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# Quantitative Profiling of S-Nitrosylated Proteins in Parkinson's Disease Paradigms for the Effects of Botanical Phenolics

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A convergent feature for most aging-related neurological diseases, such as Parkinson's Disease (PD), is excessive generation of free radicals – reactive nitrogen and oxygen species, which can contribute to neuronal cell death and link to the disease pathogenesis. Free radical nitric oxide (NO) is a signaling molecule involving in the regulation of a wide range of cellular functions from development to disease. Emerging evidence suggests that nitrosative stress due to NO over-production induces post-translational modifications of protein cysteine and modulates protein enzymatic activity in cells. S-Nitrosylation, the covalent adduction of NO to specific protein cysteine thiol, is considered as a predominant, redox-based prototypical mechanism for cell signaling. Previously, endogenous protein S-nitrosylation was detected by the biotin switch assay. Taking the advantages of both biotin switch assay and **d**ifferential **i**n-**g**el **e**lectrophoresis (DIGE), we developed a gel-based proteomics method, named as NitroDIGE, to globally and quantitatively investigate protein S-nitrosylation. Using this method, we identified a subset of S-nitrosylated proteins from both *in vitro* and *in vivo* models of Parkinsonism including pesticide rotenone-induced PD-relevant insults in SH-SY5Y cells. Moreover, we determined whether protein S-nitrosylation in cellular PD models could be modulated by different botanical phenolic compounds, including epigallocatechin gallate (EGCG) from green tea, and apocynin from *Picrorhiza kurrooa*, a herbal plant grown in the Himalayan. The NitroDIGE results demonstrated that the treatment of botanical compounds

could reduce excessive S-nitrosylated proteins in SH-SY5Y cells exposed to rotenone, indicating that these botanical phenolics could serve as effective NO scavengers to attenuate nitrosative stress and PD-relevant insults.