

Post-COVID-19 Parkinsonism and Parkinson's Disease Pathogenesis: The Exosomal Cargo Hypothesis

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Abstract: Parkinson's disease (PD) is the second most prevalent neurodegenerative disease after Alzheimer's disease, globally. Dopaminergic neuron degeneration in substantia nigra pars compacta and aggregation of misfolded alpha-synuclein are the PD hallmarks, accompanied by motor and non-motor symptoms. Several viruses have been linked to the appearance of a post-infection parkinsonian phenotype. Coronavirus disease 2019 (COVID-19), caused by emerging severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) infection, has evolved from a novel pneumonia to a multifaceted syndrome with multiple clinical manifestations, among which neurological sequalae appear insidious and potentially long-lasting. Exosomes are extracellular nanovesicles bearing a complex cargo of active biomolecules and playing crucial roles in intercellular communication under pathophysiological conditions. Exosomes constitute a reliable route for misfolded protein transmission, contributing to PD pathogenesis and diagnosis. Herein, we summarize recent evidence suggesting that SARS-CoV-2 infection shares numerous clinical manifestations and inflammatory and molecular pathways with PD. We carry on hypothesizing that these similarities may be reflected in exosomal cargo modulated by the virus in correlation with disease severity. Travelling from the periphery to the brain, SARS-CoV-2-related exosomal cargo contains SARS-CoV-2 RNA, viral proteins, inflammatory mediators, and modified host proteins that could operate as promoters of neurodegenerative and neuroinflammatory cascades, potentially leading to a future parkinsonism and PD development.

Keywords: Parkinson's disease; SARS-CoV-2; exosomes; neuroinflammation; inflammation; parkinsonism; alpha-synuclein; post-COVID-19; neurodegeneration; virus

1. Introduction

Parkinsonism is a clinical syndrome defined by the presence of resting tremor, bradykinesia, rigidity and postural instability [1]. These motor symptoms are characteristically observed in Parkinson's disease (PD) [2], which remains the primary cause of parkinsonism, but there are other disorders with the same symptoms that mirror it [3,4]. PD is the second most prevalent neurodegenerative disease worldwide after Alzheimer's disease (AD)



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Copyright: © 2022 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). and constitutes a debilitating, progressive motor disorder characterized by degeneration of the nigrostriatal dopaminergic pathway [5]. The prevalence of PD is estimated to be approximately 0.5–1% among those 65–69 years of age, rising to 3% among persons of 80 years and older [6], with an annual incidence rate of approximately 11–19/100,000 cases per year [7,8]. Although PD is generally an idiopathic disorder, there is 5–10% of PD cases that report a family history or display a clear Mendelian inheritance [9,10]. The incremental loss of dopaminergic neurons in the substantia nigra pars compacta (SNpc) and striatum is the mechanistic cause of motor manifestations, with 60–70% dopaminergic neuron loss required for the appearance of motor symptoms [11]. However, prior to motor manifestation onset, patients may display non-motor symptoms such as hyposmia, gastrointestinal dysfunction, and sleep disorders [12]. The neuropathological hallmark of PD is the misfolding and aggregation of alpha-synuclein (α -syn), which is the major protein component of Lewy bodies (LB). Indeed, formation of α -syn protein clumps within neural cells triggers the initiation of neurodegeneration processes [5].

PD is a disease of multicomplex etiology, involving the interaction of aging, genetics, and environmental variables, as well as infectious agents, such as viral infections [13,14]. Additionally, there is now a wide range of data to support the existence of viral parkinsonism, which often manifests following recovery from viral infections [4]. Although the precise mechanisms remain unclear, viruses have been implicated as potential etiological or trigger factors for both PD pathogenesis [15,16] and viral parkinsonism [4]. Recent data suggest that the emerging human severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), responsible for the ongoing pandemic that has already killed more than 6.4 M people worldwide [17], may be one of these viruses [18–20].

On cellular and molecular level, mitochondrial dysfunction, defective autophagy, oxidative stress, and neuroinflammation are all thought to play a role in PD pathogenesis and they are linked to the accumulation and spread of misfolded α -syn [21–23]. The "prion-like" cell-to-cell dissemination of amyloidogenic proteins, such as α -syn, principally refers to the formation and subsequent spread of self-propagating pathological α -syn aggregates throughout brain regions and has lately garnered considerable attention in the quest to understand PD pathophysiology [24–27]. Several in vitro studies, both in animals and continuous human cell lines, have supported this reminiscent of, yet distinct from prion diseases, mechanism of misfolded α -syn spread [28–30]. Exosomes, the nanosized vesicles and masters of intercellular communication [31], have been proposed to serve as an efficient "vehicle" of transportation for such proteins [32], mainly because they are a priori involved in several homeostatic procedures in the central nervous system (CNS) including myelination maintenance, synaptic plasticity, antigen presentation, signal transduction, neurogenesis, and trophic support for neurons [33,34]. Interestingly, many viruses, including SARS-CoV-2, have been shown to regulate exosomal biogenesis and cargo content upon release from infected host cells [35,36]. On top of that, findings from our group and others suggest that a virus-manipulated exosomal cargo could become a blueprint for disease progression even after the complete eradication of the viral agent, due to either immune response-related or drug-mediated viral clearance [37,38]. Since exosomes have a prominent position in pathogenesis and diagnosis of neurodegenerative diseases [32] and are known to be closely linked both to viral infection establishment and infectious disease progression even after virus eradication [39,40], we aim in this review to point out and discuss potential exosome-mediated mechanisms that could lead to post-COVID-19 parkinsonism and PD pathogenesis.

2. Viral Infections as Triggers for Parkinsonism and PD Development

Several studies have demonstrated that viruses may contribute to the etiology of PD and parkinsonism, despite the fact that the underlying molecular and cellular mechanisms remain obscure. The first recorded association between viral infections and parkinsonism was observed during the Spanish flu and the appearance of encephalitis lethargica, an unknown disease with parkinsonian phenotype in survivors [41]. Major human viruses,

such as hepatitis C virus (HCV) [42], herpes simplex virus-1 (HSV-1) [43], human immunodeficiency virus (HIV) [44], varicella-zoster virus (VZV) [45], West Nile virus (WNV) [46], Japanese encephalitis virus (JEV) [47,48], and Epstein–Barr virus (EBV) [49], have all been cited as risk factors for PD development or parkinsonism [3]. Notably, the role of influenza A virus (IAV) in the etiology of the transient parkinsonian phenotype [50] and in PD development [3] has been documented in several in vivo and especially in vitro studies. A case-control study found that an influenza diagnosis was linked to PD development 10 years following infection onset [51], while IAV was found postmortem in the substantia nigra of PD patients [52]. Furthermore, H5N1 infection in a mouse model resulted in Parkinson's phenomenology, sustained microglial activation, and α -syn aggregation, leading to dopaminergic neuron loss in SNpc [53]. Similarly, H1N1 infection in mice resulted in persistent microglial activation as a sign of chronic virus-induced neuroinflammation that could potentially lead to neurodegeneration [54]. More recently, another in vitro study has demonstrated that H1N1 replication can directly disrupt protein homeostasis, inducing α -syn aggregates in Lund human mesencephalic dopaminergic cells, but failing to regulate TAR DNA-binding protein 43 (TDP-43) or tau protein. Those results clearly hint at a selective effect of H1N1 virus on α -syn misfolding [55].

