Neurogenetics (2025) 26:56
https://doi.org/10.1007/s10048-025-00840-9

RESEARCH

Association of *LRRK2* R1628P variant with Parkinson's disease in Kinh Vietnamese: a cross-sectional study

Minh Duc Do[1] · Tai Ngoc Tran[2] · Linh Hoang Gia Le[1] · Thao Phuong Mai[3]

Received: 11 March 2025 / Accepted: 21 July 2025

Abstract
Parkinson's disease (PD) is a complex disorder with contributions by environmental and genetic factors. *LRRK2* R1628P is a major genetic risk factor for developing PD in Asian populations. However, the effect of this variant in Kinh Vietnamese remains unclear. This study collected DNA samples of 832 subjects comprising 190 PD patients and 642 control cases, and the *LRRK2* R1628P variant was genotyped using an allele-specific oligonucleotide PCR method. The prevalence of the GC genotype of *LRRK2* R1628P was significantly higher in the PD group than in the control group, and the *LRRK2* R1628P variant showed a significant association with PD with OR = 2.91 (95% CI = 1.50–5.62). *LRRK2* R1628P was also found to be associated with PD in subpopulations for males, early-onset, and late-onset. These results emphasize the important genetic contribution of *LRRK2* R1628P in the risk of developing PD in the Kinh Vietnamese population.

Keywords Parkinson's disease · Vietnam · *LRRK2* · R1628P · Genetic association

Introduction

Parkinson's disease (PD) is one of the most common neurodegenerative disorders and is characterized by symptoms that include tremors, muscle rigidity, and bradykinesia. PD is a global healthcare burden, with an estimated 8.5 million or more people suffering from the disease, with the prevalence increasing with age [1]. PD is a complex disease with contributions from both genetic and environmental factors [2]. Among genes associated with PD, pathogenic mutations in *LRRK2* usually cause late-onset and autosomal-dominant PD [3, 4]. The complex and large LRRK2 protein, encoded by the *LRRK2* gene, consists of major domains, including the N-terminal armadillo repeat (AMR), ankyrin-like repeats (ALRs), leucine-rich repeats (LRRs), the Ras of complex (ROC) GTPase domain, carboxy-terminal of ROC (COR), kinase domain, and the C-terminal WD40 domain [5]. The detailed functions of the LRRK2 protein are not fully understood; however, it has been suggested that overactivation of the kinase enzymatic domain in LRRK2 is an important causative change leading to the development of PD [6]. Mutations in the kinase domain, such as G2019S, have been shown to contribute to PD pathogenesis through various mechanisms, including mitochondrial dysfunction, dendrite degeneration, and reduced dopaminergic neuron viability [7–9]. However, G2019S is rarely found in Asian populations [10]. On the other hand, the *LRRK2* R1628P variant, within the COR domain, does not directly alter LRRK2 activity, but it has been described as a critical genetic risk factor among Chinese populations in Taiwan, China, and Singapore for developing PD [11–13]. In our previous study, while trying to elucidate the genetic contribution of PD in early-onset Vietnamese patients, we found a high prevalence of *LRRK2* R1628P as a risk variant for development of PD [14]. While the allelic frequency of *LRRK2* R1628P is 1.8% in Asian population [15], *LRRK2* R1628P frequency and its effect on PD risk in Kinh Vietnamese have not yet been identified. Therefore, this study

✉ Thao Phuong Mai
drmaithao@ump.edu.vn

[1] Center for Molecular Biomedicine, University of Medicine and Pharmacy at Ho Chi Minh City, Ho Chi Minh City, Vietnam

[2] Department of Neurology, University Medical Center Ho Chi Minh City, Ho Chi Minh City, Vietnam

[3] Department of Physiology-Pathophysiology-Immunology, Faculty of Medicine, University of Medicine and Pharmacy at Ho Chi Minh City, Ho Chi Minh City, Vietnam

Published online: 31 July 2025

aims to investigate the risk of developing PD in Kinh Vietnamese subjects carrying *LRRK2* R1628P, and in subgroup populations.

