

Can neurodegenerative disease be defined by four ‘primary determinants’: anatomy, cells, molecules, and morphology?

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Abstract

Traditional methods of describing and classifying neurodegenerative disease are based on the clinico-pathological concept supported by molecular pathological studies and defined by ‘consensus criteria’. Disease heterogeneity, overlap between disorders, and the presence of multiple co-pathologies, however, have questioned the validity and status of many traditional disorders. If cases of neurodegenerative disease are not easily classifiable into distinct entities, but more continuously distributed, then a new descriptive framework may be required. This review proposes that there are four key neuropathological features of neurodegenerative disease (the ‘primary determinants’) that could be used to provide such a framework, viz., the anatomical pathways affected by the disease (‘anatomy’), the cell populations affected (‘cells’), the molecular pathology of ‘signature’ pathological lesions (‘molecules’), and the morphological types of neurodegeneration (‘morphology’). This review first discusses the limitations of existing classificatory systems and second provides evidence that the four primary determinants could be used as axes to define all cases of neurodegenerative disease. To illustrate the methodology, the primary determinants were applied to the study of a group of closely related tauopathy cases and to heterogeneity within frontotemporal lobar degeneration with TDP-43 proteinopathy (FTLD-TDP).

Key words: neurodegenerative disease, primary determinants, anatomy, cells, molecules, neurodegeneration.

Introduction

Traditional methods of describing and classifying cases of neurodegenerative disease are based on the original clinico-pathological concept, viz., a distinct clinical profile in combination with ‘signature’ pathological lesions. This system was used to describe the first cases of Alzheimer’s disease (AD) [2], Pick’s disease (PiD) [139], dementia with Lewy bodies (DLB) [107], and Creutzfeldt-Jakob disease (CJD) [44,88]. Subsequently, these original descrip-

tions were refined and modified by molecular studies which resulted in the discovery of disease-specific antibodies and enabled the molecular signature of brain lesions to be established [20,59]. Ultimately, ‘consensus criteria’ have been established for the majority of disorders, e.g., AD [120,125,133,162], DLB [120], multiple system atrophy (MSA) [71,72], and progressive supranuclear palsy (PSP) [108,109], representing the coordinated views of experts in the field regarding the most important clinical and

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pathological features useful in diagnosis. As a result, neurodegenerative disorders have continued to be regarded as more or less distinct ‘entities’, neuropathologically defined by signature pathological lesions, and characterised by a specific molecular pathology [20,59].

Recent research, however, has revealed considerable heterogeneity within existing disorders [15,22], overlap between closely related entities [19,55,63,76], and the co-occurrence in individual cases of two or more co-pathologies [19,93,172]. Hence, in a recent comparative study of 1032 cases representing ten different disorders, 361 cases, approximately 35% of the sample, were excluded largely as a result of multiple pathology [25]. Not only do these exclusions ignore a large quantity of data, a bias is also created in favour of ‘typical’ or ‘pure’ examples of a disorder, thus ignoring potential intermediate, overlap, or multiple pathology cases. As a consequence, a reconsideration of existing disease entities and a new descriptive framework which can accommodate overlap and heterogeneity may be necessary [8,19,54,62,128,137].

An alternative method of describing cases of neurodegenerative disease is to use a geometrical system based on ‘ordination’, i.e., by arranging individual cases with reference to a co-ordinate frame so that their similarities and differences can be spatially represented [8,15,22,140]. In such a system, there may be no attempt to name a disorder or to classify cases into any pre-existing groups, but only to plot individual cases with reference to the co-ordinate frame. Location of a case would reveal its similarities and differences to other cases, and proximity to similar cases may reveal underlying common pathological mechanisms. To define the axes of such a co-ordinate frame, however, would require quantitative measures of a range of neuropathological variables.

This review proposes that there are four key features of neurodegenerative disease (the ‘primary determinants’) which could be used to provide such a descriptive framework, viz., the anatomical pathways affected by the disease (‘anatomy’), the cell populations affected (‘cells’), the major molecular pathology of the ‘signature’ pathological lesions (‘molecules’), and the morphological types of neurodegeneration (‘morphology’). Hence, this review discusses: (1) limitations of existing classificatory systems, (2) evidence that the four primary determinants could provide a description of cases of neurodegenerative disease, (3) whether the four determinants are ‘independent’ variables, (4) whether the four determinants should be differentially weighted, and (5) describes the application of the method to the study of a group of closely-related tauopathy cases and heterogeneity within fronto-temporal lobar degeneration with TDP-43 proteinopathy (FTLD-TDP) [22].

