1314-1320.
59. Myers RH, MacDonald ME, Koroshetz WJ, Duyao MP, Ambrose CM, Taylor SA et al. De novo expansion of a (CAG)_n repeat in sporadic Huntington's disease. *Nature Genet.* 1993;5:168-173.
60. Stevanin G, Giunti P, Belal GDS, Durr A, Ruberg M, Wood N et al. De novo expansion of intermediate alleles in spinocerebellar ataxia 7. *Hum Mol Genet.* 1998;7:1809-1813.

61. Mittal U, Roy S, Jain S, Srivastava AK, Mukerji M. Post-zygotic de novo trinucleotide repeat expansion at spinocerebellar ataxia type 7 locus: evidence from an Indian family. *J Hum Genet.* 2005;
62. Giunti P, Stevanin G, Worth P, David G, Brice A, Wood NW. Molecular and clinical study of 18 families with ADCA type II: evidence for genetic heterogeneity and *de novo* mutation. *Am J Hum Genet.* 1999;64:1594-1603.
63. Shizuka M, Watanabe M, Ikeda Y, Mizushima K, Okamoto K, Shoji M. Molecular analysis of a de novo mutation for spinocerebellar ataxia type 6 and (CAG)_n repeat units in normal elder controls. *J Neurol Sci.* 1998;161:85-87.
64. Watanabe M, Satoh A, Kanemoto M, Ohkoshi N, Shoji S. De novo expansion of a CAG repeat in a Japanese patient with sporadic Huntington's disease. *J Neurol Sci.* 2000;178:159-162.
65. Schols L, Gispert S, Vorgerd M, Menezes Vieira-Saecker AM, Blanke P, Auburger G et al. Spinocerebellar ataxia type 2: Genotype and phenotype in German kindreds. *Arch Neurol.* 1997;54:1073-1080.
66. Bauer P, Kraus J, Matoska V, Brouckova M, Zumrova A, Goetz P. Large de novo expansion of CAG repeats in patient with sporadic spinocerebellar ataxia type 7. *J Neurol.* 2004;251:1023-1024.
67. Maruyama H, Izumi Y, Morino H, Oda M, Toji H, Nakamura S et al. Difference in disease-free survival curve and regional distribution according to subtype of spinocerebellar ataxia: a study of 1,286 Japanese patients. *Am J Med Genet.* 2002;114:578-583.
68. Hagenah JM, Zuhlke C, Hellenbroich Y, Heide W, Klein C. Focal dystonia as a presenting sign of spinocerebellar ataxia 17. *Mov Disord.* 2004;19:217-220.

69. Manganelli F, Perretti A, Nolano M, Lanzillo B, Bruni AC, De Michele G et al.
Electrophysiologic characterization in spinocerebellar ataxia 17. *Neurology*. 2006;66:932-934.
70. Craig K, Keers SM, Walls TJ, Curtis A, Chinnery PF. Minimum prevalence of spinocerebellar ataxia 17 in the north east of England. *J Neurol Sci*. 2005;239:105-109.
71. Alendar A, Euljkovic B, Savic D, Djarmati A, Keckarevic M, Ristic A et al. Spinocerebellar ataxia type 17 in the Yugoslav population. *Acta Neurol Scand*. 2004;109:185-187.
72. Costa MC, Teixeira-Castro A, Constante M, Magalhaes M, Magalhaes P, Cerqueira J et al.
Exclusion of mutations in the PRNP, JPH3, TBP, ATN1, CREBBP, POU3F2 and FTL genes as a cause of disease in Portuguese patients with a Huntington-like phenotype. *J Hum Genet*. 2006;51:645-651.
73. Seixas AI, Maurer MH, Lin M, Callahan C, Ahuja A, Matsuura T et al. FXTAS, SCA10, and SCA17 in American patients with movement disorders. *Am J Med Genet A*. 2005;136A:87-89.
74. Filla A, De Michele G, Coccozza S, Patrignani A, Volpe G, Castaldo I et al. Early onset autosomal dominant dementia with ataxia, extrapyramidal features, and epilepsy. *Neurology*. 2002;58:922-928.
75. Lin IS, Wu RM, Lee-Chen GJ, Shan DE, Gwinn-Hardy K. The SCA17 phenotype can include features of MSA-C, PSP and cognitive impairment. *Parkinsonism Relat Disord*. 2006;
76. Lee-Chen GJ, Lane HY, Chen CM, Wu YR, Ro LS, Chen FL et al. Expanded trinucleotide repeats in the TBP/SCA17 gene mapped to chromosome 6q27 are associated with schizophrenia. *Schizophr Res*. 2005;

