



## OPEN ACCESS

## EDITED BY

Antonio Emanuele Elia,  
IRCCS Carlo Besta Neurological Institute  
Foundation, Italy

## REVIEWED BY

Matthew Gegg,  
University College London, United Kingdom  
Micol Avenali,  
Neurological Institute Foundation Casimiro  
Mondino (IRCCS), Italy

## \*CORRESPONDENCE

Jae-heyok Lee  
✉ jhlee.neuro@pusan.ac.kr

RECEIVED 06 November 2024

ACCEPTED 03 March 2025

PUBLISHED 02 April 2025

## CITATION

Hwangbo J, Lee MJ, Kim SJ, Park HK and Lee  
J-h (2025) Comparative analysis of methods  
for measuring glucocerebrosidase enzyme  
activity in patients with Parkinson's disease  
with the *GBA1* variant.  
*Front. Neurol.* 16:1523655.  
doi: 10.3389/fneur.2025.1523655

## COPYRIGHT

© 2025 Hwangbo, Lee, Kim, Park and Lee.  
This is an open-access article distributed  
under the terms of the [Creative Commons  
Attribution License \(CC BY\)](#). The use,  
distribution or reproduction in other forums is  
permitted, provided the original author(s) and  
the copyright owner(s) are credited and that  
the original publication in this journal is cited,  
in accordance with accepted academic  
practice. No use, distribution or reproduction  
is permitted which does not comply with  
these terms.

# Comparative analysis of methods for measuring glucocerebrosidase enzyme activity in patients with Parkinson's disease with the *GBA1* variant

Jin Hwangbo<sup>1</sup>, Myung Jun Lee<sup>2,3</sup>, Sang Jin Kim<sup>4</sup>,  
Hyun Kyung Park<sup>5</sup> and Jae-heyok Lee<sup>3,6\*</sup>

<sup>1</sup>Busan St. Mary's Hospital, Busan, Republic of Korea, <sup>2</sup>Pusan National University Hospital, Busan, Republic of Korea, <sup>3</sup>School of Medicine, Pusan National University, Yangsan, Republic of Korea, <sup>4</sup>Inje University Busan Paik Hospital, Busan, Republic of Korea, <sup>5</sup>Special Chemistry Team, Seoul Clinical Laboratories (SCL), Yongin, Republic of Korea, <sup>6</sup>Pusan National University Yangsan Hospital, Yangsan, Republic of Korea

**Introduction:** *GBA1* variants are significant genetic risk factors for Parkinson's disease (PD). Accurately measuring glucocerebrosidase (GCase) activity is crucial for understanding disease progression and developing targeted therapies. This study aimed to validate strategies for measuring blood GCase activity in patients with *GBA1*-associated PD (GBA-PD).

**Methods:** We recruited 25 GBA-PD patients and 27 matched PD patients without *GBA1* variants (non-GBA-PD). GCase activity from fresh blood was quantified using the 4-methylumbelliferyl  $\beta$ -D-glucopyranoside leukocyte assay (GCaseRaw). The GCase patient/normal control ratio (GCase ratio) was calculated for consistency. GCase activity in dried blood spot (DBS) specimens (GCaseDBS) and plasma glucosylsphingosine (GluSph) levels were measured using LC-MS/MS. The diagnostic accuracy was assessed using area under the curve (AUC) values.

**Results:** No significant differences in demographics or disease characteristics were found between GBA-PD and non-GBA-PD patients. GCase activity was significantly lower in patients with GBA-PD ( $p < 0.001$ ). The GCase ratio exhibited a higher diagnostic accuracy (AUC, 0.93) than GCaseRaw (AUC, 0.88) or GCaseDBS (AUC, 0.78). Plasma GluSph levels were higher in GBA-PD patients and were negatively correlated with the GCase ratio ( $r = -0.326$ ;  $p < 0.01$ ).

**Discussion:** The relative ratio of GCase activity showed a strong discriminatory potential, distinguishing between GBA-PD and non-GBA-PD.