The key pathophysiological processes by which viruses contribute to parkinsonism development remain unclear; however, direct neuronal damage, sustained neuroinflammation, cerebral edema due to virus-mediated damage of brain endothelium, and induction of α -syn aggregation have all been proposed as crucial neurobiological pathways of dopaminergic neuron loss and α -syn pathology [3]. Notably, due to its tendency to entrap viral particles and reduce viral replication, α -syn has been postulated to be a natural antiviral defense mechanism for neurons [56]. This notion was supported by in vivo experiments, where WNV-infected α -syn-knockout mice showed decreased survival compared to the control group [57]. Additionally, it has been suggested that viruses can cause α -syn aggregation and oligomerization through molecular mimicry mechanisms [58,59]. Taken together, these observations strongly support the notion that virus-mediated neuronal deposition of pathological α -syn may induce neurotoxicity and PD pathology.

The relationship between other members of the human *Coronaviridae* family, such as OC43 and 229E, and PD has been previously described, since antibodies against these coronaviruses were found in the cerebrospinal fluid (CSF) of PD patients [60]. The novel coronavirus SARS-CoV-2 emerged in China at the end of 2019 and triggered an outbreak of atypical viral pneumonia [61]. Due to its enhanced transmissibility, this unusual coronavirus disease, also known as coronavirus disease 2019 (COVID-19), marched fast over the world, constituting a huge public health burden [62,63]. SARS-CoV-2 spreads via infected secretions, such as saliva and respiratory droplets, through direct, indirect, or close contact with infected patients, even if COVID-19 symptomatology is absent [64,65]. While symptoms of COVID-19 are primarily systemic or respiratory, several studies demonstrate the presence of a broad spectrum of neuropsychiatric consequences including anosmia, ageusia, altered consciousness, headache, seizures, and paresthesias [66–68]. Several studies have shown that COVID-19-related neurological sequelae might persist long after the acute phase of infection [69]. The term "long" or "post"-COVID-19 syndrome refers to a syndrome observed after the acute infection period and it is characterized by the presence of a combination of COVID-19-related symptoms lasting for more than 12 weeks [70]. These symptoms cannot be explained by an alternative diagnosis and are considered a disability under the Americans with Disabilities Act (ADA) [71]. The post-COVID-19 syndrome includes a plethora of neurological manifestations such as fatigue, brain fog, cognitive impairment, and olfactory dysfunctions [72–74], many of which are also present in PD [2]. Thus, since SARS-CoV-2 shares immunopathological similarities with other viruses linked to parkinsonism, such as influenza [75], and because of COVID-19-related neurological consequences, it is reasonable to suspect that these persistent symptoms might be a prologue to a post-COVID-19 new-onset neurological disease.

3. SARS-CoV-2 Infection and PD Overlaps

3.1. Clinical Co-Manifestations

To date, only few cases of parkinsonism have been reported in literature following COVID-19 infection [19,20,76–78]. In these studies, the authors speculate a possible causative link between COVID-19 infection and a post-COVID new-onset parkinsonian phenotype, but they do not address the possibility of prodromal, pre-symptomatic PD, which became symptomatic as a result of biological or psychological stress processes associated with COVID-19. In the latter case, SARS-CoV-2 infection could act as a trigger that unmasks an underlying PD phenotype, possibly by stimulating neuroinflammatory and neurodegenerative cascades. In addition, SARS-CoV-2 infection has been demonstrated to significantly worsen motor and non-motor symptoms in people with pre-existing PD [79,80]. Considering the prevalence of post-COVID-19 syndrome [81,82], a multicenter study found that 23 out of 27 PD patients developed post-COVID-19 symptoms, with the most common long term effects of COVID-19 being the deterioration of motor function and the requirement for increased levodopa daily dose, followed by fatigue, cognitive disturbances including brain fog, and sleep disorders [83].

Probably the clinical symptoms most commonly shared between PD and COVID-19 are gustatory and especially olfactory dysfunctions. Indeed, both olfactory and gustatory impairments are among the earliest non-motor PD features [84,85]. Surprisingly, these are common early onset symptoms of COVID-19 and it has been observed that hyposmiaanosmia and dysgeusia could persist long after viral load decline, constituting a key clinical manifestation of the long COVID-19 syndrome [86,87]. Due to lack of evidence regarding the definite CNS infiltration, the olfactory route is discussed as a way for SARS-CoV-2 to gain access to the CNS. Indeed, a postmortem study demonstrated that the highest levels of SARS-CoV-2 RNA and spike protein (S protein) among various brain areas were found in the olfactory mucosal-nervous milieu, as well as in neuroanatomical areas related to the olfactory tract. In this regard, the olfactory mucosa could serve as an "anatomical bridge" for SARS-CoV-2 CNS invasion through axonal transport [88]. Furthermore, angiotensin-converting enzyme 2 (ACE2), an essential cell surface receptor responsible for S protein-mediated entry of SARS-CoV-2, was found to be expressed by epithelial cells of the human olfactory mucosa [89]. The extent of α -syn pathology in other brain regions has been substantially linked with the pathological burden in the olfactory bulb, suggesting that PD pathology extends along olfactory pathways [90]. The Braak hypothesis proposes that LB are initially found in olfactory structures, such as the olfactory bulb, and then they gradually spread towards the brain stem and ultimately to the cerebral cortex, strengthening the scenario that the earliest lesions could develop at non nigral areas [91,92]. Accordingly, Beach and colleagues have demonstrated that the olfactory bulb constitutes a primary affected area in α -synucleinopathies, including PD. In fact, it was suggested that the extent of α -synucleinopathy in the olfactory bulb strongly predicts the neuropathological confirmation of PD and reflects the severity of α -synucleinopathy in other brain regions [93]. Based on these studies, one could hypothesize that the olfactory route might pose a way for SARS-CoV-2 to gain access to the CNS, where it can modify neuropathological pathways pertinent to PD development.

Another common pathology shared between PD and COVID-19 is the deregulation and dysfunction of the gastrointestinal (GI) tract. GI symptoms and intestinal inflammation may emerge years before clinical indications of PD become apparent [94,95]. Specifically, gastrointestinal dysbiosis has been proposed to be involved in PD pathogenesis [96] and the enteric nervous system has been previously identified as a primary region for abnormal α -syn aggregation, which may then spread from the periphery to the CNS [97–99]. Specifically, the dorsal motor nucleus of the vagus nerve (DMV) receives signals from vagal parasympathetic neurons that project to the entire GI system. The DMV is involved in the PD–neuroanatomical pathway, since a monosynaptic nigro–vagal pathway that connects the SNpc to the DMV has been identified in the rat [100]. In postmortem PD studies, the DMV and the vagus nerve itself are among the most frequently afflicted structures [101,102] and they constitute principal areas of LB accumulation, even at the earliest stages of disease development [91]. In vitro research has shown that pathological α -syn may spread from the gut to the brain through the vagus nerve, with DMV being the first area of the brain to be impacted. From there, α -syn can spread to other PD brain regions including the SNpc, resulting in dopaminergic neuron loss and the appearance of the parkinsonian phenotype [103]. Interestingly, the vagus nerve has been proposed as a pathway through which SARS-CoV-2 can retrogradely invade the CNS, thus enhancing its neuroinvasiveness [104,105].

