Review

Bacterial Metabolites Mirror Altered Gut Microbiota Composition in Patients with Parkinson’s Disease

Sebastiaan Pieter van Kessel and Sahar El Aidy∗
Department of Molecular Immunology and Microbiology, Groningen Biomolecular Sciences and Biotechnology Institute (GBB), University of Groningen, Groningen, The Netherlands

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Abstract. Increasing evidence is supporting the hypothesis of α-synuclein pathology spreading from the gut to the brain although the exact etiology of Parkinson’s disease (PD) is unknown. Furthermore, it has been proposed that inflammation, via the gastrointestinal tract, potentially through infections, may contribute to α-synuclein pathogenesis, and thus to the risk of developing PD. Recently, many studies have shown that PD patients have an altered microbiota composition compared to healthy controls. Inflammation in the gut might drive microbiota alterations or vice versa. Many studies focused on the detection of biomarkers of the etiology, onset, or progression of PD however also report metabolites from bacterial origin. These metabolites might reflect the bacterial composition and as well play an important role in immune homeostasis, ultimately affecting the progression of PD. Besides the bacterial metabolites, pharmacological treatment of PD might play a crucial role during the progression and thus treatment of the disease on the immune system. This review aims to establish a link between the microbial composition with the observed alterations of bacterial metabolites and their impact on the immune system, which could have influential effect in onset, progression and etiology of PD.

Keywords: Microbiota composition, bacterial metabolites, immune modulators, Parkinson’s disease, levodopa, dopamine

INTRODUCTION

Parkinson’s disease (PD) is the second-most occurring neurodegenerative disorder worldwide [1]. The prevalence of PD increases with age and peaks at 1.5 % between 85 years and 89 years of age and 6.1-6.2 million individuals were diagnosed with PD globally in 2015-2016 [1, 2]. The main feature observed in PD patients is the aggregation of α-synuclein in Lewy bodies and loss of dopaminergic neurons in the substantia nigra pars compacta [3]. It has been postulated that α-synuclein pathology spreads out from the enteric nervous system of the gastrointestinal tract to the central nervous system in the brain [4]. Which is in agreement with the detection of α-synuclein aggregates in colonic tissue and appendix prior to the onset of PD [5, 6]. Recently, it has been shown that pathogenic α-synuclein aggregates spread from the gut to the brain in a mouse model, supporting Braak’s hypothesis of the etiology of idiopathic PD [7]. Furthermore, increasing evidence supports the involvement of the peripheral immune system in PD. Inflammation via the gastrointestinal tract, potentially through infections, may contribute to disease pathogenesis, and to the risk of PD development, which was recently reviewed in

*Correspondence to: Sahar El Aidy, Department of Molecular Immunology and Microbiology, Groningen Biomolecular Sciences and Biotechnology Institute (GBB), University of Groningen, Nijenborgh 7, 9747 AG Groningen, The Netherlands. Tel.: +31 50 36 32201; Fax: +31 50 36 32154; E-mail: sahar.elaidy@rug.nl.
Houser and Tansey proposed a model of PD pathogenesis originating from the gut where an initial inflammatory trigger could lead to a low-grade inflammation, driving shifts in the microbiota composition, and increasing gut permeability, thus allowing leakage of bacteria and their potential inflammatory metabolites [8]. This leakage in gut barrier would increase the blood-brain barrier permeability and α-synuclein pathology, which would ultimately lead to neuroinflammation followed by neurodegeneration [8]. Indeed, PD patients have an altered microbiota composition compared to healthy controls (HC) [10–22], and one of the main bacterial metabolites, short chain fatty acids (SCFA), have been implicated in α-synuclein pathology and microglia activation in a mouse model of PD [23]. Altered microbial composition could lead to a shift in circulating bacterial derived metabolites [24], and could be involved in low-grade inflammation, an important trigger for the onset of PD [8]. In this review, we aim to establish a link between the microbial composition and the reported alterations in their metabolic capacity that have profound immune modulating properties, which could potentially trigger onset, progression and etiology of PD.