## KEYWORDS

Parkinson's disease, *GBA1*, glucocerebrosidase, blood biomarkers, glycosphingolipids

## Introduction

Variants in *GBA1*, which encodes the lysosomal enzyme  $\beta$ -glucocerebrosidase (GCase), are among the most significant genetic risk factors for Parkinson's disease (PD). Studies have found that heterozygous mutations in *GBA1* can lead to decreased GCase activity, resulting in the accumulation of glycosphingolipids, which are believed to contribute to the pathogenesis

of PD by impairing autophagic processes and promoting the aggregation of  $\alpha$ -synuclein (1).

Based on their role in Gaucher's disease (GD), *GBA1* variants are classified as 'severe' (e.g., p.L483P, previously known as L444P) or 'mild' (e.g., p.N409S, N370S) (2). 'Risk' variants (e.g., p.E365K, E326K) are associated with PD risk but do not cause Gaucher's disease. Severe *GBA1* variants are associated with a higher risk of PD, younger onset, and more rapid disease progression, whereas mild and high-risk variants are associated with a more benign course (1, 2). The severity of *GBA1* variants is known to affect functional biomarker profiles in patients with *GBA1*-associated PD (GBA-PD) (3, 4). Severe variants showed the lowest GCCase levels with the steepest decline over time, as well as the lowest CSF total alpha-synuclein and highest seeding activity, indicating more aggressive pathology (5, 6).

GCCase activity is generally reduced in peripheral blood samples from patients with GBA-PD, accompanied by the accumulation of substrates, similar to the reductions observed in the brain and CSF (3). The two key substrates of GCCase are glucosylceramide (GluCer) and glucosylsphingosine (GluSph) (7). GlcSph is a more clinically useful biomarker, as it correlates with disease burden in GD. Accurate measurement of GCCase activity is crucial for understanding the biochemical impact of *GBA1* variants and for developing targeted therapies to enhance GCCase function in patients with GBA-PD. However, considerable variability in the methods used to measure GCCase activity in disease models and patient populations may impede the development of effective GCCase therapies (8, 9). This study aimed to validate widely used strategies for measuring GCCase activity in blood samples from patients with GBA-PD to assess their diagnostic efficacy and correlation with GlcSph levels.

## Materials and methods

We recruited 25 patients with GBA-PD and 27 disease duration-matched patients with PD without *GBA1* variants (non-GBA-PD). All patients fulfilled the Movement Disorder Society's diagnostic criteria for PD (10). The study was approved by the Institutional Review Board of Pusan National University Yangsan Hospital (No. 05–2023-189), and informed consent was obtained in accordance with the recommendations of the Declaration of Helsinki. To detect *GBA1* variants, the entire *GBA* gene, including all 11 exons and intron-exon boundaries, was sequenced using a long-range polymerase chain reaction approach to exclude the amplification of its pseudogene (11). *GBA* mutations were annotated according to NM\_000157.4 and NP\_000148.2. Immediately after blood collection, whole-blood and dried blood spot (DBS) samples were sent to a commercial testing laboratory for comprehensive analysis. GCCase activity (nmol/h/mg) from fresh blood was quantified using the 4-methylumbelliferyl  $\beta$ -D-glucopyranoside (4-MUG) leukocyte assay (GCCaseRaw), corrected for white blood cell counts. The GCCase activities of each patient and three controls (blank, normal control, and abnormal control) were measured simultaneously. The GCCase patient/normal control ratio (%) was also calculated for consistency (GCCaseRatio) (11). GCCase activity ( $\mu$ mol/h/L) from DBS specimens (GCCaseDBS) and plasma glucosylsphingosine (GluSph, ng/mL) concentrations were measured using liquid chromatography with

tandem mass spectrometry (LC–MS/MS). Further experimental details are provided in the [Supplementary material](#).