77. Hernandez D, Hanson M, Singleton A, Gwinn-Hardy K, Freeman J, Ravina B et al. Mutation at the SCA17 locus is not a common cause of parkinsonism. *Parkinsonism Relat Disord.* 2003;9:317-320.
78. Grundmann K, Laubis-Herrmann U, Dressler D, Vollmer-Haase J, Bauer P, Stuhmann M et al. Mutation at the SCA17 locus is not a common cause of primary dystonia. *J Neurol.* 2004;251:1232-1234.
79. Loy CT, Sweeney MG, Davis MB, Wills AJ, Sawle GV, Lees AJ et al. Spinocerebellar ataxia type 17: extension of phenotype with putaminal rim hyperintensity on magnetic resonance imaging. *Mov Disord.* 2005;20:1521-1523.
80. Minnerop M, Joe A, Lutz M, Bauer P, Urbach H, Helmstaedter C et al. Putamen dopamine transporter and glucose metabolism are reduced in SCA17. *Ann Neurol.* 2005;58:490-491.
81. Stevanin G, Durr A, Brice A. Clinical and molecular advances in autosomal dominant cerebellar ataxias: from genotype to phenotype and physiopathology. *Eur J Hum Genet.* 2000;8:4-18.
82. Sato K, Kashihara K, Okada S, Ikeuchi T, Tsuji S, Shomori T et al. Does homozygosity advance the onset of dentatorubral- pallidoluyasian atrophy? *Neurology.* 1995;45:1934-1936.
83. Sobue G, Doyu M, Nakao N, Shimada N, Mitsuma T, Maruyama H et al. Homozygosity for Machado-Joseph disease gene enhances phenotypic severity [letter]. *J Neurol Neurosurg Psychiatry.* 1996;60:354-356.
84. Ikeuchi T, Takano H, Koide R, Horikawa Y, Honma Y, Onishi Y et al. Spinocerebellar ataxia type 6: CAG repeat expansion in alpha1A voltage- dependent calcium channel gene and clinical variations in Japanese population. *Ann Neurol.* 1997;42:879-884.

85. Squitieri F, Gellera C, Cannella M, Mariotti C, Cislighi G, Rubinsztein DC et al. Homozygosity for CAG mutation in Huntington disease is associated with a more severe clinical course. *Brain*. 2003;126:946-955.
86. Trottier Y, Lutz Y, Stevanin G, Imbert G, Devys D, Cancel G et al. Polyglutamine expansion as a pathological epitope in Huntington's disease and four dominant cerebellar ataxias. *Nature*. 1995;378:403-406.
87. Martianov I, Viville S, Davidson I. RNA polymerase II transcription in murine cells lacking the TATA binding protein. *Science*. 2002;298:1036-1039.
88. Uchihara T, Fujigasaki H, Koyano S, Nakamura A, Yagishita S, Iwabuchi K. Non-expanded polyglutamine proteins in intranuclear inclusions of hereditary ataxias--triple-labeling immunofluorescence study. *Acta Neuropathol (Berl)*. 2001;102:149-152.
89. Roon-Mom WM, Reid SJ, Jones AL, MacDonald ME, Faull RL, Snell RG. Insoluble TATA-binding protein accumulation in Huntington's disease cortex. *Brain Res Mol Brain Res*. 2002;109:1-10.
90. Perez MK, Paulson HL, Pendse SJ, Saionz SJ, Bonini NM, Pittman RN. Recruitment and the Role of Nuclear Localization in Polyglutamine- mediated Aggregation. *J Cell Biol*. 1998;143:1457-1470.

Figure 1. Correlation (exponential) between age at onset (n=87, $r^2=0.41$) or age at death (n=16, $r^2=0.78$) and the size of the repeat in SCA17 affected patients [(11,15,33-36,38,47-52,54,56-58,68-70,74,79,80) and unpublished data].

Table 1. Structure of the CAG/CAA repeat in wild type and expanded alleles (11,15,33-36,38,47,50-52,54-58,70)