Materials and methods

Participants

This study recruited two groups of participants, one diagnosed with PD and the other without PD. The study protocol was approved by the Ethical Committee of the University of Medicine and Pharmacy at Ho Chi Minh City (approval number 1133/HĐĐĐ-ĐHYD). All participants were self-defined as Kinh Vietnamese. The PD group consisted of 190 unrelated PD patients whose diagnoses were confirmed by two independent neurologists from the Movement Disorder Unit, Neurology Department, University Medical Center, Ho Chi Minh City based on the International Parkinson and Movement Disorder Society Clinical Diagnostic Criteria [16]. The non-PD population comprised 642 participants who had not been diagnosed with PD at the time of recruitment. The baseline characteristics of the participants were recorded (age, gender, age at PD diagnosis, and duration of disease). Early-onset PD was defined as PD diagnosis made before the age of 50; if PD was diagnosed at 50 years old or later, it was defined as late-onset PD.

LRRK2 R1628P genotyping

DNA samples from all the participants were extracted using GeneJET™ Whole Blood Genomic DNA Purification Mini Kit (Thermo Fisher Scientific, MA, United States) according to the manufacturer's instructions. The quality of DNA samples was controlled using NanoDrop™ 2000 Spectrophotometers (Thermo Fisher Scientific). The *LRRK2* R1628P genotype was identified based on our previously developed allele-specific oligonucleotide PCR protocol [17]. Briefly, two sets of primers were designed specifically to amplify G or C nucleotides at coding position 4883 of the *LRRK2* gene by two separate polymerase chain reactions. Additionally, twenty random samples with the GG genotype and ten random samples with the GC genotype based on the PCR method were directly sequenced using ABI 3500 Biosystem (Thermo Fisher Scientific) to ensure concordance between the two genotyping methods. The protocol for direct sequencing was developed and described previously [18–21].

Table 1 Baseline characteristics of the participants

Characteristics	PD group ($N=190$)	Control group ($N=642$)	p-value
Age at PD onset/Age at recruitment (years) (Mean ± SD)	51.97 ± 9.36	51.86 ± 11.69	0.44
Disease duration (years)	4.74 ± 4.40	-	
Males/females (N)	85/105	299/343	0.66
Genotype (N, %)			< 0.01
GG	173 (91.1)	621 (96.7)	
GC	17 (8.9)	21 (3.3)	
Allele (N, %)			< 0.01
G	363 (95.5)	1263 (98.4)	
C	17 (4.5)	21 (1.6)	

Statistical analysis

The age of PD onset, duration of PD, and the age of control subjects were expressed as means and standard deviations. Categorical variables, such as gender, genotype, and allele, were expressed as direct counts and percentages. Student's T-test and a Chi-squared test were applied for statistical analyses. An odds ratio (OR) with a 95% confidence interval (95% CI) was used to assess the association between *LRRK2* R1628P and PD status.

Results

Baseline characteristics of the participants

A total of 832 subjects were recruited for this study. There were no significant differences in age and gender between the two studied groups: PD and control participants. The mean age at onset in PD patients was 51.97, with an average duration of the disease of 4.74 years. Male participants accounted for 44.7% and 46.6% in the PD and control groups, respectively. The genotyping results were totally concordant between the direct sequencing and PCR method. There was a significant difference in genotype and allelic distribution of the *LRRK2* R1628P variant between the two groups. The GC genotype was present in 8.9% of the PD group and 3.3% of the control group, while the C allele was present in 4.5% and 1.6% of the PD and control groups, respectively. All the baseline characteristics of the participants are described in Table 1.

Association of *LRRK2* R1628P and PD in the studied population and in subgroups

The genotype frequencies of *LRRK2* R1628P were under Hardy-Weinberg equilibrium in the total study population, and in the PD and control groups. No CC genotype was identified in this study; therefore, all the genetic association analysis was performed using ORs for genotypes between the PD and control groups. The *LRRK2* R1628P

