

厚生労働科学研究費補助金（創薬基盤推進研究事業 ヒトゲノムテーラーメイド研究）  
（総合）分担研究報告書

ゲノム解析によるパーキンソン病遺伝子同定と創薬・テーラーメイド研究  
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**研究要旨**

パーキンソン病治療薬であるドパミンアゴニストの副作用との関連を中心に検討した。麦角系ドパミンアゴニストでは用量依存性に心臓弁膜症の頻度が増加したが SNP 解析をすることに事前に副作用を予測できる可能性が有ると思われた。症例を集積したので今後 SNP 解析を進めていく予定である。

**A.研究目的**

パーキンソン病治療薬であるドパミンアゴニストの副作用との関連をより安全なパーキンソン病治療が可能とするために検討した。

**B.研究方法**

パーキンソン病当初210例で患者背景等の調査と心臓弁膜症検査のための心エコー検査を実施し、追跡フォロー中である。その後50例の症例追加を行った。

(倫理面への配慮)

DNA は文書同意、心エコーは口頭同意を得て実施。IRB 承認済み。

**C.研究結果**

- 1)DNA 解析は症例不十分で行っていない。
- 2)心エコーでは麦角系ドパミンアゴニストで用量依存性に心臓弁膜症の増加を確認した。

**D.考察**

心エコーでは麦角系ドパミンアゴニストで用量依存性に心臓弁膜症の増加を確認したことは新知見でありドパミンアゴニストの安全な使用に寄与すると考える。

SNP 解析により心臓弁膜症発現の可能性を予測できればより安全なパーキンソン病治療が可能となる。

**E.結論**

麦角系ドパミンアゴニストで用量依存性に心臓弁膜症の増加があり、高用量の使用は危険があるので注意を要する。

**F.健康危険情報**

麦角系ドパミンアゴニストで用量依存性に心臓弁膜症の増加することへの注意喚起

**G.研究発表**

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#### H.知的財産権の出願・登録状況 (予定を含む。)

1. 特許取得

なし

2. 実用新案登録

なし

3.その他

なし

### III. 研究成果の刊行に関する一覧表

研究成果の刊行に関する一覧表

書籍

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#### IV. 研究成果の刊行物・別刷





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Cucumber genome  
Parkinson's disease loci  
Kidney morphogenesis

## Genome-wide association study identifies common variants at four loci as genetic risk factors for Parkinson's disease

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To identify susceptibility variants for Parkinson's disease (PD), we performed a genome-wide association study (GWAS) and two replication studies in a total of 2,011 cases and 18,381 controls from Japan. We identified a new susceptibility locus on 1q32 ( $P = 1.52 \times 10^{-12}$ ) and designated this as *PARK16*, and we also identified *BST1* on 4p15 as a second new risk locus ( $P = 3.94 \times 10^{-9}$ ). We also detected strong associations at *SNCA* on 4q22 ( $P = 7.35 \times 10^{-17}$ ) and *LRRK2* on 12q12 ( $P = 2.72 \times 10^{-8}$ ), both of which are implicated in autosomal dominant forms of parkinsonism. By comparing results of a GWAS performed on individuals of European ancestry, we identified *PARK16*, *SNCA* and *LRRK2* as shared risk loci for PD and *BST1* and *MAPT* as loci showing population differences. Our results identify two new PD susceptibility loci, show involvement of autosomal dominant parkinsonism loci in typical PD and suggest that population differences contribute to genetic heterogeneity in PD.

Parkinson's disease (MIM168600) is one of the most common neurodegenerative diseases worldwide, affecting 1–2% of individuals aged  $\geq 65$  years<sup>1</sup>. Clinical features of PD result primarily from loss of dopaminergic neurons in the substantia nigra. Various medical treatments improve PD symptoms but do little to deter disease progression. Identifying genetic risk factors for PD will be helpful in elucidating the pathogenesis of the disease. Linkage studies have been successful in mapping genes for mendelian forms of parkinsonism: *SNCA* (encoding  $\alpha$ -synuclein)<sup>2</sup> and *LRRK2* (refs. 3,4) in autosomal dominant forms, and *PARK2* (encoding parkin), *PINK1*, *PARK7* (encoding DJ-1) and *ATP13A2* in autosomal recessive

forms<sup>5,6</sup>. However, mendelian forms of parkinsonism are rare compared to the far more common typical PD, a complex disorder caused by multiple genetic and environmental factors<sup>7</sup>. Association studies have evaluated variants in many candidate genes for PD<sup>7</sup>, but only a few, such as common variants of *SNCA*<sup>8-10</sup> and rare mutations of *GBA1*<sup>11</sup>, have been identified as PD-susceptibility genes with genome-wide significance. Recently, GWASs in PD have provided association evidence at several loci, but not at the genome-wide significant level<sup>12-14</sup>.

We conducted a GWAS and two subsequent replication studies for PD to identify further common variants that contribute to disease. In the GWAS stage, we genotyped 561,288 SNPs on autosomal and sex chromosomes using the HumanHap550 array (Illumina). The GWAS stage included 1,078 PD cases and 2,628 controls in the Japanese population (Supplementary Note). After SNP and sample quality control analyses, we used genotype data from 435,470 SNPs in 988 cases and 2,521 controls in the GWAS analysis (see Online Methods).

We tested for association between each SNP and PD using the Cochran-Armitage trend test with 1 d.f. The quantile-quantile plot showed a close match to test statistics expected under the null distribution (genomic inflation factor  $\lambda = 1.055$  for PD) (Fig. 1a,b). This indicates minimal overall inflation of genome-wide statistical results due to population stratification and also reveals a number of SNPs whose  $P$  values exceed those expected under the null hypothesis. Seventeen SNPs showed  $P < 5 \times 10^{-7}$ , the threshold for genome-wide significance suggested by the Wellcome Trust Case Control Consortium<sup>15</sup> (Fig. 1c). All these SNPs were located on 4q22, a region harboring *SNCA* that was previously identified by us and others as a definite susceptibility gene for PD<sup>8-10</sup>.

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