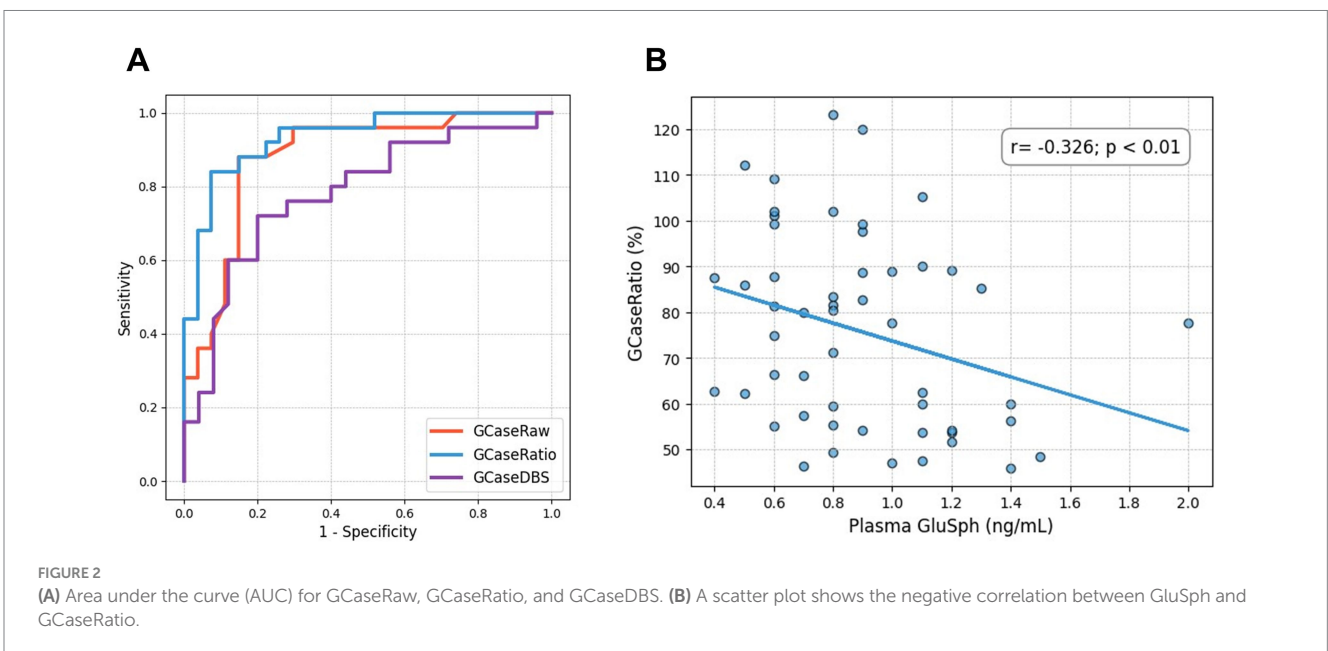
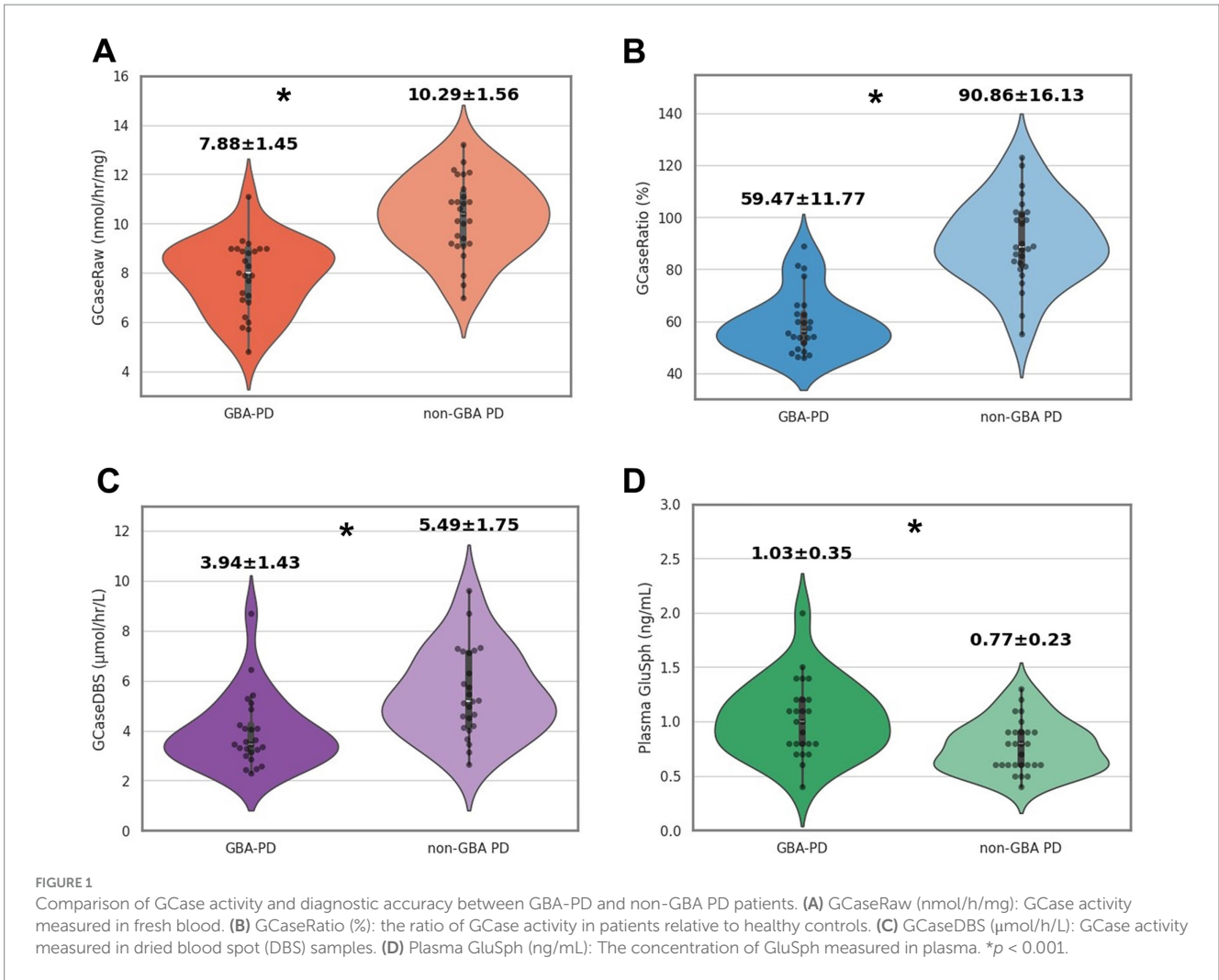
The data processing and statistical analyses were performed using SPSS (version 29.0.2). Group differences were analyzed using the Mann–Whitney *U* test for continuous variables and the  $\chi^2$  test for categorical variables. Age and disease duration were controlled using an analysis of covariance. Diagnostic accuracy was assessed using the corresponding area under the curve (AUC) values. The figures were generated using Python 3.12.5 with the matplotlib and Seaborn libraries.