Importantly, other GI manifestations, such as diarrhea, emerged as common clinical symptoms of COVID-19, while SARS-CoV-2 RNA detection in fecal samples may persist post-infection [106]. On top of that, gut microbiota imbalance due to extrapulmonary SARS-CoV-2 infection has also been observed in COVID-19 [107,108]. This warrants further investigation because GI microbiota equilibrium plays an important role in several physiological processes ensuring brain integrity and neurogenesis [109,110]. Taken together, the above observations suggest that SARS-CoV-2 infection could promote PD development and progression through a virus-exerted dysfunction of the GI system.

3.2. Inflammatory and Molecular Overlapping Pathways

Common inflammatory events unraveling during PD development and observed in the acute phase of SARS-CoV-2 infection, as well as after COVID-19 remission, may indicate a link between these two disorders. Virus-mediated sustained or aberrant neuroinflammation could be a decisive pathobiological process for the initiation of a neurodegenerative disease, such as PD, long after recovery from the viral infection [111–113]. Indeed, growing evidence indicates that SARS-CoV-2 induces neuroinflammation [114] through its neurotropic, neuroinvasive, and neurovirulence effects [115,116] or even via immune-mediated pathways [117]. SARS-CoV-2 infection also triggers systemic inflammatory responses and induces cytokine release [118]. Severe COVID-19 is characterized by a cytokine storm syndrome, which is a major cause of mortality [118,119]. Several studies have demonstrated the presence of inflammatory mediators, such as increased levels of pro- and anti-inflammatory interleukins (IL-1, IL-2, IL-6, IL-10) and tumor necrosis factor-alpha (TNF- α) in the serum of COVID-19 patients [120–123]. Interestingly, a small prospective observational study had previously found that high levels of IL-6 were linked to a higher chance of developing PD [124]. Evidently, an exacerbated systemic infection that causes a huge release of inflammatory mediators, including cytokines, chemokines, and antibodies, could lead to increased blood–brain barrier (BBB) permeability [125]. Functional and structural integrity of the BBB is pivotal in maintaining brain homeostasis [126]. A neurovascular unit (NVU) consists of multiple cell types, including brain microvascular endothelial cells (BMVECs), astrocytes, pericytes, microglia, and neurons, connected together with extracellular matrix components, and is a rigorous regulator of BBB permeability [127]. NVU disruption has been previously associated with neurodegenerative diseases [128]. In particular, BMVECs constitute an important component of NVU and are intricately interconnected through tight junction (TJ) proteins. However, inflammation affects BBB integrity and stability mainly through cytokine-induced degradation of TJ proteins [129]. SARS-CoV-2-mediated brain endothelial inflammation, upregulation of inflammatory mediators, and most significantly, disruption of BBB stability, have also been observed in human BMVECs [130]. According to in vitro studies, SARS-CoV-2 was shown to infect human BMVECs and cause a decrease in TJ protein expression [130,131]. Furthermore, incubation of human BMVECs with S protein resulted in enhanced ACE2 expression, thereby facilitating viral entry and inducing neuroinflammation [132].

When BBB becomes impaired, pro-inflammatory cytokines and factors, innate immune cells from the periphery, and SARS-CoV-2 could possibly pass through and infiltrate the CNS. In that case, the CNS professional immune cells, microglia and astrocytes, may also become activated [133,134]. Neuroinflammation is then likely to set in fast, leading to elevated production of cytokines, chemokines, reactive oxygen species (ROS), and secondary

messengers [135]. Microglia, which are highly susceptible to pro-inflammatory stimuli, are concentrated in areas harboring dopaminergic neurons, making them particularly vulnerable to inflammatory mediators [136,137]. Interestingly, the S1 subunit of S protein was found to efficiently trigger neuroinflammation, including microglia activation, release of multiple pro-inflammatory cytokines, and cause behavioral deficits in rats [138]. Consequently, these neuroinflammatory cascades lead to enhanced apoptotic activity, increased ROS levels, mitochondrial dysfunction, and eventually neurodegeneration [139,140].

Finally, cellular senescence is a core homeostatic event that provides yet another, ageand state-dependent substrate for neurodegeneration and the development of diseases like AD and PD [141,142]. Cellular senescence in the aging brain affects both neuronal and non-neuronal cells, and it is characterized by a broad array of interconnected disruptions, such as disruptions in autophagy, bioenergetics, and mitochondrial dynamics, as well as the onset of low-grade inflammation [142]. This cumulative array of dysfunction culminates in the accumulation of proteopathic seeds, including tau, amyloids, and α -syn, and tissue-wide remodeling [141]. It has been shown that SARS-CoV-2 infection induces "immunosenescence" and enhances the senescence-associated secretory phenotype (SASP) in infected tissues, via disruption of host antiviral mechanisms, such as interferon signaling pathways [143–145]. Taken together, all the aforementioned studies strongly indicate that the COVID-19 cytokine storm and innate immunity dysregulation may cause neuroinflammation and, in consequence, neurodegeneration.

Neuropathological findings in postmortem brain tissues from COVID-19 patients further support the involvement of COVID-19-related neuroinflammatory processes in PD development. A postmortem brain study of 43 COVID-19 patients has shown activation of microglia and CNS infiltration by cytotoxic T-lymphocytes, more apparent in the brainstem [146]. Regardless of COVID-19 disease severity, significant inflammatory responses such as astrogliosis, microglia activation, and perivascular T-lymphocyte infiltration were observed postmortem in both white and gray matter of patient brains [147]. Performing single-nucleus RNA sequencing and immunohistochemistry on tissue from a group of individuals who died with COVID-19 and a group of individuals who died from other causes, Yang and colleagues revealed glia transcriptomic changes that indicated a COVID-19-associated activation of inflammatory pathways. The ensuing dysregulation of homeostatic pathways could potentially lead to neurodegeneration [148]. Specifically, microglia and astrocytic subpopulations were enriched by inflammatory genes and deregulated neuroprotective ones that had been previously linked to PD and other human neurodegenerative diseases, such as the glial fibrillary acidic protein (GFAP), the interferoninduced transmembrane protein-3 (IFITM3), and others [149,150].

