<table>
<thead>
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<th>Title</th>
<th>The aetiology of idiopathic Parkinson's disease</th>
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<tr>
<td>Author(s)</td>
<td>Ramsden, DB; Parsons, RB; Ho, SL; Waring, RH</td>
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Abstract

Agents potentially involved in the aetiology of idiopathic Parkinson’s disease are discussed. These include factors regulating dopaminergic neurogenesis (Nurr 1, Ptx-3, and Lmx1b) and related proteins, together with genes involved in familial Parkinson’s disease (α-synuclein, parkin, and ubiquitin carboxy terminal hydroylase L1), and endogenous and environmental agents.

Keywords: Parkinson’s disease; environmental agents; transcription factors; α-synuclein; parkin; ubiquitin carboxy terminal hydroylase L1

Factors involved in dopaminergic neurogenesis

NUR RELATED FACTOR 1 (NURR 1) (ALSO KNOWN AS NOT, RNR-1, AND HZF-3)

Nurr 1 is a member of the superfamily of “zinc finger” transcription factors. Over 90 members of the superfamily have been described. Included among these are the hormone receptors for triiodothyronine, oestradiol, cortisol, aldosterone, vitamin D, all trans retinoic acid, and 9-cis retinoic acid. Increasingly, molecules that at one time were thought of as unlikely candidate ligands for these transcription factors are now being recognised as such. In the past few years, it has been established that bile acids modulate gene transcription via farnesyl receptors. Nevertheless, many members of the superfamily have no known ligands—so called “orphan” receptors (reviewed by Enmark and Gustafsson)—but despite this, the functions of these receptors are becoming recognised. Most recently, cholesterol entry and egress from cells has been shown to be regulated via such orphans. Also among this class of receptors is Nurr 1.

Nurr 1 was first recognised as a transcription factor that was primarily expressed in the brain and the regenerating liver (some details of the gene, cDNA, and protein are given in table 1, together with those for Ptx-3 and Lmx1b). Its close structural relation to Nur 77 led to its identification in stimulated T cells, where it functions as an intermediate early response gene, with stimulation causing a rapid increase in mRNA without the need for de novo protein synthesis. Inhibition of Nurr 1 binding to its response element led to inefficient clonal deletion of self reactive T cells. It also functions as an intermediate early gene in the central nervous system (CNS), being rapidly induced in response to focal injury, but an appreciation of its crucial importance in brain development came later, after it was
Table 1 Transcription factors involved in dopaminergic neurogenesis

<table>
<thead>
<tr>
<th>Nurr 1</th>
<th>Member of “zinc finger” superfamily of receptors; its subfamily includes nervous growth factor inducible B (NGFI-B) and neuron derived orphan receptor 1 (NOR-1).</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Human gene on 2q22–23; eight exons, spanning 8 kb. Murine, rat, and human genes have similar structures.</td>
</tr>
<tr>
<td></td>
<td>Full length mRNA has 3427 bases, 1394 are translated; the protein has 598 amino acids (66 kDa).</td>
</tr>
<tr>
<td></td>
<td>Splice variants exist—for example, Nurr 2—a novel cryptic exon located upstream in the Nurr 1 promoter region—and alternative splicing at exons 1, 2, and 6.</td>
</tr>
<tr>
<td></td>
<td>Potential regulatory region contains consensus binding sites for nuclear factor KB (NF-kB), SIM response element binding protein (CREB), and Sp1.</td>
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<tr>
<td></td>
<td>In the central nervous system (CNS) Nurr 1 expression occurs in the postmitotic late differential phase of dopaminergic precursor neuronal development, detectable from rat embryonic day 10.</td>
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<tr>
<td></td>
<td>Nurr 1 response elements: a single half site (AAAGGTCA) binds Nurr 1 as monomer; this is the same sequence as the NGFI-B response element; a direct repeat (DR3) (AAAGGTCA) binds Nurr 1/RXR as a heterodimer, Nurr 1 homodimers, and the Nurr 1/NGFI-B heterodimers.</td>
</tr>
<tr>
<td></td>
<td>Nurr 1 response elements are found in tyrosine hydroxylase (AAAGGTCA), the dopamine transporter, and other molecules such as prosopiomelanocortin.</td>
</tr>
</tbody>
</table>

Ptx-3

<table>
<thead>
<tr>
<th>Ptx-3</th>
<th>Structurally related to pentaxins—for example, C reactive protein and serum amyloid P; subfamily includes Ptx-1 and Ptx-2, and homeobox proteins such as Otx-1 and Otx-2.</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Human gene on chromosome 10.q25. has three exons.</td>
</tr>
<tr>
<td></td>
<td>cDNA has 1861 bp; protein has 381 amino acids; Ptx-3 is also a secreted, acute phase protein.</td>
</tr>
<tr>
<td></td>
<td>mRNA induced in endothelial, hepatic, and fibroblastic cells by interleukin 1β (IL-1β) and tumour necrosis factor α, but not by IL-6 and interferon γ; raised serum concentrations after bacterial lipopolysaccharide infection.</td>
</tr>
<tr>
<td></td>
<td>Expression is restricted in the CNS.</td>
</tr>
<tr>
<td></td>
<td>The Ptx-3 response element is GGCTTT.</td>
</tr>
<tr>
<td></td>
<td>There is a Ptx-3 response element in the tyrosine hydroxylase gene.</td>
</tr>
<tr>
<td></td>
<td>Mutations are associated with autosomal dominant cataracts.</td>
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</table>