## Results

The clinical features of patients with GBA-PD and non-GBA-PD are presented in [Table 1](#). There were no significant differences between GBA-PD and non-GBA-PD patients in age at onset, age at evaluation, disease duration, sex, Unified Parkinson's Disease Rating Scale Part III (UPDRS-III) scores, Hoehn and Yahr stage, Mini-Mental State Examination (MMSE), Montreal Cognitive Assessment (MoCA) performance, and levodopa-equivalent daily dose (LEDD). The heterozygous *GBA1* variants identified among the patients included p.L483P ( $n = 8$ ), p.R159W (R120W,  $n = 3$ ), p.N227S (N188S,  $n = 2$ ), p.F252I (F213I,  $n = 2$ ), p.D448H (D409H,  $n = 2$ ), p.R202\* (R163\*,  $n = 1$ ), p.I442V ( $n = 1$ ), c.115 + 1G > A ( $n = 1$ ), p.N431S (N392S,  $n = 1$ ), Rec1 [p.L483P; p.A495P; p.V499=] ( $n = 1$ ), p.G416S (G377S,  $n = 1$ ), p.V211fs (c.630delC,  $n = 1$ ), and p.G85E (G46E,  $n = 1$ ). Most of these patients (21 of 25) were classified as having severe variants (2). Among the remaining four *GBA1* variants, p.G85E was classified as mild, while p.I442V, p.N431S, and p.V211fs were categorized as unknown. GCCase activity from all specimens was significantly reduced in GBA-PD patients ( $p < 0.001$ ), compared to non-GBA-PD patients (GCCaseRaw,  $7.88 \pm 1.45$  nmol/h/mg vs.  $10.29 \pm 1.56$  nmol/h/mg,  $p < 0.001$ ; GCCaseRatio,  $59.47 \pm 11.77\%$  vs.  $90.86 \pm 16.13\%$ ,  $p < 0.001$ ; GCCaseDBS,  $3.94 \pm 1.43$   $\mu$ mol/h/L vs.  $5.49 \pm 1.75$   $\mu$ mol/h/L,  $p < 0.001$ ) ([Figures 1A–C](#)). The GCCaseRatio exhibited higher diagnostic accuracy (AUC, 0.93; 95% confidence interval [CI], 0.86–0.99) than GCCaseRaw (AUC, 0.88; 95% CI, 0.78–0.96) or GCCaseDBS (AUC, 0.78; 95% CI, 0.64–0.91) ([Figure 2A](#)). Plasma GluSph concentration was significantly higher in GBA-PD

**TABLE 1** Demographic and clinical characteristics of GBA-PDA and non-GBA-PD.

	GBA carriers ( $n = 25$ )	GBA non-carriers ( $n = 27$ )	$p$ value
Age of onset (yr)	$52.3 \pm 9.3$	$47.7 \pm 7.5$	0.078
Age at evaluation (yr)	$57.4 \pm 8.4$	$53.2 \pm 7.4$	0.08
Disease duration (yr)	$4.6 \pm 3.1$	$4.8 \pm 2.7$	0.719
Sex (Male/female)	11/14	13/14	0.773
UPDRS-III	$25.8 \pm 8.5$	$24.4 \pm 17.9$	0.135
Hoehn & Yahr	2.0 (1.0 ~ 2.5)	2.0 (1.0 ~ 2.5)	0.518
MMSE	$27.6 \pm 2.2$	$28.7 \pm 1.5$	0.071
MoCA	$25.0 \pm 4.4$	$26.8 \pm 3.1$	0.088
LEDD (mg)	$612.6 \pm 546.8$	$612.2 \pm 379.5$	0.318



patients than in non-GBA-PD patients ( $1.03 \pm 0.35$  ng/mL vs.  $0.77 \pm 0.23$  ng/mL,  $p < 0.001$ ) (Figure 1D) and was negatively correlated only with GCCaseRatio ( $r = -0.326$ ;  $p < 0.01$ ) (Figure 2B). There were no associations between blood biomarkers (GCCase activity and plasma GluSph levels) or clinical measures (UPDRS-III, H-Y stage, MMSE, and MoCA).

## Discussion

Our study revealed significant alterations in the blood GCCase activity and GlcSph levels in patients with GBA-PD, characterized by decreased GCCase activity and elevated GluSph levels. The differences between GBA-PD and non-GBA-PD were more distinct in our study than in previous research, possibly because our cohort had a higher proportion of severe variants and a markedly lower prevalence of risk variants than Western populations. Previous studies have shown that severe variants exhibit lower GCCase activity levels and demonstrate a more significant decline over time during follow-up (3, 4).