Limitations of existing classifications

Several studies have questioned whether neurodegenerative diseases are distinct or whether individual cases represent points in a ‘continuum’ of neuropathological change [8,19,20]. Hence, extensive overlap was observed between cases of AD and Parkinson’s disease (PD), interpreted as the action of common pathogenic mechanisms within vulnerable neuronal populations [137]. The authors argued that currently defined disease entities failed to deal with disease overlap and that a new classification should be considered [137]. In addition, Forstl [62] argued that the traditional clinico-pathological concept often accommodates genetically and clinically diverse conditions within the same group and therefore may have outlived its usefulness. The frequent use by authors of such terms as ‘complex syndrome’, ‘spectrum of disorders’, ‘multiple pathologies’, or even ‘continuum’ testifies to the extent to which boundaries between different disorders are more indistinct than previously thought [8,38,68,160].

Central to the argument of how neurodegenerative disease should be classified has been the status of AD [101,118]. Alzheimer’s disease is heterogeneous [145] and can be divided into clinically relevant subgroups such as sporadic AD (SAD), tangle only AD, and the various genetic subtypes of familial AD (FAD), but only one subgroup actually corresponds to the disease originally described by Alzheimer [169]. In addition, a number of descriptive terms are used to describe AD co-pathology, e.g., AD neuropathological change (ADNC), and neurofibrillary tangle (NFT)-only change in medial temporal lobe (NFT-MTL). Defining exact criteria for AD has always been difficult due to phenotypic heterogeneity, the absence of specific markers, and overlap of pathology with cognitively normal brain and related disorders [7,90]. Hence, the term ‘AD’ may describe disease subgroups with markedly different characteristics, and it has been suggested that the looser term ‘Alzheimer syndrome’

could be used or the term 'AD' dispensed with altogether [169]. If AD was to disappear as an entity, it would have significant implications for the status of many closely related disorders such as argyrophilic grain disease (AGD) [32,163,178], vascular dementia (VD) [95,106], and DLB [120].

The status of many other classically defined disorders has been equally controversial. Pick's disease [139], for example, is defined pathologically by the presence of tau-immunoreactive Pick bodies (PB) and abnormally enlarged neurons ('Pick cells'), but many cases of clinically typical PiD are at variance with these classic neuropathological features [98], e.g., some clinically typical PiD cases may lack PB [83]. Moreover, there is no convincing evidence linking the clinical symptoms of PiD with its histology, a challenge to the original clinico-pathological concept [60]. Subsequently, PiD became subsumed within the concept of 'frontotemporal dementia' (FTD) [87], but this classification also resulted in a heterogeneous group of disorders with considerable overlap between its constituent members [19]. Subsequent genetic and molecular studies have led to considerable changes in the classification and nomenclature within FTD and its neuropathological variants, viz. fronto-temporal lobar degeneration (FTLD) [37,164]. Clinical variants of FTD include the behavioural variant (bvFTD), language variants, e.g., semantic dementia (SD) and primary progressive aphasia (PPA), and motor variants such as corticobasal syndrome (CBS) and motor neuron disease (MND). In addition, pathological variants of FTLD include those with tau, transactive response (TAR) DNA-binding protein of 43 kDa (TDP-43), and fused in sarcoma (FUS)-immunoreactive inclusions [37].

Discrimination between different FTLD entities is often only possible using neuropathological criteria, the majority of which are based on the morphology and molecular composition of 'signature' pathological inclusions such as neuronal cytoplasmic inclusions (NCI), neuronal intranuclear inclusions (NII), and glial inclusions (GI), the latter including oligodendroglial inclusions ('coiled bodies'), tufted astrocytes (TA), astrocytic tangles (AT), and astrocytic 'plaques' (AP) [130]. Nevertheless, the clinical features of FTD may not predict their pathology, and neuropathological features alone cannot establish a diagnosis of FTD. In addition, studies have questioned whether some members should even be classified within FTD. Hence, corticobasal degeneration (CBD) is a predo-

minantly extrapyramidal motor disorder in which there is poor correlation between neuropathology and clinical syndrome [119]. In addition, there are FTD cases that exhibit a frontal lobe type of dementia but accompanied by a typical MND-type pathology not typical of any currently described FTD entity [30]. Consequently, FTD may define a group of cases, loosely united by clinical presentation, but with heterogeneous pathologies and therefore not easily classifiable according to clinico-pathological or any other criteria [77,79,99].

Similar problems can be observed within CJD, which in the past was regarded as a doubtful disease entity [100]. The original CJD concept [44,88] was subsequently discarded in favour of the term 'prion disease' [1,41], but there still remain problems such as overlap between CJD and other disorders, most notably with AD [19,20,76]. In addition, the prion-like behaviour of such pathological proteins as tau and α -synuclein [74,155] further blurs the distinction between classic prion diseases, tauopathies, and synucleinopathies.

The four primary determinants

This review proposes four key features, viz. the 'primary determinants', to describe the neuropathology of neurodegenerative disease: (1) anatomical pathways affected by the disease ('anatomy'), (2) cell types affected ('cells'), (3) primary molecular pathology of 'signature' pathological lesions ('molecules'), and (4) morphological types of neurodegeneration ('morphology'). How currently defined disorders may be related to these variables is shown in Table I.

