Neurodegenerative diseases are important causes of disability and death, with prominent examples including Alzheimer's disease, Parkinson's disease (PD) and motor neuron disease. Although familial clustering of these illnesses was well known before the advent of modern molecular genetics, meaningful strides in identifying the origin of neurodegenerative diseases have really only begun to be made in the past two decades. All these disorders are characterised by a small percentage of affected patients whose disease is clearly the result of Mendelian inherited genetic illness, either recessive or dominant. In particular, dominant disease is exemplified in the case of Alzheimer's disease by presenilin 2 mutations that arose in German immigrants from the Volga river region in the 17th century, and in PD by mutations in the LRRK2 protein that are linked to a founder effect dating back to the 2nd century, probably in Ashkenazi Jews.

Such autosomal dominant families enable a crucial aspect of neurodegenerative disease to be addressed, namely the identification of biomarkers that can serve to identify the earliest features of the onset of disease. These biomarkers range from proteins in cerebrospinal fluid, such as amyloid and tau, to magnetic resonance imaging scans of the brain volumes of cortex and temporal lobe structures, and positron emission tomography scans of markers of neurodegeneration, such as amyloid.

It is clear, certainly in the case of Alzheimer's disease, that by the time even mild memory impairment has developed there is widespread pathological change that is highly likely to be irreversible. Similarly, although tremor may be the best-appreciated manifestation of dopaminergic cell loss in PD, it is clearly preceded by a slowly progressive process that gradually ascends up the brainstem and may produce features of brainstem dysfunction as long as 25 years before the onset of classic PD. In general, it would probably be most useful to identify individuals who are genetically at risk for developing neurodegenerative illness, and monitor particular biomarkers, in the event that successful therapies become available.

After the initial euphoria when the first genes associated with Alzheimer's disease and PD were identified, a major issue has been the extrapolation of these findings to the much more common situation of sporadic disease in individuals who lack a clear-cut family history. So far, although genome-wide association studies (GWASs) have shown much promise, they have failed to deliver many significant advances with regard to the genetic cause of neurodegenerative disease. In particular, the power of such studies has been limited, and not uncommonly GWASs have only served
to confirm genetic targets already identified by other methods.\cite{6}
It could be argued that a sporadic case is more likely to have an
environmental cause, but the evidence for the environment playing
an important role in the causation of neurodegenerative disease is
not particularly strong.
A major advantage of genetic studies is not only that they
identify the cause of illness, but also that they shed light on
the various molecular pathways implicated in the causation of
neurodegenerative disease.\cite{7,10} This clearly has significant implications
for the development of treatments that would potentially be of benefit
for patients harbouring preclinical or manifest mutations, as well as
for patients with sporadic disease.

One major issue regarding the utility of genetics when applied to
neurodegenerative disease is that age is a major risk factor, and many
patients may not develop illness simply because they die before the
disease manifests. Confirmation of a family history of an illness being
inherited in a particular pattern may therefore be difficult. Over
and above mutation analysis, genealogical studies can be very useful in
populations where there are common founder effects and church
records. Such is the case for the original Dutch population that settled
in the Cape from the mid-1600s, and with the admixture largely of
German and French immigrants, ultimately developed into the South
African (SA) Afrikaner population. As is well known, this population has
well-established founder effects for a wide range of conditions, of
which the best-known examples are familial hypercholesterolaemia
and variegate porphyria. Furthermore, the Afrikaner population has
genealogies that range from the 1600s through the early 1800s and
later, and are well documented and recorded.\cite{8,10}

Interestingly, with respect to neurodegenerative disease, there
is some evidence for a founder effect for Huntington’s disease in SA,
possibly arising from an early Dutch settler, since there is a common
haplotype suggestive of a European origin.\cite{11,12} In the study by
Geldenhuys et al.\cite{13} published in this issue of the SAMJ, genealogies of
12 Afrikaner families were investigated in detail using the records
of the Genealogical Institute of South Africa in Stellenbosch and
other sources. The genealogical research concentrated on those
with a family history suggestive of either dominant or recessive
inheritance of PD. The 12 families were shown to be linked to a
single ancestral couple, and this finding was further supported by
confirmation of ancestral lines to the putative founder couple in an
additional 28 families, also of Afrikaner origin and with a history of
PD. The affected family members had a mean age of onset of
PD of only 52 years, which is considerably less than that in typical
idiopathic disease and suggests a genetic origin for the illness.\cite{12,13}

The founder couple was of Dutch and German ancestry and married in the
Cape in 1668.

This finding is of importance for two reasons. Firstly, given that
established genetic causes of PD have not been identified in the
Afrikaner population, it appears likely that this population carries
unique mutations that remain to be identified by genome-wide
screening.\cite{13,16} Secondly, in the event that effective treatments are
developed, particularly for presymptomatic patients, the Afrikaner
population may be considered to be at risk and requiring careful
assessment with accurate biomarkers.

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References

2. Bar-Shar A, Hyder CM, Glad N, Zahirian DP, O’Reilly-Tuttle A. Ashkenazi Parkinson’s
disease patients with the LRRK2 G2019S mutation share a common founder dating from the second to fifth
   parents affected by late-onset AD. Neurology 2014;82(9):752-760. [http://dx.doi.org/10.1212/ WNL.000000000000181]
4. Fagen AM, Xiong C, Jankovic J, et al. Longitudinal change in CSF biomarkers in autosomal-dominant
   Dis 2010;19(3):221-228.
   2009;467(7327):747-753. [http://dx.doi.org/10.1038/nature09490]
9. Wooten ZK, Pfeiffer RF, Trosho Y, Umb HS, McCord-RD, Stowell AJ. Autosomal dominant parkinsonism
   2014;104(9):419-421. [http://dx.doi.org/10.7196/SAMJ.1747]
15. Barden S, Louagie S, Brice A, Carr J. Genetic characteristics of leucine-rich repeat kinase 2 (LRRK2)
16. Rijckenberg J, Barden S, Glanzman B, Ouhosboko NU, Carr JA. The prevalence and genetics of