**ALTERED BACTERIAL-DERIVED METABOLITES IN PATIENTS WITH PARKINSON’S DISEASE**

Although it is clear that PD patients have an altered microbiota composition [10–22], which was reviewed recently [25, 26] and updated and merged in Table 1, there is a large variation among studies and there is no clear consensus about which bacteria might be involved, which might be due to several factors including sample storage, technical differences of sampling, sequencing methods, statistical approach, demographics, clinical details, and sample size [10]. Nevertheless, the altered microbiota composition could result in metabolic changes in PD patients which could play an important role in disease onset and progression of PD [24]. Therefore, many studies focused on metabolic biomarker screening (comparing healthy subjects with either familial PD or idiopathic PD), for an early detection of potential development of PD. The metabolic profiles of PD patients (in cerebrospinal fluid (CSF), blood or urine) usually reflect oxidative stress [24, 27–31] or mitochondrial dysfunction [24, 31–35]. However, many studies also observed differences in metabolites from bacterial origin, which are summarized in Table 2.

Comparing the 13 different studies in Table 1, 62% (8/13) report a decrease in species from the Lachnospiraceae family (including Blautia sp., Dorea sp., Coprococcus sp., Rosburia sp., and Clostridium XIVa sp.), 38% (5/13) report a decrease of Faecalibacterium sp., and 15% (2/13) report a decrease in Bacteroides sp. (one study reported an increase), all of which are known to be SCFAs producers [36].

In mouse models, it was shown that the gut microbiota is involved in α-synuclein aggregation pathology through their production of SCFAs [23]. Using murine models overexpressing α-synuclein, germ-free (GF) or antibiotic treated mice had reduced PD pathology compared to conventional mice. In addition, when those GF or antibiotic treated mice were administered a mixture of SCFAs, the PD pathology was restored as observed in their conventional counterparts [23]. GF mice (WT or overexpressing α-synuclein) colonized with human stool from PD patients had increased relative levels of butyrate and propionate but decreased levels of acetate compared to mice colonized with human stool from HCs [23]. These findings are in contrast with the finding that PD patients have decreased levels of absolute SCFAs and reduced relative levels of butyrate but not acetate and propionate in their stool samples compared to age matched HCs [14], which is in agreement with reduced levels of acetate found in the blood of PD patients [37]. This discrepancy is most likely because of the differences between humans and mice, specifically those born germ-free. In addition, in Sampson et al. (2016) [23] mice were recolonized with human faecal transplant, representing more acute effects as well as shifts in the microbiome based on species effects.

A decrease in Prevotellaceae or Prevotella sp. was observed in 31% (4/13) of the studies listed in Table 1. Prevotella produces (among others) hydrogen sulfide (H2S), a gasotransmitter (for review see [38]), which has been linked to PD and neuroprotection [39]. Free H2S levels in plasma, cecum, and colon of germ-free mice were significantly reduced compared to their conventional counterparts, indicating that the microbiota contributes to free H2S levels [40]. H2S breathing (40 ppm) restored the movement disorder, protected dopaminergic neurons, prevented microglia and astrocyte activation and upregulated the expression of antioxidant genes from the Nrf2 pathway in a 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine (MPTP) induced...
Table 1
Bacterial composition alterations in PD patients compared to healthy controls