Anatomy

One of the first demonstrations that a neurodegenerative disease was related to the breakdown of specific anatomical pathways was in AD [45,136]. Hence, a major feature of the pathology of AD is the disruption of afferent and efferent connections between the hippocampal formation and the rest of the brain [45]. Alzheimer's disease pathology may initially affect the temporal pole, especially the entorhinal cortex (EC), before spreading to the posterior parahippocampal gyrus (PHG) and then in a stepwise fashion to the hippocampus and association cortex, leaving primary sensory areas unimpaired until later in the disease [31,58,91,136]. The pathology may

Table I. Description of the major neurodegenerative diseases according to the four primary determinants

Disorder	Primary determinants			
	Anatomy	Cells	Molecules	Morphology
AD	GC, L	N	A β , 3R/4R tau	SP, NFT
AGD	L	N, A, O	4R tau	P-NFT, NT, GR, EN, V
CBD	FT, M, SC	N, A	4R tau	NCI
CJD	GC	N	PrP ^{Sc}	SP, V
DLB	L, C	N	α -synuclein	LB, NT, EN
FTD-MND	MC, SC	N, O	tau	NCI, GI
FTLD-TDP	FT	N, O	TDP-43	NCI, GI, V
MSA	SC	O, N	α -synuclein	GCI
NIFID	FT, L, SC	N, O	FUS	NCI, GI
PD-Dem	L, MC, SC	N	α -synuclein	LB, LT, LG
PiD	FT	N	3R tau	PB, PC
PSP	SC	N, A	4R tau	NFT, GI, AP

Disorders: AD – Alzheimer's disease, AGD – argyrophilic grain disease, CBD – corticobasal degeneration, CJD – Creutzfeldt-Jakob disease, DLB – dementia with Lewy bodies, FTDP-17 – fronto-temporal dementia and parkinsonism linked to chromosome 17, FTD-MND – motor neuron disease with dementia, MND – motor neuron disease, MSA – multiple system atrophy, NIFID – neuronal intermediate filament inclusion disease, PiD – Pick's disease, PD – Parkinson's disease, PSP – progressive supranuclear palsy; *Anatomy:* GC – general cortical, L – limbic, FT – frontotemporal, SC – subcortical; *Cells:* N – neurons, A – astrocytes, O – oligodendrocytes; *Molecules:* A β – β -amyloid, PrP^{Sc} – disease form of prion protein, FUS – fused in sarcoma, TDP-43 – transactive response (TAR) DNA-binding protein of 43 kDa; *Degeneration:* AP – astrocytic plaque, SP – senile plaques, NCI – neuronal cytoplasmic inclusions, P-NFT – pre-tangles, NFT – neurofibrillary tangles, NT – neuropil threads, GCI – glial cytoplasmic inclusions, GR – grains, EN – abnormally enlarged neurons, LB – Lewy bodies, LT – Lewy neurites, LG – Lewy grains, PB – Pick bodies, PC – Pick cells, V – vacuolation

then spread among cortical gyri and to subcortical regions via cortico-cortical and cortical-subcortical pathways respectively [5,45,136]. This hypothesis is supported by studies of the spatial patterns of SP and NFT [6,13] and of transgenic mice, in which there is selective disruption of cortico-cortical pathways [47]. Furthermore, this pattern of neurodegeneration correlates with specific neurotransmitter deficits, e.g., acetylcholinesterase-immunoreactive neurites are present at the periphery of SP, which could represent the degeneration of ascending and cortical cholinergic pathways [157].

Although many authors continue to argue that AD is a distinct entity [118], it is highly heterogeneous [42,61], and cases exhibit considerable neuropathological variation [15,19]. Variation in the anatomical spread of disease from its origin in the MTL could account for many of these differences [15,33,45]. Consequently, there may be a close relationship between the distribution of the pathology and the clinical features of individual patients [67]. For example, MTL areas are relatively spared in aphasic cases of AD, while more severe occipito-parietal degeneration, also

termed posterior cortical atrophy (PCA), is often associated with visual-spatial deficits at presentation [67].

The second commonest form of dementia is DLB, accounting for up to a quarter of all cases [120]. An essential feature of the neuropathological diagnosis of DLB is the presence of LB in the cerebral cortex and/or brain stem. Nevertheless, DLB exists in a variety of forms including neocortical, limbic [144], cerebral, and brainstem types, the neocortical subtype being the most common [85]. Many cases of DLB also exhibit ADNC [48,70,78], and therefore each pathological subtype of DLB can be divided into a 'pure' or 'mixed' form based on the degree of AD co-pathology [85]. Some studies have suggested anatomical differences in the pathways affected in AD and DLB. Brain glucose metabolism studies, for example, indicate that hypometabolism of the primary visual cortex (area V1) is more marked in DLB, whereas reductions in the posterior/temporal cortex, posterior cingulate gyrus, and frontal cortex occur in both AD and DLB [122]. Studies of regional cerebral blood flow (rCBF) report similar results, i.e., occipital hyperperfusion may be more frequent in DLB [110].