Another mechanism that may contribute to PD pathogenesis involves the renin– angiotensin system and ACE2, which are implicated in the pathophysiology of COVID-19 and may play a role in neuroinflammation-mediated neurodegeneration in PD [151,152]. ACE2 is highly expressed in several brain areas [153], including striatum [154], the substantia nigra, the olfactory bulb [155], and the brain endothelium [130,156,157]. Induced pluripotent stem cells (IPCS) derived from midbrain dopaminergic neurons were shown to be vulnerable to SARS-CoV-2 infection in vitro [158], unravelling the potentially direct neurotrophic effect of SARS-CoV-2 in strategic PD areas. Furthermore, SARS-CoV-2-induced Toll-like receptor (TLR) overactivation led to ACE2 upregulation and promoted the neurotrophic and neuroinflammatory outcomes of SARS-CoV-2 infection [159]. TLRs belong to the family of innate immune receptors and play an important role in the activation of innate immunity, including activation of glial cells. TLR-mediated stimulation of intracellular signaling pathways culminates in the release of proinflammatory mediators such as IL-6, IL-1, TNF-a, and nuclear factor-*kB* (NF-*kB*) [160]. Protein-to-protein interaction between SARS-CoV-2 S protein and TLR-4 has been previously recorded [161]. SARS-CoV-2-mediated overactivation of the TLRs may lead to hyperinflammation, ACE2 upregulation and microglia switching from the neuroprotective to the neurotoxic phenotype [159,162]. In

sequel, sustained gliosis and prolonged neuroinflammation could lead to α -syn aggregation and finally loss of dopaminergic neurons in the SNpc [112].

Aside from neuroinflammation, dysregulation of several homeostatic molecular pathways has been identified in PD onset and development. These alterations also occur during host-virus interactions as the virus attempts to direct critical cellular infrastructure towards completion of its own lifecycle. SARS-CoV-2 viral proteins were shown to post-translationally reconfigure the biological function of 24 host proteins expressed in lung. The latter act as perturbators and interact with 44 CNS proteins that are known to be implicated in PD pathogenesis [163]. Specifically, SARS-CoV-2-mediated deregulation of Rab7a and nucleoporin-62 (NUP62) could be strongly involved in PD pathogenesis, because Rab7 lysosomal protein decreases α -syn aggregation and associated neurotoxicity [164], while NUP62 is crucial for autophagosome development [165]. Furthermore, SARS-CoV-2 proteins can interact and bind to a variety of human protein trafficking molecules. Protein trafficking, translation, transcription, and ubiquitination regulation are all coordinated by these biomolecules, leading to neuroprotection, protection of BBB integrity, and neurogenesis [166]. A recent study demonstrated a direct interaction between SARS-CoV-2 nucleocapsid protein (N-protein) and α -syn, which led to the aggregation of the latter into amyloid fibrils, a highly pathogenic form of the protein, linked to PD. Co-administration of SARS-CoV-2 N protein and α -syn to a PD cell model resulted in twice the neuron loss due to neurotoxicity compared to control cells treated with α -syn alone [167].

Other important cellular processes implicated in the loss of dopaminergic neurons in SNpc are thought to be oxidative stress and mitochondrial dysfunction, endoplasmic reticulum stress, and the impairment of protein degradation systems [168–170].

A key molecular factor in PD development and progression is mitochondrial dysfunction and oxidative stress [171,172]. An imbalance between ROS generation and cellular antioxidant activity leads to oxidative stress and ROS can further affect mitochondria, attenuating adenosine triphosphate (ATP) production as well as causing damage to mitochondrial DNA [173]. In addition to causing direct cellular damage, oxidative stress can speed up neuron degeneration by inducing inflammatory or apoptotic pathways, such as NF- κ B or caspase activation [174]. In PD studies, mitochondrial dysfunction may occur months before the onset of striatal dopaminergic neuron loss [175] and PD patients have been well documented to possess reduced or deficient mitochondrial complex I activity in the SNpc [176,177]. In mice, accumulation of wild-type α -syn in dopaminergic neurons reduced mitochondrial complex I activity and elevated ROS production, leading to cell death [178]. SARS-CoV-2 seems to interact with and manipulate mitochondria in order to hijack and evade mitochondria-mediated immune response for its own replication and survival [179,180]. In this effort, SARS-CoV-2 may induce mitochondrial impairment [181,182], mitochondria-mediated oxidative stress, and mitochondrial damage through mitochondrial membrane depolarization, mitochondrial permeability transition pore opening, and enhanced ROS release [183–185]. Furthermore, the virus prevents mitophagy by blocking the binding of p62 and microtubule-associated protein 1A/1B-light chain 3 (LC3), thereby hindering viral RNA breakdown [185].

Finally, mitochondria aid the antiviral immune response by allowing release of proinflammatory cytokines [186]. ACE2 has been suggested to regulate mitochondrial function [187]. Its expression is decreased when SARS-CoV-2 S protein binds to ACE2 on microglia cells, causing ATP reduction and activation of the ROS-generating enzyme NADPH oxidase [188]. The ensuing increase in ROS production and oxygen consumption may lead to neuroinflammation and loss of neighbor dopaminergic neurons [189].

Endoplasmic reticulum (ER) stress has been linked to neurodegenerative diseases, including PD [190,191]. ER homeostasis disruption and extended ER stress lead to misfolded protein accumulation and may stimulate particular proapoptotic pathways through the activation of the transcription factor C/EBP homologous protein (CHOP) and cysteine proteases caspase-4/12 [192,193]. Growing evidence suggests that SARS-CoV-2 proteins interact with the ER compartment and may induce ER stress [194,195]. SARS-CoV-2 open reading frame 8 (ORF8) is capable of inducing ER stress by triggering the activating transcription factor 6 (ATF6) and inositol-requiring enzymes 1 (IRE1) branches of the ER stress pathway [196], potentially leading to α -syn accumulation [197]. Aside from initiating apoptotic pathways, ER stress is a powerful stimulator of NF- κ B activation and inflammatory gene transcription [198,199]. SARS-CoV-2 also appears to activate NF- κ B, causing inflammation, possibly through ER stress or via interaction with the non-structural protein Nsp5 [200]. Notably, NF- κ B is a crucial transcription factor that regulates inflammation and dopaminergic neurons loss in PD patients [201]. Hence, deregulation of this signaling pathway has been linked to PD onset and pathology [202] by favoring α -syn accumulation, aggregation, and spreading, oxidative stress-induced neuron apoptosis, neuroinflammation, and dopaminergic neuron loss [139,203,204].

When aggregation and deposition of misfolded α -syn elicit dopaminergic neuron loss, protein degradation systems come to the rescue. The ubiquitin-proteasome system (UPS) and the autophagy–lysosomal pathway (ALP) are important proteolytic systems in neurons and critical for refolding or elimination of misfolded proteins; therefore, they play a significant role in cellular homeostasis [205]. Impairment or even failure of these systems may contribute to PD pathogenesis and progression [21,206]. SARS-CoV-2 virulent components, such as ORF proteins, seem to modify autophagy formation and function, leading to SARS-CoV-2-induced autophagy disruption and potentially neuron damage [207,208]. Specifically, ORF3a was shown to impede autophagosome-lysosome (A-L) fusion and ALP formation by interacting directly with the VPS39 subunit of the homotypic fusion and protein sorting (HOPS) complex. ORF3a further damages lysosomes and impairs their function. Remarkably, this feature of HOPS-VPS39-mediated A-L fusion inhibition appears to be unique to SARS-CoV-2, since the quite similar ORF3a of SARS-CoV was ineffective in inhibiting A-L fusion [209]. Furthermore, another study found that although ORF7a protein stimulates autophagy, it also limits A-L fusion progression by downregulating the SNAP29 protein via caspase 3 (CASP3) activation, providing a mechanism through which SARS-CoV-2 uses the autophagic system to facilitate its own propagation [210]. Interestingly, a SARS-CoV-2 papain-like protease has been identified to directly cleave serine/threonine unc-51-like kinase (ULK1) and prevent ULK1-ATG13 complex formation [211]. ULK1 is an upstream autophagy orchestrator, which phosphorylates key regulatory proteins in autophagosome formation [212]. In this regard, ULK1 cleavage is expected to completely inhibit the ALP function, due to lack of autophagosome formation. Evidently, autophagy is crucially involved in the regulation of the antiviral immune response. The striking correlation between SARS-CoV-2-induced aberrant inflammation and the observed autophagy defects [213] suggests that the virus-induced cytokine storm could be mediated by the failure of autophagy mechanisms to maintain cellular homeostasis.