Table 2 Genotype and allele frequency in sub-groups

Participants	Genotype, *N* (%)				Allele, *N* (%)			
Early-onset	GG (*N* = 329)	GC (*N* = 18)	OR (95% CI)	*p*-value	G (*N* = 676)	C (*N* = 18)	OR (95% CI)	*p*-value
Early-onset PD (< 50)	73 (90.1)	8 (9.9)	2.84 (1.08–7.47)	0.03	154 (95.0)	8 (5.0)	2.71 (1.05–6.99)	0.04
Young controls (< 50)	256 (96.2)	10 (3.8)			522 (98.1)	10 (1.9)		
Late-onset	GG (*N* = 465)	GC (*N* = 20)	OR (95% CI)	*p*-value	G (*N* = 950)	C (*N* = 20)	OR (95% CI)	*p*-value
Late-onset PD (≥ 50)	100 (91.7)	9 (8.3)	2.98 (1.20–7.41)	0.02	209 (95.9)	9 (4.1)	2.90 (1.19–7.10)	0.02
Elderly controls (≥ 50)	365 (97.1)	11 (2.9)			741 (98.5)	11 (1.5)		
Male	GG (*N* = 405)	GC (*N* = 18)	OR (95% CI)	*p*-value	G (*N* = 828)	C (*N* = 18)	OR (95% CI)	*p*-value
Male PD patients	76 (89.4)	9 (10.6)	4.33 (1.66–11.27)	< 0.01	161 (94.7)	9 (5.3)	4.14 (1.62–10.60)	< 0.01
Male controls	329 (97.3)	9 (2.7)			667 (98.7)	9 (1.3)		
Female	GG (*N* = 389)	GC (*N* = 20)	OR (95% CI)	*p*-value	G (*N* = 798)	C (*N* = 20)	OR (95% CI)	*p*-value
Female PD patients	97 (92.4)	8 (7.6)	2.00 (0.80–5.01)	0.14	202 (96.2)	8 (3.8)	1.97 (0.79–4.88)	0.14
Female controls	292 (96.1)	12 (3.9)			596 (98.0)	12 (2.0)		
Whole study	GG (*N* = 794)	GC (*N* = 38)	OR (95% CI)	*p*-value	G (*N* = 1626)	C (*N* = 38)	OR (95% CI)	*p*-value
PD patients	173 (91.1)	17 (8.9)	2.91 (1.50–5.63)	< 0.01	363 (95.5)	17 (4.5)	2.82 (1.47–5.40)	< 0.01
Controls	621 (96.7)	21 (3.3)			1263 (98.4)	21 (1.6)		

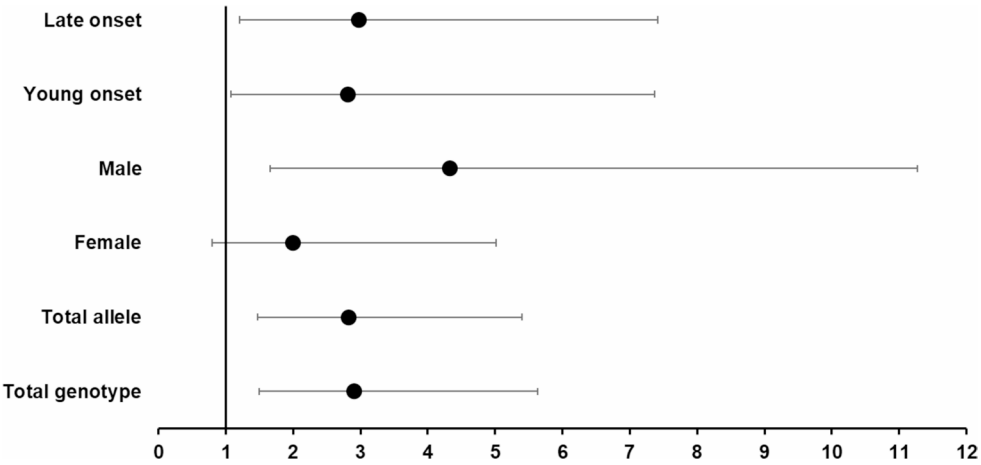

Fig. 1 Odd ratios of total studied population and subgroup populations for Parkinson's disease