GCCase activity can be measured in various samples, including leukocytes, DBSs, and cultured cells (8, 12). Our comparative analysis demonstrated that the 4-MUG leukocyte assay had better diagnostic accuracy than the mass spectrometer-based method for DBS samples. This result was expected, given its value for diagnosing GD (12). DBS samples are useful for screening clinically suspected individuals and offer advantages such as ease of collection, small blood volume requirements, and simple transportation and storage. The 4-MUG leukocyte assay, with its established specificity and sensitivity, is the gold standard for measuring GCCase activity (12).

Recent studies have used DBS to assess GCCase activity in large cohorts of patients (4, 13–15). However, the correlation between *GBA1* variant severity and GCCase activity varies across studies. The DBS assay measures the enzymatic activity in protein lysates, including cytosolic and lysosomal GCCase (8). Factors such as blood volume, hematocrit, and pre-analytical steps such as drying time can also affect the results (12). Therefore, heterozygotes may have half-normal enzyme activity, overlapping with healthy controls, making enzyme determination in DBS samples for carrier status less reliable.

The diagnostic accuracy of the 4-MUG leukocyte assay significantly improved. The relative ratio of GCCase activity, calculated for consistency, showed enhanced discriminatory potential, distinguishing between the GBA-PD and non-GBA-PD groups. Moreover, this method revealed an inverse association between GCCase activity and its substrate, plasma GluSph, a valuable biomarker for monitoring and modulating the efficacy of interventions to increase GCCase activity (7, 13).

Despite its contributions, this study had several limitations. The small sample size may restrict the generalizability of our findings. We were unable to identify an association between blood biomarkers and PD status in the current samples. Unlike previous reports (1, 2), severe variants in our cohort did not show worse clinical features, possibly due to the short disease duration. Future research with larger cohorts, including a diverse range of variant severities, is warranted to establish the reliability of these blood biomarkers in clinical

settings and to investigate the variability in GCCase activity across different populations and stages of PD.

## Data availability statement

The original contributions presented in the study are included in the article/supplementary material, further inquiries can be directed to the corresponding author.

## Ethics statement

The studies involving humans were approved by the Institutional Review Board of Pusan National University Yangsan Hospital (No. 05-2023-189), and written informed consent was obtained in accordance with the recommendations of the Declaration of Helsinki. The studies were conducted in accordance with the local legislation and institutional requirements.

## Author contributions

JH: Data curation, Validation, Writing – original draft. ML: Supervision, Writing – review & editing. SK: Supervision, Writing – review & editing. HP: Supervision, Methodology, Writing – review & editing. J-hL: Conceptualization, Funding acquisition, Supervision, Validation, Writing – original draft, Writing – review & editing.

## Funding

The author(s) declare that financial support was received for the research and/or publication of this article. This study was supported by grants from the Korea Health Technology R&D Project through the Korean Healthy Industry Development Institute, funded by the Ministry of Health & Welfare, Republic of Korea (RS-2023-00265377), and a 2024 research grant from Pusan National University Yangsan Hospital.

## Acknowledgments

We would like to thank the Seoul Clinical Laboratories (SCL) team for providing the laboratory data and protocols used in this study.

## Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

## Generative AI statement

The authors declare that no Gen AI was used in the creation of this manuscript.

## Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations,

or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.

## Supplementary material

The Supplementary material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fneur.2025.1523655/full#supplementary-material>