The pattern of temporal lobe atrophy may also differ between AD and DLB, with less hippocampal atrophy in DLB, which could explain the preservation of memory function in DLB [126].

In FTLT, which accounts for approximately 20% of all pre-senile cases of dementia [159], the pathological changes are usually more circumscribed, affecting primarily frontal and temporal lobes [156]. Nevertheless, there is often selective anatomical degeneration within this group. For example, in FTLT with transactive response (TAR) DNA-binding protein of 43 kDa (TDP-43)-immunoreactive inclusions, atrophy of the frontal lobe and temporal pole is seen in 97% of cases, but the hippocampus and subcortical areas are less affected [11,22,69]. In FTD and parkinsonism linked to chromosome 17 (FTDP-17) and CBD, however, degeneration largely affects the globus pallidus and substantia nigra and is accompanied by pathological changes in the cerebral cortex and subcortical areas [143]. In MND, cortical pathology is even more restricted to the motor cortex, although the brain stem and spinal cord may also be affected [29].

A further group of disorders exhibit a predominantly subcortical pathology including MSA, PD lacking dementia, and PSP. Hence in MSA, the substantia nigra, striatum, inferior olivary nucleus, pontine nuclei, and cerebellum are affected [18,49,105]. In some cases, there may be progressive cerebral atrophy affecting the frontal lobes [103] and the motor/premotor areas [168], the limbic system also being affected, principally in longer duration cases [138]. Although MSA is regarded as a single entity, two main subtypes are now recognized [72], viz., the cerebellar subtype (MSA-C) and parkinsonian subtype (MSA-P). The most consistent clinical syndrome, however, is parkinsonism, followed by cerebellar ataxia, and pyramidal tract signs [171]. Similarly, the anatomical distribution of pathological changes in PD is largely subcortical but with two clinical subtypes, viz., an 'akinetic-rigid' form with cell losses in the ventrolateral substantia nigra and related motor systems and a 'tremor-dominant' form with cell losses in the medial substantia nigra [89]. In addition, in PD with dementia (PD-Dem), which may be indistinguishable from DLB [28], there is spread of pathology to affect the cortical regions and hippocampus [24]. Progressive supranuclear palsy exhibits a more restricted form of subcortical degeneration, often sparing the cerebral cortex entirely [113]. Two clin-

ical phenotypes have been identified, viz., Richardson's syndrome (RS) and PSP-parkinsonism (PSP-P), the two subtypes varying in disease duration and in tau isoforms [173]. In addition, there is loss of cholinergic innervation to the thalamus and cerebral cortex in PD, but only to the thalamus in PSP [153].

Cells

The developing pathology of neurodegenerative disease may target specific cell populations. In AD, for example, it is the larger cortical pyramidal cells that are most vulnerable, smaller neurons being more resistant [80]. In addition, labelling of damaged neurons in AD is most conspicuous in lamina III of the cerebral cortex early in the disease but becomes more widespread as the pathology progresses [165]. This observation suggests a specific loss of cortico-cortical connections in AD [136], many of which use glutamate as neurotransmitter. The disease may then spread in either an orthograde or retrograde direction [45], gradually involving other neuronal types and eventually glial cells. In AD there is also loss of neurons which express the 75 kD neurotrophic receptor p75NTR [174] which preferentially binds β -amyloid ($A\beta$), and hence cells that undergo apoptosis could be mediated by this reaction. By contrast, cultured hippocampal neurons immunoreactive to the calcium-binding protein calretinin are more resistant to degeneration associated with $A\beta$ [142]. Moreover in FTLT, glutamate-immunoreactive pyramidal cells as well as calbindin D-28 γ -aminobutyric acid (GABA) neurons are lost but parvalbumin-immunoreactive cells preserved [57], consistent with loss of the cortico-cortical connections in FTLT.

A distinctive pattern of hippocampal pathology is present in CJD involving selective vulnerability of GABA neurons [75]. Hence, parvalbumin-immunoreactive neurons are severely depleted while calbindin-immunoreactive cells, which represent an early loss of inhibitory neurons, are largely preserved [75].