Lmx1b

<table>
<thead>
<tr>
<th>Lmx1b</th>
<th>This transcription factor is related to members of the LIM family of homeobox proteins.</th>
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<tbody>
<tr>
<td></td>
<td>The human gene is on 9q34 and has eight exons.</td>
</tr>
<tr>
<td></td>
<td>Genetic mutations are associated with nail-patella syndrome.</td>
</tr>
</tbody>
</table>

shown to be expressed strongly in the midbrain region. In mice in which the expression of Nurr 1 is prevented (~/~ knockout), there is a failure of development of midbrain dopaminergic neurons, with a 98% reduction in striatal dopamine and a 30% reduction in noradrenaline. In the olfactory bulb, another area that is important in idiopathic Parkinson’s disease (70% of patients with idiopathic Parkinson’s disease have olfactory bulb dysfunction, and anosia may precede other signs of the disease), Nurr 1 (~/~) mice have a 60% reduction in dopamine, although claims concerning the details of Nurr 1 expression in the olfactory bulb are conflicting. The importance of Nurr 1 for dopaminergic neurons can be seen in relation to tyrosine hydroxylase expression, as shown by the degree of coexpression of the two proteins in the adult mouse brain, namely: substantia nigra (96%), ventral tegmental area (95%), retrolubar field (91%), olfactory bulb (85%), linear nucleus raphe (91%), central grey (61%), paraventricular and periventricular hypothalamic nuclei (few), and arcuate nuclei and zona incerta (0%). In the absence of the growth of the nigral dopaminergic neurons, the animals fail to thrive and die shortly after birth. In contrast, heterozygous animals (+/~ Nurr 1 mice) are apparently healthy but have reduced midbrain dopamine values. In humans, a similar role for Nurr 1 in dopaminergic neurogenesis is assumed. Nurr 1 is not only expressed throughout life in midbrain neurons, but also in other regions unconnected with idiopathic Parkinson’s disease, suggesting that it plays an important role in maintaining the continuing health of all these cells. Exactly what the role of Nurr 1 is in the development of idiopathic Parkinson’s disease remains uncertain. Treatment of Nurr 1 deficient (~+/+) animals with MPTP (1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine) showed that they were more susceptible to the effects of the neurotoxin than normal (+/+). The identification of such a factor, which acts from early fetal life onwards, raises the possibility that differences in the amount of expression and/or the timing of the onset of expression in the fetal period may be important in predisposing these cells to an earlier that normal death and, thence, the development of idiopathic Parkinson’s disease. Other intriguing possibilities that surround Nurr 1 centre on its potential ligand binding ability and its immune responsiveness. As mentioned earlier, Nurr 1 is classed as an orphan receptor. It may act as a transcription factor without an endogenous natural ligand, either binding as a monomer to its response element, or as a dimer. However, this does not of necessity rule out the possibility that it can bind ligands, and binding of any such ligand may alter its function beneficially or deleteriously for the health of the cell. Until developments in molecular biology led to a re-evaluation of the evidence in the past decade, idiopathic Parkinson’s disease was thought to result exclusively from non-genetic causes. However, it is now generally accepted that genetics play a part. Nevertheless, as will be reviewed later, environmental causes are still thought to be of great importance. Any ability of Nurr 1 either to bind endogenous or exogenous ligands or to change in concentration in response to exposure to viruses or other noxious stimuli offers a portal to see how the health of these cells might be uniquely adversely affected by environmental factors. Furthermore, not only does Nurr 1 offer the possibility of theoretical insights, but also that of practical exploration of dopaminergic neuronal cell biology and replacement tissue for implantation. In the past it was possible to culture neuronal cells, but these cultures were highly heterogeneous mixtures of cells, making culture to culture comparisons extremely difficult. However, a culture system has been described that overcomes this problem. This involves three steps, namely: (1) the transfection of neuronal stem cells from mouse cerebellum with a Nurr 1 expression plasmid so that they overexpress Nurr 1; (2) the propagation of the cells in the presence of basic fibroblast growth factor; and (3) co-culture of the cells in the presence of type 1 astrocytes to supply other growth factors. The protocol leads to the development of a dopaminergic phenotype in approximately 80% of the resultant neurons. Such cultures should provide a model in vitro system to enable a detailed exploration of the physiology of these unique cells. Further advances in cell culture techniques, such as that described by Kawasaki et al, which allow a slightly simpler method of inducing a dopaminergic phenotype from a modified embryonic stem cell line, will also greatly aid this exploration. However, the close structural relation of Nurr 1 to other
Aetiology of idiopathic Parkinson’s disease