Overall, SARS-CoV-2 seems to interfere and disrupt several host cellular and molecular pathways involved in proper neuronal functions, potentially promoting PD pathogenesis. A summary of these overlaps is depicted in (Figure 1).



Figure 1. A schematic diagram of SARS-CoV-2 infection and Parkinson's disease (PD) development overlaps listing shared clinical manifestations, common neuroinflammatory events, and mutually activated molecular pathways.

4. The Diverse Roles of Exosomes in Viral Infection and Neurogenerative Disease

4.1. Biogenesis of Exosomes

Exosomes are one of three main subtypes of extracellular vesicles (EVs) (microvesicles, exosomes, and apoptotic bodies) secreted by the cells [214]. They are secreted from the majority of cell types and can also be isolated from body fluids, such as saliva, plasma, serum, urine, CSF, etc. [215,216]. Exosomes contain cell-specific cargos of proteins, lipids, DNAs, and coding/non-coding RNAs from the donor cells that can be preferentially delivered to targeted recipient cells. They represent a recently discovered mode of intercellular communication that may play a major role in many cellular processes in both physiological and pathological conditions [217,218].

Exosomes are EVs [219] with a cup-shaped appearance in transmission electron microscopy and size ranging from 30 to 150 nm [220,221]. Exosomes emerge from the endosomal compartment following a series of events, starting with the inward budding of the plasma membrane that gives rise to the early endosome [222]. Then, budding and modification of the limiting membrane of endosomes leads to formation of intraluminal vesicles (ILVs), whose accumulation produces late endosomes or large multivesicular bodies (MVBs) [221,223]. MVBs can either fuse with the plasma membrane and release ILVs as exosomes into the extracellular space, or with lysosomes, where ILV cargo will be degraded [224]. Biogenesis of ILVs, trafficking of MVBs, and secretion of exosomes are mainly regulated by endosomal sorting complexes required for transport (ESCRT) [225]. The ESCRT machinery consists of a set of cytosolic protein complexes that become attracted to endosomes by membrane proteins usually tagged with ubiquitin [226]. This multi-subunit protein system is essential for membrane remodeling and cargo sorting of MVBs [227], although some studies found that ILVs are also formed in the absence of ESCRT machinery (ESCRT-independent pathway), with the enzyme sphingomyelinase and tetraspanin proteins, such as CD9, CD63, and CD81, playing a pivotal role [228]. When exosomes reach the target cell, they can be internalized through specific endocytotic mechanisms, fuse directly with the plasma membrane or bind to cellular surface receptors [229–231].

Exosomal surface indicators, such as the tetraspanins CD9, CD63, and CD81, ALG 2-interacting protein X (ALIX), tumor susceptibility gene 101 protein (TSG101), and ES-CRT proteins, have all been identified and used to characterize exosomes in vitro and in vivo [31]. Because of their varied cellular origin, exosomal biomolecular composition is highly heterogeneous, bearing characteristics from both surface proteins and the cargo of their donor cells [223,232]. For example, neuron-derived exosomes are characterized

by the presence of L1 cell adhesion molecule (L1CAM), a surface exosomal marker highly expressed in neurons [233]. Furthermore, their biocompatibility and bi-layered lipid structure, which shield cargo from degradation, reduce immunogenicity and enable exosomes to pass through major biological membranes, including the BBB [219]. Considering that exosomes can cross the BBB and act as fingerprints of their cellular originators, they could be used as CNS biomarkers that can be isolated and recovered from the periphery, with minimally invasive techniques [234].

4.2. Impact of Exosomes in PD Pathogenesis

The usage of exosomes for the removal of accumulated, misfolded proteins increases under pathological conditions, particularly in proteinopathies [235,236]. Specifically, when other cellular clearance systems, such as the proteasome and ALP, fail to eliminate aggregated amyloidogenic proteins, exosomes come to the rescue [237]. Thus, exosomes may have a prominent role in PD, as they represent a potential spreading pathway for misfolded proteins, thereby contributing to pathogenesis and also to disease diagnosis through cargo analysis [238,239].

The "prion-like" mode of α -syn spread lies at the heart of PD pathogenesis, as the molecular mechanisms leading to α -syn seeding and aggregation remain unknown [240]. Exosomes, as key intercellular mediators in the CNS, may provide a valuable vehicle for the transmission of α -syn [32,236]. Unlike other cell-to-cell transmission mechanisms, such as non-classical exocytosis or transport via nanotubules, exosomes can mediate α -syn transfer over longer distances [241]. The oligometric form of α -syn is thought to be the toxic form causing neuronal death. Danzer and colleagues identified the presence of oligomeric α -syn in exosomes from continuous cell lines and primary cells and demonstrated that exosomal α -syn is more easily taken up by recipient cells than the free oligometric form of protein [242]. Other researchers used various in vitro and ex vivo cellular systems to verify the presence of α -syn in exosomes [243,244]. Considering that loss of dopaminergic neurons is associated with PD progression and worsening of motor symptoms, exosomes generated by α -syn-treated microglia exhibited a considerably higher neuron apoptosis rate than control exosomes, in an in vitro experiment [245]. Exosomes isolated from patients with PD can induce the oligomerization of soluble α -syn in recipient cells, increasing neurotoxicity and speeding up α -syn aggregate formation [246]. Additionally, serum exosomes derived from PD patients contain α -syn, which can induce behavioral and pathological features of PD in mice [247]. Taken together, data from the abovementioned studies suggest that by regulating uptake and transfer of abnormal α -syn to nearby cells, exosomes are key regulators of PD pathogenesis and its spatiotemporal evolution [248,249].

Aside from trafficking α -syn, exosomes interfere in intercellular inflammatory pathways, enhancing the possibility of PD outcomes [250]. There is abundant evidence that neuroinflammation plays a vital role in PD onset and progression [23]. A sound inflammatory response is essential for tissue repair and misfolded protein breakdown, but an excessive and delayed inflammatory response can lead to a deregulated neuroinflammatory cycle [251]. Microglia are considered to be the resident brain macrophages. By phagocytosing dead cells and helping with the removal of misfolded protein aggregates from the brain, they play an important role in the removal of extracellular α -syn species, including exosomecontained protein [252]. At the same time, microglia could be activated by exosomal α -syn, and elicit an immunological response with the release of pro-inflammatory cytokines, resulting in dopaminergic neuron death [253]. In addition to their well-established role in neuroinflammation, microglia appear to be involved in intercellular spreading of neurotoxic α -syn [254]. Furthermore, exogenous introduction of human α -syn preformed fibrils (PFFs) into primary microglial cell cultures stimulates the release of α -syn-containing exosomes, which were fully capable of inducing protein aggregation in recipient neurons [255]. This release of α -syn following PFF treatment could be an effort to monitor and control intracellular levels of misfolded protein, possibly attributed to the deregulation of the ALP pathway in microglia [255]. Autophagic activity impairment and lysosome dysfunction

11 of 29

have been previously correlated to increased release of exosomes from neuronal cells and to exosomes-mediated α -syn spread and transmission [21,237,256].