<table>
<thead>
<tr>
<th>Decreased</th>
<th>Increased</th>
<th>Method</th>
<th>PD</th>
<th>HC</th>
<th>Sample</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Prevotellaceae*, Lachnospiraeceae, Puniceicoccaceae, Roseburia, Prevotella, Blautia, Clostridium XIVa</td>
<td>Bifidobacteriaceae*, Bifidobacterium*, Rikenellaceae, Lactobacillaceae, Lactobacillus</td>
<td>16S rRNA</td>
<td>64</td>
<td>64</td>
<td>Feces</td>
<td>[10]</td>
</tr>
<tr>
<td>Prevotella copri, Eubacterium bioforme</td>
<td></td>
<td>Akkermansia muciniphila, unclassified Firmicutes</td>
<td>Shotgun metagenomics</td>
<td>31</td>
<td>28</td>
<td>Feces</td>
</tr>
<tr>
<td>Clostridium cocooides, Clostridium leptum, Bacteroides fragilis, Prevotella (ns)</td>
<td>Lactobacillus sp.</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lachnospiraceae, Faecalibacterium praunznitzii. none</td>
<td>Akkermansia muciniphila, Bifidobacterium sp.</td>
<td>16S rRNA</td>
<td>212</td>
<td>136</td>
<td>Feces</td>
<td>[17]</td>
</tr>
<tr>
<td>Coriobacteriaceae, Lachnospiraceae (Blautia sp., Dorea sp., Roseburia sp., Coprococcus sp.)</td>
<td>Bacteroides sp.</td>
<td>16S rRNA</td>
<td>38</td>
<td>34</td>
<td>Feces</td>
<td>[19]</td>
</tr>
<tr>
<td>Coprobacillaceae, Lachnospiraceae (Dorea sp.), Faecalibacterium sp.</td>
<td>Oxalobacteraceae, Balstonia</td>
<td>16S rRNA</td>
<td>38</td>
<td>34</td>
<td>Sigmoid mucosa</td>
<td>[19]</td>
</tr>
<tr>
<td>Blautia sp., Faecalibacterium sp., Ruminococcus sp.</td>
<td>Escherichia sp., Streptococcus sp., Proteus sp., Enterococcus sp.</td>
<td>16S rRNA</td>
<td>24</td>
<td>14</td>
<td>Feces</td>
<td>[20]</td>
</tr>
<tr>
<td>Lachnospiraceae</td>
<td></td>
<td>Eubacteriaceae, Bifidobacteriaceae</td>
<td>16S rRNA</td>
<td>75</td>
<td>45</td>
<td>Feces</td>
</tr>
<tr>
<td>Dorea sp., Bacteroides sp., Prevotella sp., Faecalibacterium sp.</td>
<td>Lactobacillus sp., Christensenella sp., Catabacter sp., Oscillospira sp., Bifidobacterium sp.</td>
<td>16S rRNA</td>
<td>89</td>
<td>66</td>
<td>Feces</td>
<td>[22]</td>
</tr>
<tr>
<td>Prevotellaceae, Clostridales incertae sedis IV</td>
<td>Lactobacillaceae, Verrucomicrobiaceae (Akkermansia), Bradyrhizobiaceae, Ruminococcaceae, Enterobacteriaceae</td>
<td>16S rRNA</td>
<td>72</td>
<td>72</td>
<td>Feces</td>
<td>[12]</td>
</tr>
<tr>
<td>Lactobacillus, Sediminibacterium</td>
<td>Clostridium IV, Aquabacterium, Holdemania, Sphingomonas, Clostridium XVIII, Butyrivibrio, Anaerotruncus</td>
<td>16S rRNA</td>
<td>45</td>
<td>45</td>
<td>Feces</td>
<td>[13]</td>
</tr>
<tr>
<td>Bacteroidetes, Lactobacilli, Faecalibacterium sp., Enterococciaceae, Prevotellaceae (ns)</td>
<td></td>
<td>Targeted qPCR for 9 taxa</td>
<td>34</td>
<td>34</td>
<td>Feces</td>
<td>[14]</td>
</tr>
</tbody>
</table>

*Also significant after the two-year follow up; ns, not significant.

Updated table adapted and merged from [25] and [26].
Table 2  
Bacterial metabolites significantly altered in PD patients compared to healthy controls