Nerve growth factor inducible B (NGFI-B) (also known as Nur 77/BRN2/NR1/STF59/TR5) and Neuron-derived orphan receptor 1 (NOR-1) (also known as minor/tac/chn/nor2)

Nurr 1, NGFI-B, and NOR-1 form a subfamily within the “zinc finger” nuclear receptor superfamily. Of the three, NGFI-B was the first to be characterised. Like Nurr-1, NGFI-B and NOR-1 play important roles in brain development, and both are expressed in tissues outside the CNS. The regional expression of NGFI-B and NOR-1 within the CNS is different from that of Nurr 1, with that of NGFI-B being wider, but the three do overlap, suggesting selective roles for these transcription factors in the regulation of motor function.48, 49 Table 2 summarises the expression of the three subfamily members in the CNS. Of possible relevance to idiopathic Parkinson’s disease is the fact that: (1) both NGFI-B and NOR-1 are expressed in the caudate/putamen, the target site for dopaminergic neurones from the substantia nigra, but are not expressed in the substantia nigra itself; and (2) NGFI-B, NOR-1, and Nurr 1 are involved in the regulation of dopaminergic neurone formation in the olfactory bulb, where NGFI-B is strongly expressed in the glomerular and granule cell layers.50

Human NGFI-B cDNA is 2498 bp in length, with an open reading frame of 1794 base pairs, which encodes a protein of 598 amino acids and a predicted molecular mass of 64 kDa.52-53 The NGFI-B structural gene is encoded on human chromosome 12q13.1,54 and the gene for NOR-1 is located on human chromosome 9q22, spans some 35 kb, and has eight exons.55 The NOR-1 gene gives rise to two transcripts, which when translated result in a protein containing 626 amino acids, with an approximate molecular weight of 68 kDa. All three receptors bind to a common response element—AAAAGGTTCA—as monomers.56 Nurr 1 and NGFI-B bind to AGGTCA repeats as heterodimers with RXR isoforms,7 as homodimers,57 and as a heterodimer with each other.58 NOR-1 is unusual in that it does not heterodimerise with RXR. x Ray crystallography has shown that, when NGFI-B binds as a monomer, the DNA binding domain of the receptor not only interacts with the core section of the response element (AGGTCA) in the major groove, but also with the A&A extension via the minor groove.59

Like Nurr 1, NGFI-B and NOR-1 are intermediate early genes. NGFI-B mRNA in brain was induced rapidly and transiently by growth stimulating agents,57, 60 and in hippocampal neurones in response to NMDA and muscarinic receptor stimulation.51 Both NGFI-B and NOR-1 are expressed in the fetal brain and are important signals in mitogenesis and apoptosis pathways in tissues outside the CNS.51, 54

The role of these receptors in apoptotic signalling is complex. Both NGFI-B and NOR-1 generally are regarded as proapoptotic factors in tissue outside the CNS.65, 66 This appears to be true for NGFI-B in the adult human CNS too, with high amounts of the receptor being detectable in the brains of patients with Alzheimer’s disease.67 However, as indicated above, both NGFI-B and NOR-1 are constitutively expressed in some regions of the brain in adult life where high rates of apoptotic neural death are not occurring, so obviously they have other functions, and in a model system where overexpression of NGFI-B was induced, it inhibited ceramide induced apoptosis but not the Fas–Fas ligand pathway.68 Despite these somewhat contradictory strands of evidence, an understanding of the role of NGFI-B in apoptosis and gene transcription is beginning to emerge. An essential step in the initiation of apoptosis is the release of cytochrome c from mitochondria, which then activates the caspase cascade.69 After exposure of the prostate cancer cell line LNCaP to 6-3-(1-adamantyl)-4-hydroxyphenyl)-3-chloro-2-naphthalene carboxylic acid and other proapoptotic agents, human NGFI-B was induced and the protein was shown to move from the nucleus to the mitochondrion to trigger cytochrome c release. Therefore, in its role in apoptosis, human NGFI-B is not required to initiate gene transcription. Signals directing movement out of the nucleus were contained in both the N-terminus and C-terminus of the molecule. Apoptosis was inhibited by antisense human NGFI-B mRNA. In contrast, epidermal growth factor (EGF)—a non-apoptotic stimulus—also induced human NGFI-B mRNA, but the protein produced stayed within the nucleus and was capable of initiating gene transcription.70 Therefore, it seems that the contrasting actions of human NGFI-B are modulated by its intracellular localisation, which in turn is dependent upon the nature of the signal to which the cell is exposed.