Recent advances concerning immunosenescence studied its dissemination on tissue level, via exosomes. Specifically, cell-level stressors may induce a pro-inflammatory pheno-typic shift in afflicted cells, and subsequently this shift may be communicated via specific exosomal cargo in a para- and juxtracrine manner [257]. Notably, interferon-responsive genes and proteins, such as the IFITM3 protein, may be loaded during such transmissions, representing a tissue-level signal of inflammation [258]. Depending on the cargo and cell of origin, exosomes may conversely ameliorate the SASP [259], thereby abating inflammation [260,261].

4.3. Exosomes as Biomarkers in PD Diagnosis

To date, the diagnosis of PD depends on the clinical manifestations of the disease and it is determined by the presence of motor symptoms [2]. PD diagnosis may be difficult, especially in early pre-symptomatic stages, due to the absence of motor symptoms [262]. Hence, a low clinical diagnostic accuracy rate in the preclinical phase has been reported [263]. The usage of exosomal cargo as a potential "biomarker" or "early indicator" of PD pathology and progression has piqued great interest. Notably, exosomal α -syn has been proposed as a potential biomarker for PD in multiple studies [238,239,246,264]. Shi and colleagues found that CNS-derived exosomal α -syn was considerably higher in PD patients than in controls and it had a significant relationship with disease severity [238]. Similarly, a longitudinal investigation revealed that α -syn levels in neuronal exosomes were significantly higher in patients with early-stage PD compared to control groups, and that higher α -syn levels were linked to the progression of motor impairment [264]. Another study found that levels of CNS-derived exosomal α -syn were lower in early-stage PD patients compared to individuals with essential tremor and the control group [239]. In salivary EVs from PD patients, it was demonstrated that absolute levels of α -syn oligomers and the ratio of α -syn oligomers over total α -syn were increased compared to healthy controls, indicating that they could be used as diagnostic biomarkers [265]. Mean levels of neuron-derived exosomal α -syn have been proposed to distinguish PD from other cases of atypical parkinsonism and neurodegenerative diseases, as a twofold increase was observed in patients with preclinical and established PD compared to the other etiologies [266].

As far as other neurospecific exosomal cargo proteins are concerned, it has been shown that CNS-derived exosomal tau levels were considerably higher in PD patients compared to controls, and notably but not significantly increased compared to those of AD patients [267]. Furthermore, levels of clusterin, apolipoprotein A1 (apoA1), and the complement C1r subcomponent were significantly lower in PD patients at Hoehn and Yar stages II and III (a scale for assessing the functional impairment caused by PD) compared to healthy controls [268]. Conversely, neuron-derived exosomal protein deglycase DJ-1 was higher in PD patients compared to controls [269].

In addition to misfolded proteins, exosomes serve as a conduit for transport of other RNA species such as microRNA (miRNA). Exosomal miRNAs regulate gene expression in recipient cells at a post-transcriptional level, thereby interfering with several physiological processes in the CNS, including homeostasis, neuron growth, cell migration, and brain endogenous immunity [270]. Mounting evidence has proposed a pivotal role for exosomal miRNAs in neurodegenerative diseases, including PD [271]. Firstly, they can inhibit protein synthesis after cellular uptake of exosomes [272]. Secondly, they can directly bind to TLRs and trigger neuroinflammation [273], and thirdly, they can induce oxidative stress pathways leading to neurotoxicity [274]. Given the diverse roles of miRNAs in PD pathogenesis, several studies have focused on their diagnostic value. Gui and colleagues studied the alterations in the miRNA profiles of CSF-derived exosomes from PD patients, finding that 16 exosomal miRNAs were elevated and 11 miRNAs were downregulated in PD in comparison with the control group. Characteristically, miR-1 and miR-19b-3p were identified to be considerably decreased in PD-CSF exosomes. MiR-153, miR-409-3p, miR-

10a-5p, and let-7g-3p, on the other hand, were increased in that patient group [275]. Another study in serum exosomes from PD patients observed a drop in miR-19b expression and an elevation in miR-195/miR-24 expression in PD patients compared to healthy controls [276]. Finally, exosomal miRNAs were successfully used to differentially diagnose PD stages from healthy controls, showing that those miRNAs could serve as specific biomarkers both for early PD detection and PD progression [277].

4.4. Exosomes and SARS-CoV-2 Infection

Exosomes play a critical role in viral infections [278]. Exosomes and viruses share structural and physicochemical features, such as size, shape, biochemical composition, and biomolecule transportation pathways within cells [279,280]. Thus, exosomes constitute a new frontier in the realm of viral infections, including SARS-CoV-2.

A proposed way of viral spreading is via exosomes that contain viral particles or components. In the case of respiratory viruses, several studies showed that viral antigens are present in circulating exosomes recovered from lung transplant recipients infected with rhinovirus and respiratory syncytial virus [281]. In SARS-CoV-2 infection, exosomal cargo contains viral proteins or peptide fragments, such as the N and S proteins [282,283], whose presence has been linked to enhanced viral propagation, host immune reaction, and induction of a cytokine storm [284]. Barberis and colleagues identified for the first time viral genetic material in the exosomal cargo of COVID-19 patients, suggesting that SARS-CoV-2 may also be using the endocytic pathway to spread [285].

The "Trojan exosome hypothesis", in which retroviruses employ EVs to penetrate host cells, boost viral propagation, and elude the immune response, was introduced by Gould and colleagues [286] and was later supported by several reports [40]. In SARS-CoV-2 infection, the virus uses multiple steps to achieve entry into the host cell, including ACE2-mediated receptor binding and transmembrane serine protease-2 (TMPRSS2)-mediated intracellular cleavage [287]. Recent data revealed that EVs carry and transfer ACE2 between different types of cells [288]. This led to the development of a competitive inhibitory therapy against SARS-CoV-2, in which ACE2-expressing EVs compete for the SARS-CoV-2 S protein S1 domain, limiting viral infection [289].

Exosomes released during viral infection contain inflammatory markers that cause a strong inflammatory response, acting as pathogen-related molecular patterns, thereby enhancing pathogenicity [290]. For example, exosomal CD9 has been shown to be involved in the route for EV-mediated viral transmission, by speeding up lentiviral infection and improving transduction effectiveness in B- and T-lymphocytes [291]. In addition, CD9 cooperates with TMPRSS2 to cleave viral fusion glycoproteins, thus facilitating the entry of coronaviruses, such as MERS-CoV, into lung cells [292]. These findings suggest that CD9 and other exosomal tetraspanins could facilitate SARS-CoV-2 infection. Proteomic analysis of plasma-derived exosomal cargo from COVID-19 patients revealed that circulating exosomal proteins are strongly correlated with pathological procedures leading to COVID-19 tissue damage, such as immune hyperactivation, coagulopathy induction, and inflammation [285]. Monosialodihexosyl ganglioside (GM3)-enriched exosomes are positively connected with disease severity in COVID-19 cases [293].