In FTLT, GI can be observed in oligodendroglial cells in the hippocampus, PHG, and amygdala [134]. In addition, a fundamental cytoskeletal alteration of oligodendrocytes occurs in MSA [18,50,170] resulting in the formation of characteristic 'glial cytoplasmic inclusions' (GCI) [135] which can be observed in the substantia nigra, striatum, inferior olivary nucleus, pontine nuclei, and cerebellum [105]. A close association between GCI and microtubules has also been

demonstrated [129], aberrant or ectopic expression of cdk5 and MAPK leading to abnormal phosphorylation of microtubule cytoskeletal proteins and the formation of inclusions. In MSA cases with frontal lobe atrophy [103], there are cell losses in laminae V/VI of the cerebral cortex, and GCI are often found in white matter. In addition, inclusions are found in the granule cell layer of the dentate gyrus and pre-frontal cortex and 'dot-like' structures or grains in the PHG [4]. The GCI may represent a pathological change synchronous with or preceding that of neuronal loss in MSA [84]. In addition, TA [82,102,175] are present in the motor cortex and striatum in PSP [51]. Neurons affected in PSP also appear to be functionally related, NFT occurring in interconnected extrapyramidal and oculomotor structures [151]. The presence of astrocytic pathology is regarded as a diagnostic feature of PSP [82] which may distinguish the disorder from the closely related CBD [81,109].

Molecules

The molecular pathology of 'signature' pathological lesions has played a highly significant role in diagnosis, the identification of new disease entities, and the development of theories of pathogenesis [20,59]. Studies of pathological lesions, however, reveal considerable molecular diversity [20]. In AD, for example, A β exists in several forms, the most common being A β _{42/43}, found largely in SP, whereas the more soluble A β ₄₀ is also found in association with blood vessels [121,146] and may develop later in the disease [46]. In addition, A β deposits may be associated with a variety of additional molecular constituents [20] including apolipoprotein E (Apo E) [176], α -antichymotrypsin, sulphated glycosaminoglycans, and complement factors [166]. A β -immunoreactive deposits also occur in DLB, but the ratio between the isoforms may differ from AD. In DLB, the predominant form of A β is A β _{42/43}, as in AD, but the level of A β ₄₀ is reduced compared with AD [117].

The majority of disorders have either tau- or α -synuclein-immunoreactive pathology. Within the tauopathies, PiD is characterised by tau with three microtubule repeats (3R tau), while PSP and CBD are composed of four-repeat (4R) tau [50,127]. Cellular inclusions in these disorders, however, are also associated with additional molecular constituents. Hence, PB in PiD are immunoreactive to ubiquitin

and Alz-50 [111] and in the synucleinopathy DLB [27], LB are also reactive for intermediate filaments (IF) [65], neurofilament (NF) proteins [66], cyclin dependent kinase-5 [34], α -B crystallin [112], and polyubiquitinated chains [86]. Furthermore, aggregates of abnormal intermediate filaments (IF) immunoreactive for α -internexin have been identified as a component of inclusions in neuronal intermediate filament inclusion disease (NIFID), a rare subtype of FTLD [10,30,36,92]. Subsequently, 'fused in sarcoma' (FUS) protein was identified as a major pathological protein in this disorder [23,132,177]. In addition, a significant number of cases of FTLD are linked to the product of the transcriptional repressor gene (*TARDP*), viz. TDP-43 [131], suggesting that these diseases may form another molecular group, viz., the TDP-43 proteinopathies.

Morphology

There are six main types of morphological degeneration observed in neurodegenerative disease. First, extracellular protein deposits are deposited in the neuropil e.g., A β in AD [73] or the disease form of prion protein (PrP^{Sc}) in CJD [152]. Second, intracellular protein aggregates develop as inclusions in cell bodies, nuclei, and the processes of neurons and glial cells. These include the various types of NCI, including NFT in AD, LB in PD and DLB [120], PB in PiD [111], and tau-reactive neurons in CBD [81]. In addition, GI, including the GCI characteristic of MSA [135], occur in a variety of disorders including FTLD-TDP, AGD, and CBD. Third, some disorders exhibit extensive neuropil threads (NT) or dystrophic neurites (DN) in specific brain regions such as in FTLD-TDP [22] and PD-Dem [24,149]. Fourth, disorders such as PD-Dem also possess Lewy grains (LG) which are α -synuclein-immunoreactive and which resemble the tau-reactive argyrophilic grains (AG) commonly observed in AGD [32,163,178], AD [148], and elderly, cognitively normal brains [52,94].