Export of human NGFI-B from the nucleus is also a means of modulating gene transcription via interaction with the retinoid signalling system. After nerve growth factor induced phosphorylation of NGFI-B serine residue 105, the NGFI-B–RXR complex leaves the nucleus, reducing the availability of RXR for heterodimerisation with RAR, which thus reduces the transcriptional activity of the RAR–RAR complex.71 Export of the RXR–

Table 2  Regional expression of Nurr 1, NGFI–B, and NOR–1 mRNA in rat and mouse brain

<table>
<thead>
<tr>
<th>Area of brain</th>
<th>Nurr 1</th>
<th>NGFI-B</th>
<th>NOR–1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Neocortex</td>
<td>++</td>
<td>++</td>
<td>A</td>
</tr>
<tr>
<td>Caudate/putamen</td>
<td>++</td>
<td>A</td>
<td>A</td>
</tr>
<tr>
<td>Hippocampus</td>
<td>+</td>
<td>+</td>
<td>++</td>
</tr>
<tr>
<td>Olfactory bulb area</td>
<td>+</td>
<td>++</td>
<td>++</td>
</tr>
<tr>
<td>Ventral tegmental</td>
<td>+</td>
<td>+</td>
<td>++</td>
</tr>
<tr>
<td>Substantia nigra</td>
<td>++</td>
<td>++</td>
<td>+</td>
</tr>
<tr>
<td>Subiculsum</td>
<td>++</td>
<td>+</td>
<td>A</td>
</tr>
<tr>
<td>Locus coeruleus</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Cerebellum</td>
<td>++</td>
<td>++</td>
<td>A</td>
</tr>
<tr>
<td>Spinal cord</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

A, early, neonatal life; B, later life.
++, strong expression; +, moderate expression; –, weak or no expression.

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NGFI-B complex from the nucleus has also been suggested as the mechanism whereby retinoids inhibit the activation induced apoptosis of immature thymocytes. It was suggested that this occurred because of the reduced ability of NGFI-B to initiate gene transcription, but it may be the result of the inability of the RXR-NGFI-B heterodimer to interact with the mitochondrion, in contrast to NGFI-B alone.

The recent work on the role of NGFI-B in apoptosis has been carried out largely in non-CNS cells, and whether the same actions and mechanisms apply in the CNS remains to be seen. However, NGFI-B is inductive in the dopaminergic target areas in the striatum in response to burst stimulation of the medial forebrain bundle, and both NGFI-B and NOR-1 are inducible in response to therapeutic drugs (haloperidol) and substances of abuse (cocaine and morphine). The induction of NGFI-B and NOR-1 was suggested as a mechanism whereby retinoid signaling was disturbed, so that it might be of relevance in schizophrenia. In contrast, compulsive running was shown to downregulate striatal NGFI-B and NOR-1 expression. Thus, these two transcription factors appear to be involved in dopaminergic-related personality characteristics. However it is still unclear whether Nurr 1 has similar properties to NGFI-B, and whether and how the expression of NGFI-B and NOR-1 changes and, if it does, how such changes coincide with any alterations in the expression of Nurr 1 in idiopathic Parkinson's disease. Because of the complex way that all three principle members of the NGFI-B family act as individuals and interact with each other and other liganded nuclear receptors, such as the retinoid and glucocorticoid receptors, these proteins have the capacity to modulate the transcription of many genes, only a few of which have been recognised, and to act as both survival and proapoptotic factors, not necessarily by modulating events in the cell nucleus. This complexity is increased by the fact that further proteins are formed from the same genes by either exon splicing or the use of different transcription start sites and promoters. These also have transactivator properties; the Nurr 1 related protein (TINUR) derived by differential splicing is induced in T cells undergoing apoptosis.

The elucidation of the actions of all three major proteins should give insights into dopaminergic neuronal cell survival and death in the substantia nigra, either because the function of Nurr 1 in these cells has changed or because the functions of NGFI-B or NOR-1 in neurones in target sites have changed, causing a lack of support for the incoming dopaminergic neurones. In turn, such knowledge may give insights into the biochemical basis of some of the behavioural and personality features of the disease, in addition to the cause of the neuronal death.

However, zinc finger nuclear receptors are not the only transcription factors that are of interest in dopaminergic neurone development and survival. Two others which are members of different families are being increasingly recognised as important. These are Lmx1b and Ptx-3. Both are homeobox proteins.

Lmx1b and Pentaxin 3 (Ptx-3)

Although Nurr 1 expression is essential for the final differentiation of stem cells into dopaminergic neurones, it cannot initiate and complete this process by itself. Neuronal development and differentiation occur as a consequence of the actions of successive waves of transcription factors. In the early phases of the transformation of stem cells sonic hedgehog and fibroblast growth factor 8 (FGF-8) appear to be principal players. Another transcription factor that acts at this early stage is Lmx1b. The expression of this factor is stimulated by FGF-8 and, as part of this cascade, Lmx1b in turn stimulates another transcription factor, Wnt1.

Lmx1b is a member of the LIM homeodomain protein family and was first recognised because of its role in dorsal–ventral limb patterning. It is expressed in numerous tissues where it affects skeletal, cranial, renal, and eye structures, and the trajectory of motor neurones in limbs. Subsequent studies have shown that loss of function mutations in the human gene are responsible for the nail-patella syndrome. Its role in dopaminergic neuronal development is only just beginning to be elucidated. It is expressed in the neural tube at an early stage in the genesis of mesencephalic dopaminergic neurones in response to FGF-8 stimulation, where it maintains the expression of another transcription factor Wnt1, and in the normal adult midbrain. Lmx1b knockout mice fail to develop the full repertoire of dopaminergic neurones and their gene products. Although Nurr 1 and tyrosine hydroxylase are still expressed, there is a failure of expression of Ptx-3.

