Midnolin is a strong genetic risk factor for Parkinson's disease in Japanese and British populations.

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Parkinson's Disease (PD) is a common neurodegenerative disease. Although more than 20 causal genes for PD have been identified from patients with familial PD, the majority of PD cases are sporadic and the detailed onset mechanism remains unclear. Our previous genetic analysis revealed that the copy number loss of *Midnolin* (*MIDN*) is found in 10.5% of patients with sporadic PD in a Yamagata population cohort. Furthermore, we showed that MIDN regulates neurite outgrowth and expression of Parkin E3 ubiquitin ligase in PC12 cells. Here, we attempted to replicate the genetic association between *MIDN* and PD in a large British population cohort. We examined copy number variations and single nucleotide polymorphisms of the *MIDN* gene in 2,860 controls and 2,168 PD patients. We found significant copy number loss in the *MIDN* gene in 6.55% of patients with PD (odds ratio = 4.35). In addition, when a deletion spanning more than 50,000 bp was defined as the copy number loss, the odds ratio dramatically increased to 22.3. No significant differences for two frequent single nucleotide polymorphisms (rs3746106 and rs3746107) were found. Taken together, we show the strong genetic association of *MIDN* with PD development in a British population and in a Japanese population, suggesting *MIDN* is a universal genetic risk factor for PD.