	Repeat number	Structure of the repeat							
		CAG ₃	CAA ₃	CAG ₇₋₁₁	CAACAGCAA	CAG ₉₋₂₁	CAACAG		
Wild type	25-42*	CAG ₃	CAA ₃	CAG ₇₋₁₁	CAACAGCAA	CAG ₉₋₂₁	CAACAG		
Koide et al. 1999 (11) spo, <i>de novo</i>	63	CAG ₃	CAA ₃	CAG ₉	CAACAGCAA	CAG₉	CAA ₃ CAG ₉ CAACAGCAA	CAG ₁₉	CAACAG
Shatunov et al. 2004 (57) spo, <i>de novo</i>	55	CAG ₃	CAA ₃	CAG ₉	CAACAGCAA	CAG₁₅	CAACAGCAA	CAG ₁₇	CAACAG
Nakamura et al. 2001 (34)	55	CAG ₃	CAA ₃	CAG ₉	CAACAGCAA	CAG₁₆	CAACAGCAA	CAG ₁₆	CAACAG
Fujigasaki et al. 2001 (35)	46	CAG ₃	CAA ₃	CAG ₉	CAACAGCAA	CAG₂₆		CAACAG	
Nakamura et al. 2001 (34)	48	CAG ₃	CAA ₃	CAG ₆	CAACAGCAA	CAG₃₁		CAACAG	
Nakamura et al. 2001 (34)	47	CAG ₃	CAA ₃	CAG ₈	CAACAGCAA	CAG₂₈		CAACAG	
Nakamura et al. 2001 (34) spo	47	CAG ₃	CAA ₃	CAG ₆	CAACAGCAA	CAG₃₀		CAACAG	
Zuhlke et al. 2001 (33)	51	CAG ₃	CAA ₃	CAG ₉	CAACAGCAA	CAG₃₁		CAACAG	
Silveira et al. 2002 (47)	43	CAG ₃	CAA ₃	CAG ₉	CAACAGCAA	CAG₂₃		CAACAG	
Stevanin et al. 2003 (36) spo, reduced penetrance	46	CAG ₃	CAA ₃	CAG ₁₁	CAACAGCAA	CAG₂₄		CAACAG	
Stevanin et al. 2003 (36) spo	44	CAG ₃	CAA ₃	CAG ₉	CAACAGCAA	CAG₂₄		CAACAG	
Zuhlke et al. 2003 (55) spo, homoZ	47	CAG ₃	CAA ₃	CAG ₉	CAACAGCAA	CAG₂₇		CAACAG	
Zuhlke et al. 2003 (54) reduced penetrance	48	CAG ₃	CAA ₃	CAG ₉	CAACAGCAA	CAG₂₈		CAACAG	
Oda et al. 2004 (38) 4 spo, 1 homoZ	44-47	CAG ₃	CAA ₃	CAG _x	CAACAGCAA	CAG_y		CAACAG	
Brusco et al. 2004 (15) spo, reduced penetrance?	45	CAG ₃	CAA ₃	CAG ₉	CAACAGCAA	CAG₂₅		CAACAG	
Brusco et al. 2004 (15)	45	CAG ₃	CAA ₃	CAG ₈	CAACAGCAA	CAG₂₆		CAACAG	
Toyoshima et al. 2004 (50) homoZ	48	CAG ₃	CAA ₃	CAG ₆	CAACAGCAA	CAG₃₁		CAACAG	
Bruni et al. 2004 (58)	52	CAG ₃	CAA ₃	CAG ₉	CAACAGCAA	CAG₃₂		CAACAG	
Wu et al. 2004, 2005 (51) spo	46	CAG ₃	CAA ₃	CAG ₆	CAACAGCAA	CAG₂₉		CAACAG	
Craig et al. 2005 (70)	52	CAG ₃	CAA ₃	CAG ₉	CAACAGCAA	CAG₃₂		CAACAG	
Craig et al. 2005 (70)	44	CAG ₃	CAA ₃	CAG ₉	CAACAGCAA	CAG₂₄		CAACAG	
Maltecca et al. 2003 (56) paternally unstable	53-66	CAG ₃	CAA ₄	CAG₄₄₋₅₇	CAACAG				
Zuhlke et al. 2001 (33) maternally unstable	53-55	CAG ₃	CAA ₃	CAG₄₅₋₄₇	CAACAG				
Zuhlke et al. 2005 (52) paternally unstable reduced penetrance	49-53	CAG ₃	CAA ₃	CAG₄₁₋₄₅	CAACAG				

spo: sporadic cases; homoZ: homozygous cases; *the structure of the wild-type alleles has not been determined in all cases.

Table 2. Frequency of the most commonly associated neurological signs reported in SCA17 patients (11,33-38,47-57,68-70,74,79)

No. of families	51
No. of patients	122
Mean age at onset (range)	34.6 +/- 13.2 (3-75 years)
Cerebellar ataxia	97% (78/80)
Dementia	77% (54/70)
Psychiatric symptoms	67% (36/54)
Pyramidal signs	57% (23/40)
Abnormal movements	56% (42/75)
<i>Dystonia</i>	64% (28/44)
<i>Chorea, choreoathetosis</i>	36% (16/45)
Parkinsonism	50% (24/48)
Epilepsy	35% (15/43)