Later and at almost the same time as Nurr 1 is expressed, another transcription factor—Ptx-3—appears (embryonic day 11.5 in the rat). In the CNS, this factor is found only in mesencephalic dopaminergic neurones, unlike Nurr 1 and the other factors mentioned above, but its expression does not by itself lead to the formation of the final dopaminergic phenotype. In Nurr 1 deficient (−/−) mice, Ptx-3 is expressed normally in the progenitor cells but these do not survive. However, the importance of Ptx-3 for these neurones can be seen by the fact that a Ptx-3 response element (GGCTTT) is present in the 5' flanking regions of the human, rat, and mouse tyrosine hydroxylase genes, and binding of the transcription factor to this element results in pronounced upregulation of transcription. Ptx-3 expressing neurones are reduced in number in parkinsonian substantia nigra and in that of the 6-hydroxydopamine lesioned rat. However, whether the neuronal loss in these situations is related to Ptx-3 function, or the reduction in Ptx-3 is simply a consequence of the death of these neurones, is uncertain. Nevertheless, it is principally the Ptx-3 expressing neurones that die.
Aetiology of idiopathic Parkinson's disease

Genetic and environmental aetiological factors

The above discussion has concentrated on transcription factors that are involved in dopaminergic neurogenesis and have functions, as yet ill defined, in the adult CNS. Whether they have a role in the aetiology of idiopathic Parkinson's disease is very uncertain, but they clearly have the potential to be involved in this. By definition, the causes of idiopathic Parkinson's disease are as yet unknown. Over the past two decades, scientific opinion has varied between two extreme poles: from there being only environmental causes, to the position where genetic factors are considered to be the dominant aetiological feature. One major stimulus to this refocusing of emphasis on to genetics has stemmed from the recognition that a new class of rotenone-like compounds might exist in the environment. Whether they have a role in the aetiology of idiopathic Parkinson's disease are as yet unknown. Over the past two decades, scientific opinion has varied between two extreme poles: from there being only environmental causes, to the position where genetic factors are considered to be the dominant aetiological feature. One major stimulus to this refocusing of emphasis on to genetics has stemmed from the recognition that a new class of rotenone-like compounds might exist in the environment.

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Whether either of these opposing opinions or a combination of the two is correct remains to be seen, but because most effort has been directed to elucidating the genetic basis of familial Parkinson's disease. Consequently, these developments will be reviewed first.

FAMILIAL GENETIC LOCI

To date, the genetic loci that have been found to be associated with Parkinson's disease with fairly typical symptoms are:

- A locus on chromosome 4q, which encodes the protein α-synuclein. The mutations involved are A30P and A53T.101,102
- A locus on chromosome 6q, which encodes the protein parkin. Multiple mutations are involved.100–108
- A locus on chromosome 4p, which encodes the protein ubiquitin C-terminal hydrolase (UCHT). The mutation involved is I93M.109
- A locus on chromosome 4p, which encodes an unknown protein.110
- A locus on chromosome 2p13, which encodes two unknown proteins,111,112 and cytochrome b.113

In addition, there are other loci associated with atypical symptoms. For example, a locus on chromosome 17q21–22, which encodes the protein tau, and which is associated with frontotemporal dementia,114–116 and a locus on chromosome 19q13, which is associated with rapid onset dystonia Parkinson's disease.117

There are other loci that are associated with other modes of inheritance than the autosomal dominant transmission described in the original family with the α-synuclein mutation. These include:

- Autosomal recessive—several mutations in the parkin gene.118–120
- Autosomal dominant inheritance because of parkin gene mutation.119
- Maternal transmission—mutations in mitochondrial DNA.120

Other loci are associated with both unusual features and mode of transmission—for example, a 12S ribosomal RNA gene point mutation causing disrupted protein synthesis resulting in parkinsonism, deafness, and neuropathy.121

Despite the increasing number of kindred being described, familial parkinsonism accounts for a relatively small proportion of the total patient population; therefore, the reason for the interest in these cases, apart from that of knowing the details of the causal mutation in each, is that they may shed light on the aetiologies of sporadic cases. This is proving to be the case to a surprising extent, although the mutations in the familial cases are not found in sporadic idiopathic Parkinson's disease.122–125 (In fact, it has been suggested that another relatively common mutation in the UCHT gene, S18Y, is protective.122) What has been highlighted from this work is the importance of two inter-related pathways: α-synuclein fibril formation and ubiquitin targeted protein catabolism.