5. SARS-CoV-2-Related Exosomal Cargo and Its Potential Roles in Post-COVID-19 Parkinsonism and PD Pathogenesis

Given the established role of exosomes both in pathophysiological neuronal processes, and PD development and progression [294,295], as well as their emerging significance in SARS-CoV-2 infection and propagation [285], we believe that cascading from SARS-CoV-2 infection to post-COVID-19 parkinsonism and, possibly PD onset via exosomal cargo, should be at the research forefront. The putative roles of SARS-CoV-2-related exosomal cargos in the development of viral parkinsonism and/or PD pathogenesis are outlined and described in the next two paragraphs.

5.1. Exosomal Cargo and Induction of Post-COVID-19 Neuroinflammation

Following COVID-19 recovery and viral clearance, exosomes could be at the center of neuroinflammatory crossroads. Experimental studies in other several systemic inflammatory conditions, such as obesity [296] and rheumatoid arthritis [297], have outlined a strong relationship between peripheral systemic inflammation and neuroinflammation [298,299]. Exosomes could operate as physical bridges between these two conditions since they can traverse the BBB. In vivo proof of exosomes acting as neuroinflammatory mediators under systemic inflammation conditions has recently been obtained. Specifically, in a mouse model that received serum-derived exosomes from lipopolysaccharide (LPS)-challenged mice, brain gliosis, CNS expression of pro-inflammatory cytokine mRNA and inflammation-associated miR-155 were all increased [300]. In addition, exosomes generated by peripheral immune cells, such as activated monocytes and macrophages, were shown to be taken up by neurons and astrocytes, resulting in pathological cargo dissemination and neurotoxicity [301].

Serum exosomes from PD patients revealed increasing levels of IL-1 and TNF- α inflammatory mediators in comparison with the control group, while intravenous or intrastriatal administration of PD exosomes to mice induced α -syn aggregation, microglia activation, and neurodegeneration of dopaminergic neurons, leading to worsening of motor symptoms [247]. Conversely, exosomes containing pro-inflammatory cytokines, such as IL-1, can effectively be shed by glial cells [302]. This glia-derived insidious exosomal cargo can spread to neurons, contributing to a vicious cycle of neuroinflammation and neurodegeneration [245], a phenomenon further associated with older age [303].

The presence of inflammatory mediators in exosomes derived from SARS-CoV-2 infected cells could potentially enhance the model of neuroinflammation and ensuing neurodegeneration via peripheral systemic inflammation, possibly promoting a cellular milieu that favors PD development and progression mechanisms. Exosomal analysis from COVID-19 patients revealed high levels of tenascin-C (TNC) and fibrinogen- β (FGB) compared to controls. Both TNC and FGB induce release of pro-inflammatory cytokines via NF- κ B signaling, leading to the presence of TNF- α , IL-6, and chemokine CCL5 upon exposure of hepatocytes to exosomes from COVID-19 patients. In this regard, a potential "window" of inflammatory insults to distant tissues should be examined [304].

Current knowledge so far suggests that the SARS-CoV-2 S protein seems to play a central role in exosome-mediated regulation of neuroinflammatory events pertinent to neurodegeneration. Thus, S protein or S-derived fragments were discovered in plasma exosomes isolated from COVID-19 patients, with an increased exosomal presence in clinical cases with moderate rather than severe disease. Multiomics exosomal analysis identified several molecules involved in immune responses, inflammation, and activation of both coagulation and complement pathways in infected patients compared to the control group of healthy subjects [284].

Furthermore, an in vitro study demonstrated that ectopic expression of SARS-CoV-2 S protein in HEK-293T cells generated a large number of exosomes highly loaded with miR-148a and miR-590. These exosomal miRNAs decreased gene expression of ubiquitin specific peptidase 33 (USP33), a deubiquitinase enzyme (DUBs)-stabilizer of its target protein, and of interferon regulatory factor 9(IRF9). They also deregulated the USP33-IRF9 network following their internalization in human microglia cells. IRF9 had been previously identified as a protective functional protein in CNS homeostasis, and its absence could result in severe neurological damage in glial cultured cells due to interferon (IFN)-α-mediated overexpression of IFN-γ-like genes [305]. Reduced microglial USP and IRF9 levels effectively induced the production of important inflammatory gene pathways such as TNF-β, NF-κB, and IFN-β, culminating in neuroinflammatory cascade activation [306]. Apart from that, exosomes recovered from plasma of COVID-19 patients revealed the presence of S protein-derived fragments fully capable of inducing the immune system response. Evidently, exosomes from patients with mild disease severity exhibited higher amounts of MHC class II-antigen-presenting protein able to interact with CD4+ T-cells and

boost their proliferation and activation [284]. MHC II overexpression, CD4 activation, and invasion of the CNS can all cause IFN-mediated phagocytic conversion of brain myeloid cells [307]. The ensuing neuroinflammation and dopaminergic neuron loss in the SNpc could conceivably lead to a PD phenotype [308,309].

Neuroinflammation mediated by host regulatory factors may also be conferred by SARS-CoV-2-manipulated exosomes. High-mobility group box 1 (HMGB1) is a nuclear protein involved in several CNS procedures such as inflammation, apoptosis, and autophagy regulation [310]. Elevated levels of HMGB1 in serum and CSF from PD patients have been observed [311]. Notably, inhibition of HMGB1 has been shown to reduce microglia-mediated neuroinflammation, neuron dopaminergic loss, and progression of PD pathology in PD animal models [311,312]. Neurofilament light chain (NfL) levels are a protein-indicator of axonal damage and serve as a biomarker for several neurodegenerative diseases, including PD [313,314]. At the same time, it has been suggested that NfL levels may potentially reflect neuroinflammatory processes leading to neurodegeneration in the early stages of multiple sclerosis development [315]. Analysis of the exosomal cargo of neuron-derived EVs (NDEV) isolated from post-COVID 19 patients with or without neurological symptoms showed high levels of HMGB1 and NfL compared to the control group, thereby implicating SARS-CoV-2 infection in the regulation of the two pro-PD development factors [316].

5.2. The Periphery-Exosomes-CNS Axis as a Promoter of Post-COVID-19 Parkinsonism and PD Development

Loaded with SARS-CoV-2 components and RNA, as well as virally-induced neuroregulatory molecules, exosomes are fully capable of accessing hard-to-reach neuroanatomical areas, such as the olfactory bulb [88], the hypothalamus [317], the DMV, and the brainstem [317–319]. A possible route allowing access to exosomes traveling long distances from peripheral tissues that are prime sites of infection, such as the intestine and the lungs, to the brain could be through retrograde axonal transport from peripheral nerves [320,321]. In that case, SARS-CoV-2-related exosomes could end up disrupting normal homeostatic molecular mechanisms in brain areas that have been previously associated with PD pathogenesis [322–324]. Indeed, a COVID-19 postmortem study detected major neurological damage, but only low levels of SARS-CoV-2 RNA in the brains of expired patients [325]. Furthermore, cortical accumulation of total α -syn was observed following viral eradication in a SARS-CoV-2 intranasally-infected hamster model without any indication of inflammation and neurodegeneration [326]. Extending the Braak hypothesis, one could argue that any neurological sequelae and neuropathological outcomes observed in COVID-19 survivors may emerge both directly, due to virus-exerted effects, and indirectly, through molecular and neuroinflammatory mediators, carried by SARS-CoV-2-related exosomes remaining in circulation even after elimination of the virus.