variant showed a statistically significant association with PD in genotype and allele analysis with OR = 2.91 (95% CI = 1.50–5.63) and 2.82 (95% CI = 1.47–5.40), respectively (Table 2). The studied population was further divided into subgroups based on age (early onset/late-onset) and gender (male/female). The frequencies of genotypes and alleles of *LRRK2* R1628P in these subpopulations are listed in Table 2. Additional calculations were performed, and the results show that *LRRK2* R1628P is statistically associated with PD in males (OR = 4.33, 95% CI = 1.66–11.27), early-onset (OR = 2.84, 95% CI = 1.08–7.47), and late-onset group (OR = 2.98, 95% CI = 1.20–7.41). The GC genotype did not show a significant increased risk of developing PD in female subjects, with OR = 2.00 (95% CI = 0.80–5.01). The calculated ORs of the total study population and subgroups are shown in Fig. 1.

Discussion

Although LRRK2 is a large and complex protein with seven different domains, it has been suggested that the overall function of LRRK2 is regulated mainly by the kinase domain [6]. LRRK2 has been reported as being involved in different neuronal functions, such as synaptic vesicle trafficking, regulating neuroinflammation, and promoting neuronal apoptosis via ASK1 phosphorylation [22–24]. Located in the COR domain, *LRRK2* R1628P harbors a substitution of a highly basic polar arginine with a neutral nonpolar proline. Even though this substitution is not in the kinase domain, it can indirectly upregulate kinase activity by turning its adjacent amino acid residue S1627 to the phosphorylation site Cdk5, leading to conditional neuronal death [25]. These mechanistic findings could explain the fact that *LRRK2* R1628P is a

consistent genetic risk factor for PD in Asian populations. Similarly, other rare causal *LRRK2* variants located in the COR (Y1699C, L1795F) or ROC domains (R1441C/H/G) have been reported to significantly increase LRRK2 kinase activity [26–30].

Our findings show that *LRRK2* R1628P statistically increases the risk of developing PD by up to 2.91 times in Kinh Vietnamese. Subgroup analyses al showed that this variant significantly increases PD risk in male, early-onset, and late-onset populations with OR = 4.33, 2,84, 2.98, respectively. These results are consistent with the data for Chinese populations in Taiwan, Singapore, and mainland China but not with Europeans [11–13, 31, 32]. Other studies also show a concordant effect of R1628P and PD in other Asian populations, such as Thais and Malaysians [33, 34]. Another reason why the effect of *LRRK2* R1628P on PD is faint in other populations is the markedly low frequencies of this variant in Europeans, Hispanics, and Africans [35, 36]. In short, *LRRK2* R1628P seems to be a signature marker for PD in East Asian populations but not in other populations. This finding once again emphasizes the importance of studying disease-specific genetic associations in diverse ethnicities to develop a comprehensive understanding of the pathogenesis of complex diseases such as PD. Furthermore, the Kinh Vietnamese show distinct genetic-associated characteristics that require thorough investigations in regard to complex, heterogenous diseases. Recent studies showed that Kinh Vietnamese share signature genetic variants associated with hypertension, acute myocardial infarction, and type 2 diabetes mellitus with other Asian populations [37–42], however, novel variants were also identified [43].

This study has several limitations. First, *LRRK2* R1628P was analyzed in the absence of other genetic variants associated with PD, while previous studies have shown that the risk of developing PD is modified when multiple variants are integrated [44]. Second, complete clinical information on PD patients was not available; therefore, there are unresolved questions about how *LRRK2* R1628P affects the PD phenotype in the Kinh Vietnamese population. Third, the statistical power calculation was not performed, particularly for the subgroup analyses. Fourth, the control group was relatively young, and they were not entirely excluded from the risk of developing PD. Given the current estimated prevalence of PD in Vietnam [45] and the minor allele frequency of *LRRK2* R1628P, it is expected to the greatest degree that seven controls with GG genotype will develop PD, and this change would not significantly affect the results of this study.

In conclusion, we found that *LRRK2* R1628P is significantly associated with PD in Kinh Vietnamese and in different subgroups. However, comprehensive genetic studies combining both monogenic and polygenic models are required to understand fully the complex and heterogeneous genetic nature of PD, especially in a country like Vietnam, with more than 100 million residents who are getting older and facing the threat of PD.

Author contributions T.M and M.D designed the study; T.T and T.M recruited the participants; L.L, M.D performed genotyping; T.M and M.D wrote the manuscript. The manuscript was critically revised and approved by all the authors.