<table>
<thead>
<tr>
<th>Study</th>
<th>Sample</th>
<th>PD</th>
<th>Healthy</th>
<th>Method</th>
<th>Decreased (FC, PD vs HC)</th>
<th>Increased (FC, PD vs HC)</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>[29]</td>
<td>CSF</td>
<td>34</td>
<td>35</td>
<td>GC-MS</td>
<td>none</td>
<td>none</td>
<td>Lumbar puncture after fasting.</td>
</tr>
<tr>
<td>[31]</td>
<td>CSF</td>
<td>31</td>
<td>95</td>
<td>FT-ICR-MS</td>
<td>none</td>
<td>p-cresol sulfate (9.29); Quinic acid (1.7)</td>
<td>Lumbar puncture; 18 patients without PD medications and 11 with PD medication.</td>
</tr>
<tr>
<td>[90]</td>
<td>CSF</td>
<td>48</td>
<td>57</td>
<td>GC/LC-MS</td>
<td>none</td>
<td>none</td>
<td>Postmortem (within 4 hours) collection of lateral ventricular CSF.</td>
</tr>
<tr>
<td>[91]</td>
<td>CSF</td>
<td>10</td>
<td>10</td>
<td>1D 1H-NMR</td>
<td>none</td>
<td>none</td>
<td>Six patients started dopaminergic treatment at the time of CSF collection.</td>
</tr>
<tr>
<td>[55]</td>
<td>CSF, Plasma</td>
<td>20</td>
<td>20</td>
<td>GC-TOF-MS</td>
<td>none</td>
<td>none</td>
<td>PD baseline; Samples were collected without overnight fasting, between 8-9 AM.</td>
</tr>
<tr>
<td>[48]</td>
<td>CSF, Plasma</td>
<td>49* NA</td>
<td>LC-GC-MS</td>
<td>Correlation with the progression of PD: Benzoic acid (CSF: r = –0.42, plasma: ns)</td>
<td>Correlation with the progression of PD: indoleacetic acid (CSF:0.29, plasma: ns)</td>
<td>Placebo treated PD patients from study from 1989. Lumbar puncture for CSF samples and blood samples were collected after overnight bed rest (between 6 and 10 AM before breakfast).</td>
<td></td>
</tr>
<tr>
<td>[92]</td>
<td>CSF, Plasma</td>
<td>22</td>
<td>28</td>
<td>GC/LC-MS</td>
<td>3-(4-hydroxyphenyl)acetic acid (NA)</td>
<td>indole (NA)</td>
<td>Lumbar puncture and plasma samples from non-fasting patients; Samples were age, sex, and sampling-date matched</td>
</tr>
<tr>
<td>[93]</td>
<td>CSF, Plasma</td>
<td>26</td>
<td>14</td>
<td>LC-MS</td>
<td>none</td>
<td>none</td>
<td>Lumbar punctures were performed between 09.30 and 10.00 am after overnight fasting; Blood was drawn from the cubital fossa immediately after the lumbar puncture.</td>
</tr>
<tr>
<td>[37]</td>
<td>Plasma</td>
<td>43</td>
<td>37</td>
<td>2D 1H-NMR</td>
<td>trimethylamine (NA), acetate (NA), threonate (NA)</td>
<td>none</td>
<td>Samples were obtained from drug-naïve PD patients with age and gender-matched healthy controls.</td>
</tr>
<tr>
<td>[94]</td>
<td>Plasma</td>
<td>53</td>
<td>46</td>
<td>LC-ECA</td>
<td>none</td>
<td>none</td>
<td>53 PD patients (41 iPD, 12 LRRK2&lt;sup&gt;G2019S&lt;/sup&gt;) were compared to 31 healthy family members (21 positive and 10 negative for LRRK2 mutation) and 15 non-related controls.</td>
</tr>
<tr>
<td>[28]</td>
<td>Serum</td>
<td>35</td>
<td>7</td>
<td>GC/LC-MS</td>
<td>indoleacetic acid (0.67)</td>
<td>phenyllactate (1.84); 3-(4-hydroxyphenyl)lactate (1.23)</td>
<td>Blood was withdrawn after 4 hours of fasting.</td>
</tr>
<tr>
<td>[33]</td>
<td>Serum</td>
<td>41</td>
<td>40</td>
<td>DiscoveryHD4&lt;sup&gt;TM&lt;/sup&gt; Metabolon Platform</td>
<td>catechol sulfate (0.62)</td>
<td>none</td>
<td>Mass spectrometry-based; Blood was withdrawn after fasting from 41 idiopathic early-stage Parkinson’s patients (disease duration &lt;1 year).</td>
</tr>
</tbody>
</table>
[30] Serum 43 42 CIT-LC-MS none 
vanillic acid (3.48) (mainly dietary source) 
Determined of PD patients not developing dementia \( (n=27) \) and PD patients that did develop dementia \( (n=16) \). Blood was withdrawn at baseline.

[32] Serum 28 18 LC-MS none 
one none 
In the morning before any food or drink. PARK2 PD patients; Blood was withdrawn after overnight fasting.

[24] Serum 6 19 LC-MS indoleacetic acid (0.82); hippuric acid (0.52); 3-hydroxyhippuric acid (0.39); catechol sulfate (0.62); 3-(3-hydroxyphenyl)propionic acid (0.49); Indole-3-methyl acetate (0.70); 2-Furoylglycine (0.37) 
one none 

[68] Serum 48* 10 LC-MS phenylethylamine (0.34d, 0.16e) tyramine (1.70d, 2.44e) 

[95] Serum 80 20 LC-FT-ICR-MS none none 
39 rapid progressing PD Patients and 41 slowly progressing PD patients. No fasting was required. No medication was allowed in the morning. Samples were taken at the morning exam between 8 AM and 12 PM.

[35] Urine 106 104 LC-MS none 
3-(4-hydroxyphenyl)acetic acid (1.96–2.16); tryptamine (2.22–3.31); indoleacetic acid (1.66–3.23); phenylacetic acid (2.36–2.71) 

[34] Urine 92 65 GC/LC-MS none 
3-(4-hydroxyphenyl)acetic acid (1.66a, 2.78b, 5.85c); indoleacetic acid (2.64a, 3.49b, 1.88c); aminobenzoic acid (6.63a, 25.43b, 16.74c); hydroxybenzoic acid (4.30a, 4.26b, 6.68c); 

[14] Feces 34 44§ GC-MS acetate (0.43f, 0.71g), butyrate (0.38f, 0.57g), propionate (0.48f, 0.61g) 
§34 age matched controls and 10 young healthy controls. Fold changes derived from figure compared to young controls§ and age matched controls§. All subjects were on an omnivorous without special dietary habits or restrictions. During the last 3 months no intake of antibiotics, probiotics, or prebiotics was reported.