Fifth, abnormally enlarged neurons (EN), defined as having an irregularly enlarged or swollen cell body in which the largest diameter of the perikarya is at least three times the nuclear diameter [9], are a common feature of many disorders including AD [64], PiD, CBD, and AGD [163]. Enlarged neurons are also present in CJD, especially in cases with severe white matter degeneration [17,96,104]. In PSP, however, EN are less numerous and where present confined to

limbic regions [124,167]. There are also different types of EN. Hence, in PiD and CBD [14,16], there is uniform swelling of the neuronal perikaryon resulting in the characteristic 'ballooned' neurons, these cells being referred to as either Pick cells (PC) in PiD or ballooned neurons (BN) in CBD [126]. In addition, there are swollen achromatic neurons (SAN) in which the cell body is more irregularly enlarged, the Nissl substance uniformly pale, powdery, and eosinophilic, and the cell nucleus displaced to the cell margin [113]. Finally, there are swollen cells which occur in inherited neurovisceral disorders such as Niemann-Pick disease type-C in which swelling of the cell is associated with abnormalities in lipid storage [35,53]. Hence, EN in neurodegenerative disease lack specificity to any particular disease [64] but may indicate particular types of pathological change. Ballooned neurons occur after infarction and could represent an attempt at regeneration following axonal damage [3]. Enlarged neurons could also be a stress response since many swollen neurons are immunoreactive to α -B-crystallin induced by neuronal stress and which may have a protective function [123]. In addition, peripheral nerve transection, which separates nerve cells from their targets, may also lead to EN [141].

Sixth, significant vacuolation is a feature of many disorders, most notably CJD ('spongiform change') [152], but also to varying degrees AD, DLB, and FTLD, the latter often present as microvacuolation in superficial cortical laminae [22]. In the sporadic subtype of CJD (sCJD), clustering of vacuoles occurs in association with either neuronal perikarya or PrP^{Sc} deposits [17], while in the cerebellum of the variant subtype of CJD (vCJD), clusters of vacuoles in the molecular layer are negatively correlated with surviving Purkinje cells [21]. Hence, the degree of vacuolation could be an indication of the extent of neuronal loss in a region.

Independence of primary determinants

An important consideration is whether the four primary determinants are independent variables. If variables are inter-correlated, however, degeneration of a specific anatomical pathway may predict cell type affected, molecular pathology, or type of neurodegeneration. If this hypothesis is correct, then only certain combinations of anatomy, cells, molecules, and morphology would define neurodegenerative disease. Hence, in AD, which has tau-immunoreactive NFT, LB may also be present, and there is a strong correla-

tion between the presence of cortical α -synuclein-immunoreactive LB and degeneration of the substantia nigra [97]. In addition, in FAD linked to the *APP*₇₁₇ mutation, extrapyramidal features were present in all members of a single family and LB were present in a proportion of individuals [147]. Moreover, cortical LB in DLB are composed of intermediate filaments (IF) and a granular matrix, while brain stem LB have an electron-dense core and radially oriented filaments [65]. These results suggest that it is degeneration of a specific anatomical pathway, e.g., the extrapyramidal system, that could determine the molecular pathology, e.g., in this case, α -synuclein-immunoreactive LB. However, there is no specific relationship between grains (GR) and molecular pathology, GR being α -synuclein- or tau-immunoreactive in PD-Dem [149] and AGD [32,163,178] respectively.

In AD, cortical and subcortical NFT are composed of morphologically similar paired helical filaments (PHF), but cortical and subcortical PHF have a different molecular composition [161]. In addition, within the tauopathies, diseases may have morphologically similar tau-immunoreactive inclusions [56] but exhibit regional differences in distribution, especially in PSP, PD and CBD, which could be associated with different types of tau abnormality. Furthermore, in Niemann-Pick disease, the clinical spectrum of the disease is heterogeneous, rapid progression being associated with axonal spheroids and slow progression with NFT and neuronal dystrophy [158]. The NFT have a similar composition to those of AD but a different morphology reflecting their regional origin. In addition, frontal lobe atrophy could occur in both PSP and DLB associated with either NFT or LB respectively [43]. Differences in the neuronal population affected in the frontal cortex or in patient genotype could account for these differences. Positive correlations have also been observed among the densities of LB, LN, and LG in PD-Dem, suggesting that they could result from degeneration of the same neurons, LB aggregating in cell bodies and LN and LG in adjacent neurites and synapses respectively [24].

Studies that directly correlate a molecular pathology with loss of a specific cell type are rare. However, McKenzie *et al.* [115] found that specific areas of MTL secreted large quantities of amyloid precursor protein (APP), and that more APP-immunoreactive neurons were found in these areas in head injury patients, which could explain the high density of SP in the temporal lobe in AD [12] and the subsequent

spread of pathology [45]. In PSP, tau mRNA isoforms containing 4R tau are increased in the brainstem but not in the frontal cortex or cerebellum, which could predict the eventual anatomical distribution of these inclusions [40].

Weighting of primary determinants

Of the four primary determinants, molecular pathology has had the most profound impact over the last 25 years [20,54]. Should therefore this variable be regarded as the most fundamental? Classification based on molecular pathology, however, is often at variance with more traditional concepts based on anatomy. For example, AD and DLB are closely related and overlap extensively in clinical and pathological features [20], but AD is a tauopathy and DLB a synucleinopathy and therefore different at the molecular level. In addition, PSP is a tauopathy, but also an example of 'atypical parkinsonism' and therefore clinically related to the synucleinopathies PD, MSA, and DLB [154]. Recent research has criticised the concentration on 'signature' pathological lesions and their

molecular determinants and has questioned whether this emphasis has been detrimental to the study of neurodegenerative disease as a whole [39]. Hence, given current uncertainties regarding which variables are 'important' or 'fundamental', it is suggested that all four determinants should be given equal weight.