Funding This study was supported by University of Medicine and Pharmacy at Ho Chi Minh City, Vietnam under grant number 196/2023/HĐ-ĐHYD.

Data availability No datasets were generated or analysed during the current study.

Declarations

Ethics approval The studies involving human participants were reviewed and approved by the Ethics Committee of the University of Medicine and Pharmacy at Ho Chi Minh City, Vietnam (Approval number 1133/HĐĐĐ-ĐHYD).

Competing interests The authors declare no competing interests.

References

1. Lees AJ, Hardy J, Revesz T (2009) Parkinson's disease. Lancet 373:2055–2066. https://doi.org/10.1016/S0140-6736(09)60492-X
2. Warner TT, Schapira AHV (2003) Genetic and environmental factors in the cause of parkinson's disease. Ann Neurol 53:S16–S25. https://doi.org/10.1002/ana.10487
3. Paisán-Ruíz C, Jain S, Evans EW et al (2004) Cloning of the gene containing mutations that cause PARK8-Linked parkinson's disease. Neuron 44:595–600. https://doi.org/10.1016/j.neuron.2004.10.023
4. Zimprich A, Biskup S, Leitner P et al (2004) Mutations in *LRRK2* cause Autosomal-Dominant parkinsonism with pleomorphic pathology. Neuron 44:601–607. https://doi.org/10.1016/j.neuron.2004.11.005
5. Mata IF, Wedemeyer WJ, Farrer MJ et al (2006) LRRK2 in parkinson's disease: protein domains and functional insights. Trends Neurosci 29:286–293. https://doi.org/10.1016/j.tins.2006.03.006
6. Cookson MR (2010) The role of leucine-rich repeat kinase 2 (LRRK2) in parkinson's disease. Nat Rev Neurosci 11:791–797. https://doi.org/10.1038/nrn2935
7. Lee JH, Han J, Kim H et al (2019) Parkinson's disease-associated LRRK2-G2019S mutant acts through regulation of SERCA activity to control ER stress in astrocytes. Acta Neuropathol Commun 7:68. https://doi.org/10.1186/s40478-019-0716-4
8. Lin C-H, Tsai P-I, Wu R-M, Chien C-T (2010) LRRK2 G2019S mutation induces dendrite degeneration through mislocalization and phosphorylation of Tau by recruiting autoactivated GSK3β. J Neurosci 30:13138–13149. https://doi.org/10.1523/JNEUROSCI.1737-10.2010
9. Walter J, Bolognin S, Poovathingal SK et al (2021) The Parkinson's-disease-associated mutation LRRK2-G2019S alters dopaminergic differentiation dynamics via NR2F1. Cell Rep 37:109864. https://doi.org/10.1016/j.celrep.2021.109864
10. Correia Guedes L, Ferreira JJ, Rosa MM et al (2010) Worldwide frequency of G2019S LRRK2 mutation in parkinson's disease: A