PD mouse model [41]. Similar results were found in a 6-hydroxydopamine (6-OHDA) and rotenone induced PD rat model receiving 30 or 100 \( \mu \)mol/kg NaHS (an H\(_2\)S donor) [42]. Similarly, H\(_2\) another and potentially overlooked gasotransmitter, which can be produced by gut microbiota, such as Blautia sp., Clostridium spp., might have an important link to PD as it has been described to neutralize toxic hydroxyl radicals, downregulate the expression of proinflammatory factors, and preserve cerebrovascular reactivity [43]. Intriguingly, 0.08 ppm of H\(_2\) in drinking water reduced the loss dopaminergic neurons by 16\% compared to the control in the substantia nigra and slightly improved the mobility in an open-field test using a MPTP induced PD mouse model [44]. Similarly, the protection of dopaminergic neurons, by drinking hydrogenated water, was also observed in a 6-OHDA rat model [45]. Bacterial species representing the genera of bacteria altered in PD have been tested for their production of H\(_2\) [46]. Blautia coccoides and Clostridium leptum, which are reported to be underrepresented in PD patients (Table 1) produced the highest levels of H\(_2\) (1.6 and 0.62 \( \mu \)mol/10\(^8\) cells) [46], and therefore might contribute to the availability of molecular H\(_2\) which potentially plays a role in neuroprotection.

Other organic metabolites produced by Clostridium species [47] were found to be differentially present in serum, urine, and CSF samples of PD patients (Table 2). For example, an increase in 3-phenyllactate, and 3-(4-hydroxyphenyl)lactic acid and a decrease of indoleacetic acid (IAA) was observed in serum of patients with idiopathic PD and familial PD (PARK2 mutations) [24, 28], although in urine, an increase of 3-(4-hydroxyphenyl)acetic acid and IAA was observed [34, 35]. In addition, a minor but significant correlation was observed between IAA and the progression of PD in CSF but not in plasma, however these samples were stored for 25 years before analysis on LC/GC-MS, which could influence the accuracy of sample analysis [48]. IAA is produced via oxidative decarboxylation or deamination of indolepyruvate or tryptamine, respectively. Levels of IAA and tryptamine, produced by Ruminococcus gnarus and Clostridium sporogenes [49], are strongly dependent on the microbiota as GF mice showed ~30 fold decrease in IAA cecal or fecal levels and a corresponding ~10 fold decrease in tryptamine levels when compared to their conventional raised counterparts [50, 51]. Congruously to the increased IAA levels in urine, an increase in tryptamine was detected in urine of PD patients in one of the studies [35]. Importantly, IAA was shown to modulate inflammatory responses reducing pro-inflammatory cytokine production by macrophages stimulated with LPS and palmitate or attenuating the cytokine mediated lipogenesis through the aryl hydrogen receptor (AHR) in hepatocytes [51]. Furthermore, IAA has an anti-inflammatory activity in LPS-stimulated BV2 microglial cells [52]. Taken together, data available suggest that altered levels of IAA, which are caused by changes in microbial composition, might play a role in attenuating inflammation in PD patients.

P-cresol sulfate (sulfonated by the liver), which is exclusively produced by gut bacteria [53], mainly by species belonging to Clostridiaceae (Clostridium clusters I, IV, IX, XI, XIII, XVIII, XVI) and Bacteroidaceae families [54] (Table 1), is also observed to be ~10 fold increased in in the CSF of PD patients [31] but not in blood samples [24, 28]. However, differential metabolite levels in blood do not necessarily reflect CSF levels [55]. P-cresol has a profound effect on the inflammatory response of macrophages and T-cells [56–58]. In murine peritoneal exudate cells (the adherent fraction, mainly macrophages) and in a J774.1 macrophage cell line, pre-treatment with p-cresol at non-cytotoxic levels was able to inhibit IL-12 production after stimulation with heat-killed Lactobacillus casei [56]. The same effect was observed later in murine peritoneal exudate cells and RAW276.3 macrophage cell-line stimulated with LPS or LPS and IFN\(_\gamma\) [58]. In addition, p-cresol sulfate increased IL-10 levels but did not alter levels of TNF\(_\alpha\) [58]. In a hypersensitive mouse model, p-cresol and p-cresol sulfate correlated negatively with ear swelling, suggesting that p-cresol (sulfate) attenuates T cell mediated immune response [57]. When \textit{in vitro} CD3\(^+\) splenocytes were stimulated with p-cresol or p-cresol sulfate a decrease in IFN\(_\gamma\) and an increase IL-4 levels were observed, which was confirmed by a decreased Th1/Th2 ratio (CD3\(^+\)/CD4\(^+\) splenocytes, intracellular stained for IFN\(_\gamma\) (Th1) or IL-4 (Th2) production), but no difference between untreated and p-cresol treated cytotoxic T-cells or regulatory T-cells were found [57].

