

## Biochemical Changes and Cardiovascular Function in Parkinson's Disease: Precautionary Notes

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Parkinson's disease (PD) is the second most important neurodegenerative disorder in the elderly population, after Alzheimer's disease. With a prevalence ranging from 35.8 per 100,000 to 12,500 per 100,000 and annual incidence estimates ranging from 1.5 per 100,000 to 346 per 100,000 in different countries [1-3], PD represents today a major age-related problem of health [4,5]. Meta-analysis of the world wide data indicates a rising prevalence of PD with age (from 41 per 100,000 at 40-49 years to 1,903 per 100,000 at over age 80). PD also shows a characteristic distribution by geographic location (a prevalence of 1,601 per 100,000 in patients from North America, Europe and Australia, and a prevalence of 646 per 100,000 in Asian patients) [6]. PD is more prevalent in males (1,729 per 100,000, >65 yrs) than in females (1,644 per 100,000), with a peak prevalence in the age group of  $\geq 90$  years (4,633 cases per 100,000), and a mean prevalence of 1,680 per 100,000 in people older than 65 years of age [7]. Prevalence and incidence Male/Female ratios increase by 0.05 and 0.14, respectively, per 10 years of age. Incidence is similar in men and women under 50 years (M/F ratio <1.2), and over 1.6 times higher in men than women over 80 years [8].

PD-related neurodegeneration is likely to occur several decades before the onset of the motor symptoms (rigidity, bradykinesia, resting tremor, postural instability) [9], resulting from the confluence of genomic defects, epigenetic aberrations and diverse environmental risk factors (toxins, drugs, pesticides, brain microtrauma, focal cerebrovascular damage).

Different genes distributed across the human genome have been associated with PD, including *GBA*, *ADH1C*, *TBP*, *SCA17*, *HDL4*, *ATXN2*, *MAPT*, *SNCA*, *PARK1-22*, *LRRK2*, *PINK1*, *CHCHD2*, *UCHL1*, *APOE*, and many others [10,11]. All these genes are under the influence of the epigenetic machinery (DNA methylation, chromatin remodeling, histone modifications, miRNAs) that regulates their expression in different tissues and may contribute to selective nigrostriatal dopaminergic neurodegeneration. PD neuropathology is characterized by a selective loss of dopaminergic neurons in the substantia nigra pars compacta, with widespread involvement of other brain structures and peripheral tissues [9].

PD exhibits multiple biochemical changes in body fluids and in brain tissues, including neurotransmitters, neurotrophic factors, Lewy body components, abnormal proteins encoded by mutant PD-associated genes, transition metals, calcium and calcium-binding proteins, inflammation factors, ROS and mitochondrial anomalies, proteasome dysfunction, conformational changes in proteins, abnormal protein removal and degradation, hormonal dysregulation, apoptosis and alterations in transduction pathways [12,13]. Recent data indicate that endocrine dyscrasia and the subsequent loss of cell cycle control represent pathogenic events in the development of age- and sex-related neurodegenerative diseases, including Alzheimer's disease, stroke and PD [13]. However, a major question is whether these changes are primarily associated with pathogenic mechanisms or are the consequence of chronic treatment with antiparkinsonian drugs in the case of PD.

The introduction of L-DOPA in the 1960s represented a breakthrough in the treatment of PD, and it continues to be the most effective symptomatic therapy in Parkinsonian disorders [14]. Levodopa (L-DOPA) is the natural isomer of the amino acid D,L-dihydroxyphenylalanine which was isolated from the bean of *Vicia faba* in the early 1910s by Torquato Torquati, and chemically defined by Markus Guggenheim in 1913. In 1938, Peter Holtz discovered the enzyme L-dopadecarboxylase, which converts L-DOPA into dopamine [15]. Dopamine is transformed into noradrenaline by dopamine- $\beta$ -hydroxylase. Both catecholamines are important neurotransmitters involved in different higher activities of the central nervous system. In addition to dopamine precursors (L-DOPA), other symptomatic treatments for PD include dopamine agonists (amantadine, apomorphine, bromocriptine, cabergoline, lisuride, pergolide, pramipexole, ropinirole, rotigotine), monoamine oxidase (MAO) inhibitors (selegiline, rasagiline), and catechol-O-methyltransferase (COMT) inhibitors (entacapone, tolcapone) [16]. The initial complication of long-term L-DOPA therapy is the "wearing-off" phenomenon [17,18], together with motor fluctuations and dyskinesia, which develop during the use of both L-DOPA and dopamine agonists [14,19-21]. Polypharmacy with antidepressants, antipsychotics, urological drugs, analgesics, antihistaminics and cholinesterase inhibitors also contributes to severe complications associated with the anticholinergic burden in PD [22]. Furthermore, gastrointestinal complications (constipation, sialorrhea, dysphagia, difficulty in mastication, choking/aspiration) [23], cardiovascular problems [24], neuroendocrine changes and psychiatric disorders are frequent in Parkinsonian patients chronically treated with conventional antiparkinsonian drugs [16,23]. The onset of these complications is also influenced by the genomic background of the patients [11]; and the efficacy and safety of the drugs currently consumed by those who suffer a Parkinsonian disorder is highly dependent on their pharmacogenomic profile [25-29]. Genes involved in the pharmacogenetic network include pathogenic, mechanistic, metabolic, transporter and pleiotropic genes, and all these genes are also under the influence of potential epigenetic aberrations [30-32]. In recent years, novel evidence has demonstrated the impact of pharmacogenetics on the efficacy and safety of most antiparkinsonian drugs [16,26-29]. In the particular case of L-DOPA, the *ANKK1*, *BDNF*, *LRRK2*, and *PARK2* genes are pathogenic genes potentially involved in its effects. The *CCK*, *CCKAR*, *CCKBR*, *DRD1*, *DRD2*, *DRD3*, *DRD4*, *DRD5*, *GRIN2A*,