systematic review. Parkinsonism Relat Disord 16:237–242. https://doi.org/10.1016/j.parkreldis.2009.11.004
11. Ross OA, Wu Y-R, Lee M-C et al (2008) Analysis of Lrrk2 R1628P as a risk factor for parkinson's disease. Ann Neurol 64:88–92. https://doi.org/10.1002/ana.21405
12. Zhang P, Wang Q, Jiao F et al (2016) Association of LRRK2 R1628P variant with parkinson's disease in ethnic Han-Chinese and subgroup population. Sci Rep 6:35171. https://doi.org/10.1038/srep35171
13. Lu C-S, Wu-Chou Y-H, van Doeselaar M et al (2008) The LRRK2 Arg1628Pro variant is a risk factor for parkinson's disease in the Chinese population. Neurogenetics 9:271–276. https://doi.org/10.1007/s10048-008-0140-6
14. Do MD, Tran TN, Luong AB et al (2023) Clinical and genetic analysis of Vietnamese patients diagnosed with early-onset parkinson's disease. Brain Behav 13:e2950. https://doi.org/10.1002/brb3.2950
15. Sherry ST, Ward MH, Kholodov M et al (2001) DbSNP: the NCBI database of genetic variation. Nucleic Acids Res 29:308–311. https://doi.org/10.1093/nar/29.1.308
16. Postuma RB, Berg D, Stern M et al (2015) MDS clinical diagnostic criteria for parkinson's disease. Mov Disord 30:1591–1601. https://doi.org/10.1002/mds.26424
17. Le LHG, Mai TP (2025) Establishing ASO PCR protocol for identifying R1628P variant in LRRK2 gene. Vietnam Med J 71:201–204. https://doi.org/10.51298/vmj.v547i2.12990
18. Mai P-T, Le D-T, Nguyen T-T et al (2019) Novel GDAP1 mutation in a Vietnamese family with Charcot-Marie-Tooth disease. Biomed Res Int 2019:7132494. https://doi.org/10.1155/2019/7132494
19. Do MD, Pham DV, Le LP et al (2021) Recurrent PROC and novel PROS1 mutations in Vietnamese patients diagnosed with idiopathic deep venous thrombosis. Int J Lab Hematol 43:266–272. https://doi.org/10.1111/ijlh.13345
20. Thao MP, Tuan PVA, Linh LGH et al (2018) Association of HLA-B∗38:02 with antithyroid drug-induced agranulocytosis in Kinh Vietnamese patients. Int J Endocrinol 2018:7965346. https://doi.org/10.1155/2018/7965346
21. Do MD, Mai TP, Do AD et al (2020) Risk factors for cutaneous reactions to allopurinol in Kinh vietnamese: results from a case-control study. Arthritis Res Therapy 22:182. https://doi.org/10.1186/s13075-020-02273-1
22. Usmani A, Shavarebi F, Hiniker A (2021) The cell biology of LRRK2 in parkinson's disease. Mol Cell Biol 41:e00660–e00620. https://doi.org/10.1128/MCB.00660-20
23. Rui Q, Ni H, Li D et al (2018) The role of LRRK2 in neurodegeneration of Parkinson disease. Curr Neuropharmacol 16:1348–1357. https://doi.org/10.2174/1570159X16666180222165418
24. Yoon J-H, Mo J-S, Kim M-Y et al (2017) LRRK2 functions as a scaffolding kinase of ASK1-mediated neuronal cell death. Biochim Biophys Acta (BBA) Mol Cell Res 1864:2356–2368. https://doi.org/10.1016/j.bbamcr.2017.09.001
25. Y S, J M, P Z, et al (2016) Parkinson-Related LRRK2 mutation R1628P enables Cdk5 phosphorylation of LRRK2 and upregulates its kinase activity. PloS one 11:. https://doi.org/10.1371/journal.pone.0149739
26. Muda K, Bertinetti D, Gesellchen F et al (2014) Parkinson-related LRRK2 mutation R1441C/G/H impairs PKA phosphorylation of LRRK2 and disrupts its interaction with 14-3-3. Proc Natl Acad Sci U S A 111:E34–43. https://doi.org/10.1073/pnas.1312701111
27. West AB, Moore DJ, Choi C et al (2007) Parkinson's disease-associated mutations in LRRK2 link enhanced GTP-binding and kinase activities to neuronal toxicity. Hum Mol Genet 16:223–232. https://doi.org/10.1093/hmg/ddl471
28. Henry AG, Aghamohammadzadeh S, Samaroo H et al (2015) Pathogenic LRRK2 mutations, through increased kinase activity, produce enlarged lysosomes with reduced degradative capacity and increase ATP13A2 expression. Hum Mol Genet 24:6013–6028. https://doi.org/10.1093/hmg/ddv314
29. Lange LM, Levine K, Fox SH et al (2025) The LRRK2 p.L1795F variant causes parkinson's disease in the European population. Npj Parkinsons Dis 11:1–10. https://doi.org/10.1038/s41531-025-00896-2