In contrast to P-cresol sulfate, catechol sulfate, a product of bacterial and human co-metabolism, was found to be decreased in PD patients [24, 33]. Catechol is an intermediate bacterial product from the benzoate degradation pathway [59, 60]. Notably, higher bacterial metabolism of catechol seems to be associated with inflammation as concluded from the higher relative abundance of bacteria representing...
the benzoate pathway are higher in a murine colitis model during the active disease compared to remis-

For example, *Ralstonia pickettii*, which is

known to produce and degrade catechol [61, 62] was

reported to be increased in the sigmoid mucosa of

PD patients (Table 1) potentially reflecting inflam-
mation [19], which is in agreement with the reported

higher abundance of bacteria representing the ben-
zoate degradation pathway [60].

Molecular mimicry by extracellular amyloid pro-
teins produced by bacteria have been proposed as
one potential trigger inducing misfolding of neuronal
proteins via cross-seeding [63]. Recently the amy-
lloid protein produced by *Escherichia coli* (curli) has
been implicated in α-synuclein pathology in rats and
*Caenorhabditis elegans* [64]. Rats orally adminis-
tered with wild type *E. coli* or *E. coli* lacking the
curli-gene revealed increased α-synuclein aggregates
in the brain and gut of rats (hippocampus, stria-
tum, and enteric nervous system) when treated with
wild type *E. coli*. Furthermore, increased expres-
sion of IL-6, TLR2 and TNF were observed in the
striatum or rats treated with wild type *E. coli*
[64]. Various species from the *Enterobacteriaceae* family (*E. coli*), *Salmonella typhimurium* *Citrobac-
ter sp.*, *Citrobacter freundii*, *Cronobacter sakazakii,* and *Proteus mirabilis* produce curli [65]. Impor-
tantly, 31% (4/13) of the studies reported increased
abundance of *Enterobacteriaceae spp.* [11, 12, 14,
20] (Table 1). Intriguingly, oral administration of
*P. mirabilis* in a MPTP induced PD mouse model
induced neuronal damage, motor deficits, neuroin-
flammation and α-synuclein aggregation [66]. The
authors suggested that higher levels of LPS by *P.*
*mirabilis* induced the observed neuronal damage.
However, the fact that *P. mirabilis* produces curli
could be another factor involved in the observed PD
pathology.