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*GRIN2B*, *HCRT*, *HOMER1*, *LMO3*, and *OPRM1* genes are mechanistic genes whose products influence L-DOPA efficacy and safety. L-DOPA is a substrate of enzymes encoded by the *COMT*, *CYP1A2*, *CYP2B6*, *CYP2C19*, *CYP2D6*, *CYP3A4*, *CYP3A5*, *DBH*, *DDC*, *G6PD*, *MAOB*, *TH*, *UGT1A1*, and *UGT1A9* genes responsible for its metabolism. *SLC6A3* is the major transporter of L-DOPA; and *ACE*, *ACHE* and *APOE* are pleiotropic players in L-DOPA effects [16]. *ADORA2A* SNPs and *HOMER1* variants may be associated with L-DOPA-induced dyskinesia and psychotic symptoms [33,34]. A haplotype integrating -141CIns/Del, rs2283265, rs1076560, C957T, TaqIA and rs2734849 polymorphisms at the *DRD2/ANKK1* gene region might also be associated with L-DOPA-induced motor dysfunction [35]; and *SLC6A3* is a genetic modifier of the treatment response to L-DOPA in PD [36].

In a search for novel therapeutic options for PD [37,38], we had the opportunity of evaluating basal biochemical conditions and cardiovascular function in PD patients without any treatment at the moment of their first diagnosis, and in PD patients chronically treated with antiparkinsonian drugs for more than one year. Both groups exhibited substantial biochemical and cardiovascular differences. In addition to changes in blood biochemical (i.e., urea, creatinine, phosphorous, alkaline phosphatase, folate, cyanocobalamin) and hematological parameters (neutrophils, basophils) [38], the most significant differences were found in plasma neurotransmitters and hormones. For instance, as expected, basal dopamine levels in untreated patients were below 20 pg/mL ( $11.22 \pm 0.29$  pg/mL) (mean  $\pm$  SE) whereas basal dopamine levels in treated patients ranged from 21 to 30,000 pg/mL ( $2,139.23 \pm 804.72$  pg/mL) ( $p < 0.001$ ). Chronic treatment with antiparkinsonian drugs reduces the levels of plasma serotonin, FSH, LH and estrogen, and tends to increase the levels of adrenaline, histamine, ACTH, cortisol, and testosterone in a non-significant mode. Changes in neurotransmitters and endocrine parameters are highly influenced by the genomic profile of each patient [37,38].

When PD patients are stratified by their cardiovascular function, as assessed with EKG, 39.50% show an abnormal EKG, 19.32% are borderline, and 41.18% exhibit a normal EKG. Significant differences have been found in plasma neurotransmitter levels (dopamine, noradrenaline, adrenaline, serotonin, histamine) and hormones (prolactin, cortisol, LH, estrogens). High levels of noradrenaline, dopamine, histamine and serotonin, and lower levels of prolactin, LH, testosterone and estrogens are more frequent among patients with abnormal EKG. It appears that a persistent overload of catecholamines and, to a lesser extent, histamine might contribute to cardiovascular dysfunction in PD patients. Since these patients undergo long-term periods of treatment with different antiparkinsonian drugs, which chronically alter neurotransmitter levels and hormonal regulation, some reflections are pertinent: (i) it is likely that the chronic overstimulation of the dopaminergic system at central and peripheral levels may become deleterious for cardio-cerebrovascular function and hormonal regulation; (ii) since the central dopaminergic dysfunction precedes the clinical onset of the disease by several decades, it is urgent to identify predictive biomarkers to protect the population at risk of suffering PD; (iii) the progression of PD for the past 50 years, in terms of gradual increase in prevalence and incidence rates, indicates that environmental toxicity may contribute to accelerate selective dopaminergic neurodegeneration; therefore, a better scrutiny of environmental risk factors is necessary to implement preventive programs in susceptible persons; (iv) most post-mortem neurochemical studies might be contaminated by chronic polypharmacy; (v) novel drugs and bio products for the treatment of PD should address dopaminergic neuroprotection to reduce premature neurodegeneration

rather than dopaminergic overstimulation; and (vi) since biochemical changes and therapeutic outcomes are highly dependent upon the genomic profiles of PD patients, personalized treatments should rely on pharmacogenetic procedures to optimize therapeutics [16].

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