α-Synuclein is a member of a small family of proteins (other members being β-synuclein and persyn). Under normal circumstances, it is strongly expressed in neurones in a limited
number of areas of the brain, including the dopaminergic neurones of the substantia nigra (a feature in common with parkin in contrast to ubiquitin carboxy terminal hydroxylase\textsuperscript{136}), and comprises about 2\% of total brain protein.\textsuperscript{127} Its physiological role is ill defined, but it is present in nerve terminals. Its importance was recognised because of the fact that, together with proteasome and synphilin-1, and in whole and partially digested forms, it is a major component of Lewy bodies, which are a cardinal feature of the pathology of the parkinsonian brain. Of added importance are the facts that the proteins composing Lewy bodies are heavily ubiquitinylated and they are resistant to proteolysis.\textsuperscript{136,137} The mutations discovered in the initial parkinsonian families were thought either to render α-synuclein more resistant to proteolysis or to have a greater tendency to form fibrils, and in these ways accelerate Lewy body formation, thereby effectively clogging up the cytosol of the neurone and killing it.\textsuperscript{138}

In support of this relatively simple scenario was the discovery of the mutation in the ubiquitin C-terminal hydroxyxylase gene. The ubiquitin targeted pathway of intracellular protein catabolism utilises initially three classes of proteins, corresponding to the three steps in the first phase of the pathway—ubiquitin activation, ubiquitin conjugation, and target protein ligation—to attach the polyubiquitin tail to the protein to be destroyed. Ubiquitin C-terminal hydroxyxylases in the final step release ubiquitin from this polyubiquitin tail for re-use after digestion of the target protein by the 26S proteasome complex.\textsuperscript{139} An inability to release ubiquitin from the polyubiquitin tail, as a result of deficient ubiquitin C-terminal hydroxylase activity, with the resultant absent or incomplete digestion of the target protein, could allow the accumulation of the building blocks for neurotoxic fibrils.

The first difficulty with this simple scenario in which toxicity occurs because of cytosolic blockage is the Japanese families with parkin gene defects. These defects give rise to an early onset form of Parkinson’s disease. In the few individuals who underwent necropsy no Lewy bodies were found. While the function of the parkin gene product was unknown, this difficulty could be explained away, but it is now clear that the gene gives rise to a ubiquitin ligase.\textsuperscript{139} These enzymes are of crucial importance for attaching the initial ubiquitin to the target protein and then extending the ubiquitin chain. Lack of Lewy bodies in individuals with gross genetic mutation that inactivate the enzyme presumably arises from the fact that α-synuclein and other proteins are not ubiquitinylated, so they do not progress to the point where partially digested material is available for fibril formation. Hence, simple cytosol blockage by insoluble proteins is not the only cause of cell death, which, therefore, may be caused by the inability to clear soluble proteins in these cases.

Second, in most sporadic cases investigated no mutation in the α-synuclein gene has been found and it is not clear from in vitro experiments that the variant α-synucleins have a significantly greater rate of fibril formation when compared with that of the wild-type, which nevertheless does form fibrils.\textsuperscript{136} These facts pose questions of how Lewy body formation occurs in sporadic Parkinson’s disease and how this is related to cell death. Factors that may be more relevant than the rate of fibril formation are interactions with other proteins, such as synphilin-1\textsuperscript{137}; the rates of formation of soluble oligomers of α-synuclein, a step that precedes fibril formation,\textsuperscript{138,139} which affects mitochondrial function\textsuperscript{140}; and the nucleation of fibril formation.\textsuperscript{139} In the last instance, the role of iron as the instigator of fibril nucleation has been suggested to be important.\textsuperscript{141} In health, the pigmented dopaminergic neurones normally have relatively high concentrations of both iron and copper, and in the clinical phase of the disease increased amounts of low molecular weight iron and copper compounds are released in the cerebrospinal fluid.\textsuperscript{142} Thus, the iron released from one dead or dying cell may be available to propagate fibril nucleation in other cells.

Third, it is worth repeating that none of the genetic abnormalities seen in the familial cases is seen in most of the patients. Therefore, if the inability to degrade α-synuclein and other proteins is not only the basis of Lewy body formation but the ultimate reason why the neurone dies, a defect must exist that precedes and precipitates this. Such a conclusion is supported by the existence of the well characterised familial cases that result from mitochondrial DNA mutations where genome DNA mutations can be discounted.\textsuperscript{143} This leads back to themes that are familiar to those in the immediate field: oxidative stress, mitochondrial complex I underactivity and energy production, excitotoxicity, and dopamine metabolism. In addition, as pointed out by Goldberg and Lansbury, one consequence of events before fibril formation occurring being of prime importance may be that a therapeutic approach directed solely at inhibiting the polymerisation of protein into fibrils might not be beneficial.\textsuperscript{138}

**ENDOGENOUS GENERATION OF SELECTIVE NEUROTOXINS**

The evidence that the substantia nigra in idiopathic Parkinson’s disease experiences free radical mediated oxidative stress has been reviewed exhaustively on numerous occasions,\textsuperscript{144} and the abnormally low mitochondrial complex I activity well documented previously,\textsuperscript{145} so neither will be discussed in detail here. That overexcitation of receptors such as the α1B-adrenergic receptor might lead to neurodegenerative disease also continues to receive support, as in the recent findings in multiple system atrophy.\textsuperscript{146} However, in idiopathic Parkinson’s disease the things that are not clear are: (1) whether oxidative stress precedes complex I inhibition or vice versa, and (2) how excitotoxicity relates to the two. The MPTP model of idiopathic Parkinson’s disease would suggest that underactivity of complex I leads to oxidative stress. This
reduced activity could occur because of the presence of some inhibitory neurotoxin, or as a result of the accumulation of random replication errors in mitochondrial DNA. In terms of neurotoxins, two classes of compounds have been investigated extensively: cysteine-dopamine reaction products and MPP⁺-like molecules.