The neurological consequences of SARS-CoV-2 infection, according to Ahmed and colleagues, could be attributed, at least in part, to exosomal mRNA and transcriptional factors (Tfs) carried from the lungs to the brain areas [327]. These exosomal Tfs have the ability to regulate cellular gene expression transcriptionally and induce neuronal alterations consistent with imminent neurodegeneration. Among 19 exosomal Tfs found overexpressed during the acute phase of SARS-CoV-2 infection, BCL3, JUND, MXD1, IRF2, IRF9, and STAT1 were observed to activate genes associated with PD pathogenesis in strategic areas of the brain, such as the medial and lateral substantia nigra and the superior frontal gyrus region. These genes are implicated in a variety of physiological activities, including signal transduction, neuron death, and immunological surveillance. Evidently, their Tf-mediated dysregulation could contribute to neurodegeneration and PD pathology. For example, STAT1 triggers microglia activation and dopaminergic neurons' autophagy under hypoxia, including COVID-19 manifested hypoxia [328–330].

Exosomes may be further implicated in the association between SARS-CoV-2 and PD via the transfer of protein expression regulators from the periphery, through the BBB and

into the CNS. It has been suggested that such factors could interact with proteins that are highly expressed in the CNS and are linked to PD. A relevant study demonstrated that 24 host lung proteins were subjected to post-translational modifications by SARS-CoV-2 viral proteins. Then, they were taken up and transported out of the lungs into the CNS by exosomes, leading to local disruption of protein–protein interactions [163].

Finally, recent studies have verified the presence of SARS-CoV-2 viral proteins in brain-derived exosomes, potentially enhancing their role in SARS-CoV-2 propagation and pathogenicity. Indeed, cargo profiling of neuron-derived EVs (NDEV) and astrocyte-derived EVs (ADEV) recovered from the plasma of COVID-19 patients revealed significantly higher levels of critical SARS-CoV-2 S1 and N proteins, in all COVID-19 affected subgroups compared to controls. Notably, mean ADEV and NDEV levels of N protein could be used to distinguish the group of patients who developed long COVID-19 with neuropsychiatric manifestations from the long COVID-19 group without such complications and the recovered COVID-19 patients without long COVID-19 [283]. Furthermore, SARS-CoV-2 spike-derived fragments were found to be efficiently exhibited in exosomes from recovered patients who had previously suffered from both mild and severe COVID-19 [284].

In vitro investigations have demonstrated that DMV neurons are vulnerable to oxidative stress and that oxidative stress enhances intercellular α -syn propagation [331]. SARS-CoV-2 could exploit inflammatory exosomal cargo [306] to induce oxidative stress in the DMV, facilitate α -syn aggregation, and eventually promote post-COVID-19 parkinsonism through SARS-CoV-2 S and N proteins. This hypothesis could be supported by the fact that both viral proteins have been shown to increase total α -syn and phosphorylation at Ser129 (pS129) levels [332], speed up the ability of endogenous α -syn to form amyloid fibrils [167], and ultimately induce LB-like pathology [332].

Collectively, it is possible that the exosomal presence of these viral proteins illuminates connecting routes linking COVID-19 to PD. Given that SARS-CoV-2 viral components persist in exosomes during the acute and potentially the post-COVID-19 phase, one could reasonably hypothesize that the COVID-19-related exosomal cargo could act as a neurode-generative promoter and probable elicitor of parkinsonism manifestation.

6. Conclusions

Although the role of viruses in PD pathogenesis is still debated, various studies have found a link between viruses and parkinsonism, suggesting that they may operate as an initiating trigger of primary PD or secondary parkinsonism. The outbreak of the COVID-19 pandemic led to the realization that elimination of the virus after recovery does not always signal the end of the disease, as many patients are burdened with post-COVID-19 manifestations. One of the great concerns of the medical community at this point is the likelihood that SARS-CoV-2 infection could lead to parkinsonism, a notion strongly supported by the PD-like symptoms observed in some patients during the acute or post-COVID-19 phase. Extending the hypothesis of post-COVID-19-induced parkinsonian phenotype, we present herein clinical, inflammatory, and molecular overlaps that have started to emerge and constitute a neurobiological connective network between these two diseases. Exosomes are key regulators of intercellular communication and have been shown to play a crucial role in neurodegenerative diseases. SARS-CoV-2 manipulates exosomes, altering their cargo and, as a result, their function, so that they may serve as a vehicle for viral spread. In doing so, these SARS-CoV-2-related exosomes may efficiently transport SARS-CoV-2 genetic material and viral proteins from the periphery, being the gut or lungs, or other tissues, in the CNS via BBB crossing. SARS-CoV-2 related exosomes, in particular, can potentially transmit SARS-CoV-2 fragments, transcriptional factors, and inflammatory mediators to brain cells, resulting in prolonged neuroinflammation and α -syn aggregation, which collectively contribute to PD development or a possible deterioration in people with genetic predisposition towards PD. Visualization of the hypothetical role of SARS-CoV-2related exosomes and their cargo in PD pathogenesis is depicted in (Figure 2). In conclusion, we postulate in this review that cargo analysis of SARS-CoV-2-related exosomes, especially

brain-derived ones, could serve as a compass for delineating underlying virus-mediated pro-PD development mechanisms and for detecting the much-dreaded post-COVID-19 parkinsonism storm. To this end, experimental and clinical studies will be conducted to validate our hypothesis.



Figure 2. A hypothetical quasi-infectious model of CNS proteopathic seeding, with SARS-CoV-2 as the model virus. At step 1, SARS-CoV-2 neuroinvasion can occur either as a primary event by infecting neurons, or following infection of non-neuronal cells, such as brain endothelial cells, olfactory epithelial cells, or cells from peripheral infected tissues. Successful infection either of non-neuronal cells (2) or neurons (3) could lead to the production of exosomes that could be transmitted transynaptically (3), or intercellularly (4). The quasi-infectious concept indicates that the exosomal cargo is pathogenic and may be enhanced by the presence of viral components (5). SARS-CoV-2 S and N proteins could potentiate the formation of amyloid fibrils by endogenous α -syn in recipient cells. At the same time, exosomes could transmit α -syn to other brain cells in a "prion-like" mode. Exosomal immunomodulatory molecules could enhance neuroinflammatory processes in both neuronal and glia cells, while transcriptional regulators and miRNAs might activate intracellular signaling pathways and regulate gene transcription pertinent to neuroinflammatory phenotype turnover could enhance neuroinflammation further, resulting in enhanced neurodegeneration.

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