Introduction: Parkinson’s disease (PD) has systemic manifestations beyond the progressive loss of dopaminergic nigrostriatal neurons. Accordingly, recent studies implicated the role of gut dysbiosis on PD pathology and progression. In this study we performed comparative analysis of urinary metabolites profiling to detect candidate metabolites mirroring gut dysbiosis in PD.

Methods: A total of 64 urine samples obtained from healthy controls were analysed by reverse phase (RP)/UPLC-MS/MS methods with positive and negative ion mode electrospray ionization (ESI) and HILIC/UPLC-MS/MS with negative ion mode ESI. Welch’s two-sample t-test was performed on log transformed data and p<0.05 was considered significant.

Results: A total of 6 polyamine metabolites were significantly altered in PD patients. Additionally, we found 11 metabolites associated with the gut microbiome were differently abundant in PD. Polyamines have been linked to intestinal inflammation and dysbiosis. Accordingly, in our study we found some crucial polyamine metabolites to correlate with specific gut microbiome metabolites.

Conclusion: Compositional and metabolic alterations in the PD microbiota are highly associated with gut function. Our results suggest a plausible link between altered bacterial and polyamines metabolism, which could impact on pathophysiological processes. Functional microbiome analyses could have clinical utility for biomarker and therapeutic development in PD.