## References

- Blandini F, Cilia R, Cerri S, Pezzoli G, Schapira AHV, Mullin S, et al. Glucocerebrosidase mutations and synucleinopathies: toward a model of precision medicine. *Mov Disord.* (2019) 34:9–21. doi: 10.1002/mds.27583
- Parlar SC, Grenn FP, Kim JJ, Baluwendrat C, Gan-Or Z. Classification of GBA1 variants in Parkinson's disease: the GBA1-PD browser. *Mov Disord.* (2023) 38:489–95. doi: 10.1002/mds.29314
- Huh YE, Usnich T, Scherzer CR, Klein C, Chung SJ. GBA1 variants and Parkinson's disease: paving the way for targeted therapy. *J Mov Disord.* (2023) 16:261–78. doi: 10.14802/jmd.23023
- Huh YE, Chiang MSR, Locascio JJ, Liao Z, Liu G, Choudhury K, et al.  $\beta$ -Glucocerebrosidase activity in GBA-linked Parkinson's disease: the type of mutation matters. *Neurology.* (2020) 95:e685–96. doi: 10.1212/WNL.0000000000009989
- Lerche S, Wurster I, Roeben B, Zimmermann M, Riebenbauer B, Deuschle C, et al. Parkinson's disease: Glucocerebrosidase 1 mutation severity is associated with CSF alpha-Synuclein profiles. *Mov Disord.* (2020) 35:495–9. doi: 10.1002/mds.27884
- Brockmann K, Quadalti C, Lerche S, Rossi M, Wurster I, Baiardi S, et al. Association between CSF alpha-synuclein seeding activity and genetic status in Parkinson's disease and dementia with Lewy bodies. *Acta Neuropathol Commun.* (2021) 9:175. doi: 10.1186/s40478-021-01276-6
- Surface M, Balwani M, Waters C, Haimovich A, Gan-Or Z, Marder KS, et al. Plasma glucosylsphingosine in GBA1 mutation carriers with and without Parkinson's disease. *Mov Disord.* (2022) 37:416–21. doi: 10.1002/mds.28846
- Ysselstein D, Young TJ, Nguyen M, Padmanabhan S, Hirst WD, Dzakmo N, et al. Evaluation of strategies for measuring lysosomal glucocerebrosidase activity. *Mov Disord.* (2021) 36:2719–30. doi: 10.1002/mds.28815
- den Heijer JM, Cullen VC, Pereira DR, Yavuz Y, de Kam ML, Grievink HW, et al. A biomarker study in patients with GBA1-Parkinson's disease and healthy controls. *Mov Disord.* (2023) 38:783–95. doi: 10.1002/mds.29360
- Postuma RB, Berg D, Stern M, Poewe W, Olanow CW, Oertel W, et al. MDS clinical diagnostic criteria for Parkinson's disease. *Mov Disord.* (2015) 30:1591–601. doi: 10.1002/mds.26424
- Hwangbo J, Lee MJ, Kim SJ, Lee J. The frequency of Korean patients with Parkinson's disease carrying GBA mutations in a subgroup with age at onset  $\leq$  55 years old. *J Mov Disord.* (2023) 16:207–9. doi: 10.14802/jmd.22191
- Dardis A, Michelakakis H, Rozenfeld P, Fumic K, Wagner J, Pavan E, et al. Patient-centered guidelines for the laboratory diagnosis of Gaucher disease type 1. *Orphanet J Rare Dis.* (2022) 17:442. doi: 10.1186/s13023-022-02573-6
- Alcalay RN, Wolf P, Chiang MSR, Helesicova K, Zhang XK, Merchant K, et al. Parkinson's progression markers initiative. Longitudinal measurements of glucocerebrosidase activity in Parkinson's patients. *Ann Clin Transl Neurol.* (2020) 7:1816–30. doi: 10.1002/acn3.51164
- Omer N, Giladi N, Gurevich T, Bar-Shira A, Gana-Weisz M, Glinka T, et al. Glucocerebrosidase activity is not associated with Parkinson's disease risk or severity. *Mov Disord.* (2022) 37:190–5. doi: 10.1002/mds.28792
- Marano M, Zizzo C, Malaguti MC, Bacchin R, Cavallieri F, De Micco R, et al. Increased glucosylsphingosine levels and Gaucher disease in GBA1-associated Parkinson's disease. *Parkinsonism Relat Disord.* (2024) 124:107023. doi: 10.1016/j.parkreldis.2024.107023