The salient feature of MPP⁺ is the aromatic quaternary N-methyl, which allows it to bind to complex 1 but, because such a charged molecule would not pass the blood–brain barrier, intra CNS routes of synthesis are required, as in the case of the conversion of MPTP to MPP⁺ by monoamine oxidase B. One such route is N-methylation, with simple pyridines, β carbolines, and tetrahydroisoquinolines as substrates. Members of these classes of compounds are present in the food chain, the general environment, and in the human brain and cerebrospinal fluid. Enzymes that can convert them into their N-methylpyridinium analogues are also present in the mammalian brain. In an apparently analogous fashion to MPP⁺, the N-methyl derivatives are selectively neurotoxic, interact with the dopamine uptake system, and inhibit mitochondrial respiration. In the case of β carbolines, the molecule can be N-methylated at two sites, and the kinetics of the two reactions are different. However, the enzyme(s) responsible has not been isolated and cloned, so it is not clear whether the two activities observed represent different actions of the same enzyme or two entirely different ones. Following on from earlier work by Matsubara et al., who showed that β carboline concentrations in the cerebrospinal fluid of patients with Parkinson’s disease were higher than those of control subjects, Gearhart et al have shown increased β carboline 9N-methyltransferase activity in the frontal cortex of parkinsonian brain compared with that of non-parkinsonian brain. Thus, there appears to be both higher amounts of substrate and one form of enzyme activity in the disease population.

Our own work in this area has concentrated on nicotinamide-N-methyltransferase (NNMT), which, apart from catabolising the amide form of vitamin B₃, has a wide substrate specificity that enables it to generate a variety of potentially toxic N-methylpyridinium ions. Its expression is dominated by an as yet undetermined, non-coding, genetic polymorphism, which results in a quarter of the general population having high hepatic enzymic protein and activity values. Because nicotinamide is an integral part of NADH, which is the electron and hydrogen donor for complex 1, catabolism of nicotinamide could conceivably have an effect on intracellular NADH values. Thus, NNMT links, albeit tenuously, the ability to produce N-methylpyridinium ions, the metabolism of NADH, complex 1 activity, and the genetics of 25% of the general population. In exploring the hypothesis that NNMT may be an aetiological factor in idiopathic Parkinson’s disease, some of our initial findings are that the enzyme is expressed in neurones and in higher amounts in two regions of the brain (caudate nucleus and cerebellum) in Parkinson’s disease compared with control brain (cerebellum, fig 1). The enzyme is expressed in the substantia nigra, but the destruction of so many neurones that has occurred in this area by the time subjects reach necropsy makes comparisons between parkinsonian and non-parkinsonian material difficult to interpret.

**Figure 1** Expression of nicotinamide-N-methyltransferase (NNMT) protein and mRNA in control (non-Parkinsonian) and Parkinsonian cerebellum. (A) Protein expression in non-Parkinsonian cerebellum. Counterstain only (blue) is present. (B) Protein expression in the Parkinsonian cerebellum. Brown staining indicating the presence of NNMT protein is present solely in the neurones of the granular layer, with little or no staining in the white matter and the molecular layer. (C) mRNA expression in the non-Parkinsonian cerebellum. Little expression indicated by blue/purple staining was present in the granular layer. (D) mRNA expression in the Parkinsonian cerebellum. Pronounced blue/purple staining indicating the presence of NNMT mRNA is present solely in the granular layer, with no staining in either the white matter or the molecular layer.
How NNMT relates to β-carboline N-methyltransferases and tetrhydroisquino- 
line N-methyltransferase is unclear, but as Gearhart et al pointed out, these may all be the 
same entity.49 If so, the collective evidence from the three areas would present a strong 
case for N-methylpyridinium ion formation being an important aetiological factor.

A second area of biochemistry where the generation of neurotoxins has been explored is 
that of dopamine metabolism. The arguments as to whether dopamine itself is deleterious to 
the neurone when considered in relation to L-DOPA treatment have been well rehearsed 
previously and will not be repeated here. One aspect of endogenous dopamine metabolism 
that has not received wide attention is that of its interaction with cysteine. Work in this area has 
been carried out in the main by the group led by Dryhurst. This group has shown that under 
mild oxidising conditions cysteine and dopamine or other catecholamines react to- 
gether to form a variety of compounds, including dihydrobenzothiazines, which are potent 
inhibitors of complex 1, and free radical species.152-158 If the products of these reactions 
are involved in the aetiology of the disease, because the neurone has evolved to generate 
dopamine, factors that control the intracellular concentration of the other reactant (cysteine) 
would be important. Within the hepatocyte, the enzyme cysteine dioxygenase is one such 
factor. Therefore, we explored the possibility that this enzyme, which has been shown to be 
expressed in brain previously,159 is expressed in dopaminergic neurones. To date, we have 
shown that, in the rat, the enzyme is present in numerous brain regions and the highest 
unstimulated activity can be seen in the basal ganglia and olfactory bulb.160 Inspection of 
chromosome 5 sequence data in GenBank shows a potential Ptx-3 response element 
within 2 kb of the transcription start site of the gene, suggesting that this exclusively dopamin- 
ergic transcription factor may be involved in the regulation of expression. Initial immuno-
histochemistry shows that the enzyme is present in neurones,161 and further work is 
under way to characterise expression in the human substantia nigra. Relatively little work 
has been done on the genetics of cysteine dioxygenase regulation, but some phenotyping 
studies suggest that most of the population has a low to medium degree of constitutive activity, 
with a small proportion being in a high activity group.162 A low activity would favour a high 
intracellular cysteine concentration and hence the formation of toxic reaction products.