**BACTERIAL-MEDIATED SIDE EFFECTS
OF PARKINSON’S DISEASE TREATMENT**

Orally administered PD medication could have an
effect on gastrointestinal (GI) function and therefore
on the microbial composition alterations in
PD patients. For example, the COMT-inhibitors,
anticholinergics and levodopa/carbidiopa (border-
line significant) were associated with microbiota
alterations within PD patients [17]. Furthermore,
COMT-inhibitors were significantly associated with
an increase of *Lactobacillaceae* and a decrease of
*Clostridiales Family IV (Incertae Sedis)* [12]. In 54%
(7/13) of the studies *Lactobacillaceae* or *Lactobacil-
lus* were reported to be increased in PD patients
(Table 1). Some *Lactobacillus* species are known
to produce tyramine [67] and tyramine has been
proposed as a biomarker for PD patients because
of the significantly higher levels of tyramine com-
pared to HC observed in the blood circulation (2.4
and 1.7 fold, respectively) [68], Table 2. Although
other studies did not find an increase in tyramine, an
increase in the downstream metabolite of tyramine,
3-(4-hydroxyphenyl) acetic acid, was observed in PD
patients [34, 35], potentially supporting increased
levels of tyramine. The authors associated the human
aromatic amino acid decarboxylase (AADC, also
known as DOPA decarboxylase (DDC)) with the
observed levels, without speculating about possible
contribution of gut bacteria. Tyramine is abundant in
fermented foods particularly produced by lactic acid
bacteria (*Lactobacillus sp.*, *Enterococcus sp.*) harboring
tyrosine decarboxylases (TDC), which are also
commensals in the human GI-tract [67, 69, 70]. Tyra-
mine is produced in the small intestinal content of rat,
indicating that small intestinal bacteria contribute to
tyramine levels *in vivo*. In addition, tdc-gene abun-
dance correlated positively (*r* = 0.82, *n* = 10) with the
disease duration of PD [71], supporting the increased
abundance of *Lactobacillaceae* or *Lactobacillus*
found in PD patients. Besides the decarboxylation
of tyrosine to tyramine, the study also showed that bac-
teria harboring TDC can effectively decarboxylate
levodopa to dopamine, and might compromise the
levels of levodopa in the gut, before it can reach the
brain [71], which was later independently confirmed
in human stool samples and using a TDC inhibitor in
mice colonized with *E. faecalis* [72]. Co-prescribed
decarboxylase inhibitors, mainly carbidopa, prevent
peripheral decarboxylation of levodopa treatment by
the human AADC (DDC), which however do not
affect the bacterial TDCs [71]. The inadequate block-
ing of bacterial TDC might result in higher levels
of luminal dopamine produced by the gut bacte-
ria (65). Thus, because of levodopa treatment, PD
patients are exposed to higher circulating levels of
dopamine compared to matched HCs. Indeed, serum
dopamine levels (sulfonated by the liver) are found
to be 30–40 times higher compared to HC [24] and
serum dopamine levels correlated with the dosage of
levodopa [73]. Comparing healthy and PD sub-
jects on either a low dose (400 mg/day) or a on
a high dose (700 mg/day) of levodopa showed that
PD patients on a high dosage of levodopa have
significantly more dopamine in their peripheral blood lymphocytes (PBLs), however, (nor)epinephrine or DOPAC levels were not altered [74]. In contrast, non-treated PD patients have low dopamine levels in their PBLs, even ~3 fold lower than in healthy subjects, but after treatment showed an ~30 fold increase in the PBL dopamine content [75]. Likewise, higher levels of dopamine were detected in plasma of levodopa treated PD patients (~2.5 fold increase) compared to HC or de novo PD patients and no significant differences were observed between HC and de novo PD patients [76].

The high levels of dopamine exposure in PD patients, resulting from bacterial and human levodopa metabolism, could affect immune homeostasis, as dopaminergic systems are involved in either the adaptive and innate immune system, recently reviewed [77, 78]. Dopamine receptors are widely expressed on human leukocytes and dopamine, through its receptors, can modulate T-cell response, and might act as autocrine or paracrine signaling molecule in the cells of the immune system [78]. Importantly, the percentage of Dopamine Receptor D5 (DRD5) positive CD4+ T-cells correlated negatively with the UPDRS-III (Unified Parkinson’s Disease Rating Scale, Part III, motor examination) score [76], indicating that the severity (progression) of the disease, and thus the disease duration [79] and drug treatment might be associated with reduced DRD5+ CD4+ T-cells. A follow up study investigating CD4+ T cell subsets (T helper cells, Th1, Th2, Th17; and T regulatory cells, Treg) showed an overall decrease of CD4+ T cells in de novo PD patients and treated PD patients attributed by a decrease in most T-cell subsets except for Th1. Remarkably, there were little differences observed between the de novo PD and treated PD patients except for Treg mediated inhibition of T effector cell (Teff, mixture of T helper cells) proliferation by dopamine. Treg subsets from healthy subjects, de novo PD patients, and treated PD patients showed similar Treg mediated inhibition of Teff proliferation, which is almost abolished by dopamine except for Treg cells isolated from treated PD patients, those cells appeared to be insensitive to dopamine [80]. This finding is consistent with an earlier report showing that dopamine prevents inhibition of murine Teff proliferation by Treg cells [81]. Furthermore, it was shown that the effect of dopamine was mediated through DRD1-like receptors (DRD1 or DRD5) [81], which is in agreement with the negative correlation observed between disease severity (and thus indirectly disease and treatment duration) and DRD5+ CD4+ T-cells in PD patients [76]. This Treg insensitivity might potentially be originated from the of long-term levodopa treatment of PD patients. In addition, DRD2-like receptors (D2, D3, D4) seem to be involved in the dopaminergic immune pathway in PD. DRD3 knock out (KO) mice or RAG1 KO mice (which are devoid of T and B cells) reconstituted with DRD3-deficient splenocytes or DRD3-deficient CD4+ T cells resulted in a strong neuroprotection in MPTP-induced PD, showing a fundamental role of DRD3 expressed on CD4+ T cells in the degeneration of dopaminergic neurons. Furthermore it was shown that DRD3 deficient CD4+ T cells are unable to acquire the Th1 effector phenotype, indicating that dopaminergic signaling (by dopamine or agonists) through DRD3 would produce Th1 cells which are key in neurodegeneration observed [82]. Which is in agreement with the higher Th1/Th2 ratio observed in progressing PD patients but not in de novo PD patients, potentially through dopamine mediated Th1 differentiation in combination with the inability of Treg cells to inhibit Teff cells [80].