Application

An important practical question concerns what categories of anatomy, cells, molecules, and neurodegeneration should be used to define the descriptive axes. The multiplicity of possible defining variables suggests the use of a multivariate data analysis method such as principal components analysis (PCA) [15,22]. Principal components analysis simplifies a description of cases based on multiple variables by selecting two or three axes which describe sources of maximum variation in the data, i.e., 'the principal components' (PC). Hence, a PCA enables the degree of similarity and dissimilarity between cases to be studied based on quantitative estimates of their neuropathological characteristics [15,22]. The result of a PCA is a scatter plot of cases in relation to the PC in which the distance between cases reflects their similarity or dissimilarity, based on the defining histological features. Each PC therefore accounts for a proportion of the total variance in the data, PC1 accounting for the greatest amount of the variance and remaining PCs for diminishing amounts of the remaining variance. Such a system appears to have the requisite multivariate geometry and simplicity necessary to provide a possible framework for describing neurodegenerative disease. The following examples are based on relatively small numbers of cases and a restricted range of descriptive variables to illustrate the methodology.

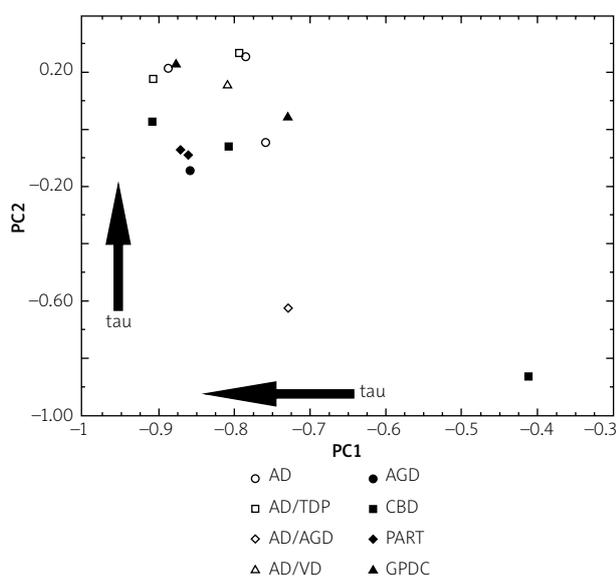


Fig. 1. Principal components analysis of 15 tauopathy cases (AD – Alzheimer's disease, AGD – argyrophilic grain disease, CBD – corticobasal degeneration, GPDC – Guamanian Parkinson's disease dementia complex [GPDC], PART – primary age-related tauopathy) using variables derived from the four primary determinants. A plot of the cases in relation to the first two principal components (PC 1 and 2 (Armstrong, unpublished data).

Example 1: Investigating the relationships between closely related tauopathies

The objective was to investigate similarities and differences among 15 closely related tauopathy cases traditionally classified as AD, AGD, CBD, Guamanian Parkinson's disease dementia complex (GPDC), or primary age-related tauopathy (PART). The defining variables include: (1) anatomy: frontal and temporal lobes and substantia nigra, (2) cells: neurons, astrocytes, oligodendrocytes, (3) molecules: tau, A β , and TDP-43, and (4) morphology: NCI, NT, GR, AT, GI, SP, EN, and

vacuolation. A plot of the 15 cases in relation to the first two principal components is shown in Figure 1.

Several features are evident from this plot. First, the majority of cases form a single cluster towards the upper left of the plot, the two remaining cases (AD/AGD, CBD) being more atypical. Second, within the main cluster, there is no obvious clustering of cases with similar co-pathology such as AD or TDP-43, although the two PART cases do occupy closely related positions. Third, several neuropathological variables are correlated with the factor loadings of the cases on the PC but overall there is a general increase in tau pathology with increasingly negative loadings on PC1 and positive loadings on PC2. Hence, if a new tauopathy case were to be added to this analysis, it would be possible to determine: (1) from its location, whether the new case was a typical or an atypical tauopathy, (2) the affinity of the new case relative to previous cases, and (3) the relative location of the case along a continuum of severity of tau pathology.