30. Kalogeropulou AF, Purlyte E, Tonelli F et al (2022) Impact of 100 LRRK2 variants linked to parkinson's disease on kinase activity and microtubule binding. Biochem J 479:1759–1783. https://doi.org/10.1042/BCJ20220161
31. Berg D, Schweitzer KJ, Leitner P et al (2005) Type and frequency of mutations in the LRRK2 gene in Familial and sporadic parkinson's disease*. Brain 128:3000–3011. https://doi.org/10.1093/brain/awh666
32. Di Fonzo A, Tassorelli C, De Mari M et al (2006) Comprehensive analysis of the LRRK2 gene in Sixty families with parkinson's disease. Eur J Hum Genet 14:322–331. https://doi.org/10.1038/sj.ejhg.5201539
33. Pulkes T, Papsing C, Thakkinstian A et al (2014) Confirmation of the association between LRRK2 R1628P variant and susceptibility to parkinson's disease in the Thai population. Parkinsonism Relat Disord 20:1018–1021. https://doi.org/10.1016/j.parkreldis.2014.06.013
34. Gopalai AA, Lim S-Y, Chua JY et al (2014) LRRK2 G2385R and R1628P mutations are associated with an increased risk of parkinson's disease in the Malaysian population. Biomed Res Int 2014:867321. https://doi.org/10.1155/2014/867321
35. Simpson C, Vinikoor-Imler L, Nassan FL et al (2022) Prevalence of ten *LRRK2* variants in parkinson's disease: A comprehensive review. Parkinsonism Relat Disord 98:103–113. https://doi.org/10.1016/j.parkreldis.2022.05.012
36. Shu L, Zhang Y, Sun Q et al (2019) A comprehensive analysis of population differences in LRRK2 variant distribution in parkinson's disease. Front Aging Neurosci 11:13. https://doi.org/10.3389/fnagi.2019.00013
37. Tran NQ, Truong SD, Ma PT et al (2022) Association of KCNJ11 and ABCC8 single-nucleotide polymorphisms with type 2 diabetes mellitus in a Kinh Vietnamese population. Med (Baltim) 101:e31653. https://doi.org/10.1097/MD.0000000000031653
38. Truong S, Tran NQ, Ma PT et al (2022) Association of ADIPOQ Single-Nucleotide polymorphisms with the two clinical phenotypes type 2 diabetes mellitus and metabolic syndrome in a Kinh Vietnamese population. Diabetes Metab Syndr Obes 15:307–319. https://doi.org/10.2147/DMSO.S347830
39. Tran TT, Mai TP, Tran HCB et al (2021) Association between AGT M235T and left ventricular mass in Vietnamese patients diagnosed with essential hypertension. Front Cardiovasc Med 8:608948. https://doi.org/10.3389/fcvm.2021.608948
40. Tran DC, Do MD, Le LHG et al (2023) Predictive value of ACE I/D genetic polymorphism for 12-month all-cause mortality in patients with acute myocardial infarction. Medicine 102:e34976. https://doi.org/10.1097/MD.0000000000034976
41. Tran DC, Le LHG, Thai TT et al (2024) Effect of AGTR1 A1166C genetic polymorphism on coronary artery lesions and mortality in patients with acute myocardial infarction. PLoS ONE 19:e0300273. https://doi.org/10.1371/journal.pone.0300273
42. Tran DC, Le LHG, Thai TT et al (2023) Association between ACE I/D genetic polymorphism and the severity of coronary artery disease in Vietnamese patients with acute myocardial infarction. Front Cardiovasc Med 10. https://doi.org/10.3389/fcvm.2023.1091612
43. Mai TP, Luong BA, Ma PT et al (2024) Genome-wide association and polygenic risk score estimation of type 2 diabetes mellitus in Kinh Vietnamese-A pilot study. J Cell Mol Med 28:e18526. https://doi.org/10.1111/jcmm.18526

44. Wang C, Cai Y, Zheng Z et al (2012) Penetrance of LRRK2 G2385R and R1628P is modified by common PD-associated genetic variants. Parkinsonism Relat Disord 18:958–963. https://doi.org/10.1016/j.parkreldis.2012.05.003
45. GBD 2019 Diseases and Injuries Collaborators (2020) Global burden of 369 diseases and injuries in 204 countries and territories, 1990–2019: a systematic analysis for the global burden of disease study 2019. Lancet 396:1204–1222. https://doi.org/10.1016/S0140-6736(20)30925-9