THE GENETICS OF “NON-FAMILIAL” PARKINSON’S DISEASE: CANDIDATE GENES

The work outlined in the previous section may be categorised as a “candidate toxin” approach 
to elucidate the aetiology of idiopathic Parkinson’s disease. However, the general emphasis 
on genetics has led to other themes such as xenobiotic metabolism and links with 
Alzheimer’s disease. Polymorphic alleles are sought that are more or less common in the 
idiopathic Parkinson’s disease population compared with the control population, controls 
being either age and sex matched to varying extents, or sibling pairs. Many genes have been 
investigated and a few phenotypic studies carried out. Examples of genes investigated in 
some recent studies are CYP1A1,163 the dopamine D2 receptor gene,144 tau,145 and 
apolipoprotein E.146 In addition, associations between Parkinson’s disease and combinations 
of genetic loci, such as α synuclein and apo lipoprotein E alleles147 have been investigated. 
On the whole, the results of such studies have been unconvincing. One group will present 
evidence of an allele being positively associated with the development of idiopathic Parkinson’s 
disease, only for another group either to fail to find the correlation with the disease or to give 
another interpretation. An example of this is the case of the NAT2 alleles, where Bandmann 
and colleagues claim a positive association between the “slow acetylator” genotype and 
the development of idiopathic Parkinson’s disease in what they call a “familial” Parkinson’s 
disease group—a group composed of individuals with at least one affected relative—as 
opposed to the classic, “large family” studies, which identified the mutant α synuclein and 
parkin genes referred to earlier. This was suggested in a smaller scale phenotypic study 
too.170 In contrast, Harhangi et al had failed to find this connection in randomly selected 
patients with idiopathic Parkinson’s disease and claim that the genotype is a marker of 
mortality in the general population.171 We also failed to find this connection,165 although 
patient selection was not identical to that of Bandmann et al.

The question arises, therefore, of how to interpret the results of such studies. Where two 
or more groups have put forward opposing findings, has one side simply got it wrong? If so, 
how does one tell which? In the case of CYP2D6 alleles, which were suggested to be 
important by both separate, early phenotyping172 and genotyping173 results, the weight of 
evidence from repeat studies by other groups has tipped the scales against these 
conclusions.165 174-176 Nevertheless, it would be depressing to think that such a process would 
have to be gone through for every candidate gene that is dreamt up. It may be argued that 
whole genome scanning will obviate this problem. However, in the case where it has been 
most successful in identifying susceptibility loci in a common multigene disease—diabetes 
mellitus, type 1—the genetic link in families is stronger than in idiopathic Parkinson’s disease, 
much larger population groups and family clusters were studied, and controls were 
carefully matched. Thus, if one accepts the multigene hypothesis, it presents huge logistical 
problems in terms of sample acquisition and classification to achieve adequate statistical 
power to recognise small differences in allelic frequencies. Moreover, the case for a geneti- 
cally based aetiology is still strongly chal- 
lenged,180 and although the multigene hypoth- 
thesis may form a convenient way of explaining a baffling problem, it is not necessarily correct.
In an essential monogenic disease such as familial amyloidotic polyneuropathy a single mutation in a single gene can give rise to greatly different phenotypic forms of expression. In the case of the Met30 variant transhyretin, the Portuguese expression is one of lower limb involvement and renal failure, whereas in a Danish family the heart is the organ primarily affected. Presumably, this arises in part from the interaction of different levels of gene products in the two populations. A similar scenario (in this case a combination of apolipoprotein E and α synuclein alleles), compound by the effects of exposure to varieties of natural (such as homocysteine) and man made toxins (such as lead), might also explain the multifarious features of the entity we call idiopathic Parkinson’s disease.

Conclusions
We are some way from unravelling the conundrum of the aetiology of idiopathic Parkinson’s disease, although two big advances have been made. The first is the elucidation of the genetic defects in large affected kindreds, which has pointed to the importance of defects in ubiquitin and defects in large alpha synuclein in Parkinson’s disease, although two big advances have been made.

37 www.molpath.com
Homo sapiens chromosome 12 working draft sequence,


54 Homo sapiens chromosome 12 working draft sequence,


Aetiology of idiopathic Parkinson's disease


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