Besides levodopa, which results in higher exposure to peripheral dopamine, blocking DDC to avoid peripheral conversion of levodopa to dopamine, might have a profound influence on the immune system. Recently, it has been reported that carbidopa, a DDC inhibitor, has immunosuppressive properties as it prevents T-cell proliferation and T-cell autoimmunity in a mouse model [83]. Furthermore, it has been demonstrated that carbidopa is an AHR- ligand [84], and therefore might play a role in the immune system, as AHR is an important contributor to the adaptive immune system by modulating T-cell differentiation, reviewed recently [85].

Importantly, proliferation of murine B-cell enriched lymphocyte cultures isolated from spleen, lymph nodes and Peyer’s patches are inhibited by dopamine in a concentration dependent manner (1–100 μM), which coincided with immunoglobulin production (IgA, IgM, IgG) [86]. IgA is known to shape the microbiota composition, reviewed here [87], and thus a decrease in IgA production due to the exposure to dopamine could potentially lead to alteration in the microbiota composition. In a recent study, inflammatory markers in fecal samples of PD patients we compared to their HCs counterparts. The mean levels of the angiogenesis factor (Flt1), the pro-inflammatory cytokines IL-1α, and CXCL8 were significantly higher in PD patients. Importantly, consumption of probiotics was associated with significantly higher levels of the chemokines...
CCL4 (MIP-1β), and CCL17 (TARC), and the pro-inflammatory cytokine IL-7 [88]. Unfortunately, the potential effect of anti-Parkinson medication on the fecal immune profiles was not included in the analysis, which could have a profound effect on the outcome (discussed above).

**CONCLUSION**

Microbial dysbiosis might be a contributing factor to the onset and/or progression and severity of PD. Altered bacterial composition might result in a change in bacterial metabolites as detected in PD patients, contributing to the immune homeostasis, and potentially detrimental for the onset and progression of the disease. Equally important is the pharmacological treatment of PD, which might further contribute to a disturbed immune system. Nonetheless, it remains to be elucidated what drives the modulation of the microbial composition in PD patients. Many studies have focused on the metabolic profile of PD patients in CSF, blood, or urine in order to find potential biomarkers for the etiology, onset, or progression of the disease. Many of these altered metabolites are bacterial products, reflecting a deviation in the microbial composition of PD patients, and therefore might act as an important biomarker for microbial dysbiosis. In addition, those bacterial-derived metabolites show important immunomodulatory properties, which might be important for the progression of the disease.

The main metabolites found have phenol/indole moieties and are mainly produced by bacteria from the Clostridia class and are also known SCFAs producers. Notably, alterations in SCFAs were not reported in the majority of metabolomics studies, most likely because of the methods used for the untargeted metabolomics. Because SCFAs have a potential effect on the α-synuclein pathology, targeted metabolomics for SCFAs should be performed in future metabolomics studies, as they might give clues about abnormal levels in PD patients potentially influencing PD pathology. Furthermore, altered levels of SCFAs could be linked with the levels of p-cresol and IAA as these metabolites are produced mainly by Clostridia [47, 54], the main butyrate producing bacteria in the gut [89]. Taken together, further research on the metabolites produced by the gut microbiota is necessary to unravel the complex interaction of multiple facets of metabolites originating from altered microbial composition and pharmacological treatment on the immune system in PD patients to give further insights on the role of gut microbiota and their metabolites on the onset, progression and etiology of the disease. Standardized methods of stool sampling and sequencing technology should be developed to generate more consensus among metabolomic and microbiota studies. Additionally, studies should be conducted with focus on determining the fecal metabolome from PD patients in context of the pathology and progression of the disease. Composition of the diet as well as medication are confounding factors that influence that changes in the microbiome thus should be taken into consideration in the data analyses.

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**CONFLICT OF INTEREST**

The authors have no conflict of interest to report.

**REFERENCES**