Example 2: Investigation of subtypes of FTLD-TDP

The second example is a study of neuropathological heterogeneity within FTLD with TDP-43-immunoreactive pathology (FTLD-TDP). These cases have a complex neuropathology comprising NCI, NII, GI, and DN. Four pathological subtypes of FTLD-TDP have been proposed [37,114,150] based on the type and regional distribution of the various types of inclusion. Hence, type 1 cases (Mackenzie-type 2) are characterized by long DN in superficial cortical laminae with few or no NCI or NII, type 2 (Mackenzie-type 3) by numerous NCI in superficial and deep cortical laminae with infrequent DN and sparse or no NII, type 3 (Mackenzie-type 1) by pathology predominantly affecting the superficial cortical laminae with numerous NCI, DN and varying numbers of NII, and type 4 by numerous NII, and infrequent NCI and DN especially in neocortical areas. The defining variables were: (1) anatomy: frontal and temporal lobes, (2) cells: neurons and oligodendroglia, (3) molecules: TDP-43, and (4) neurodegeneration: NCI, NII, DN, and GI. Hence, quantitative estimates of density of TDP-43-immunoreactive neuronal and glial inclusions were made in frontal and temporal regions of 94 cases of FTLD-TDP [22]. A PCA of the data is shown in Figure 2 and shows that cases representing the four subtypes exhibit considerable overlap, subtypes 1 and 4 being the most distinctive

and located towards the bottom and top of the plot respectively. Cases of subtype 2 and 3 were less distinct, with a greater degree of overlap. Hence, new cases could be added to the analysis over time and their location relative to PC1 and PC2, and therefore to all previous cases, established. Location of a new case would suggest to which subtype the case may belong. Hence, in Figure 2, new case A would be most likely to be an example of subtype 1 and case B of subtype 4. New cases C and D are more difficult to classify, although it is probable that they have more affinity with subtypes 2 and 3.

Further applications

More extensive applications of the methodology could include all cases of neurodegenerative disease from a single neuropathological centre and ultimately from several contributing centres. A major problem in attempting to apply this approach on a larger scale, however, is the lack of comparative quantitative data of sufficient scope, detail, quality, and consistency to define all possible cases. Most quan-

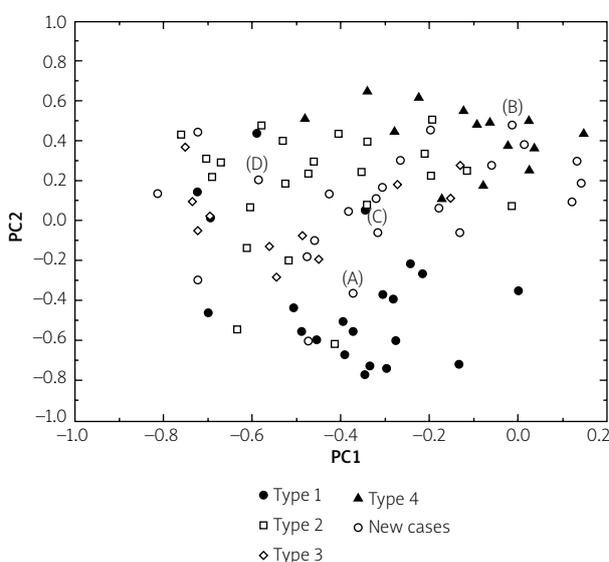


Fig. 2. Principal components analysis of 94 cases of frontotemporal lobar degeneration with TDP proteinopathy (FTLD-TDP) based on the densities of TDP-43 immunoreactive neuronal and glial inclusions in frontal and temporal cortex. Identified on the plot are the subtypes of disease based on the system of Cairns *et al.* (2007). Cases marked A, B, C, D are new cases added to the existing plot (data from Armstrong *et al.* 2010).

titative studies of a disorder quantify only signature pathological lesions [11], while others confine observations to a restricted number of anatomical regions or cell types, whereas all aspects of anatomy, cells, molecules, and morphology would need to be measured in each case. Nevertheless, the recent detailed comparative study of a large number of cases of ten neurodegenerative diseases, albeit using semi-quantitative data [25], demonstrates that it is feasible to collect comparative data across a large number of cases and disorders, enabling a descriptive system to be developed based on the four primary determinants.

Conclusions

This review proposes that four primary determinants could be used as the basis of a system to describe the neuropathology of neurodegenerative disease and which can take into account disease heterogeneity, overlap, and the presence of multiple pathologies. Such an approach has a number of advantages. First, it could describe all cases of neurodegenerative disease, not just those that may fit more traditional concepts. Second, it would emphasise the continuous nature of neurodegenerative disease by incorporating disease heterogeneity and overlap to their true extent [8,19]. Third, it would remove the necessity to classify new cases within an existing system, especially those which exhibit more complex multiple pathologies, as each case would be regarded as unique and would be located within a space defined by the primary determinants. Fourth, it potentially reveals the similarities and differences between cases included in the analysis, emphasising that common pathological mechanisms may be involved in different disorders. A major limiting factor in applying such a system on a large scale, however, is the current lack of detailed quantitative data of sufficient quality across cases and disorders [25].

Disclosure

Author reports no conflict of interest.

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