The genetics of Parkinson’s disease

....From family studies to diverse population scale genome wide assessments

Sara Bandres-Ciga, PharmD, M.S, PhD,
Staff Scientist
Centre for Alzheimer’s and Related Dementias, CARD, NIH
@sarabandres1
Table of contents

● Parkinson’s disease as a “non-genetic disease”
● Molecular genetics pre-history
  ○ Autosomal dominant PD: SNCA as the major starting point
  ○ LRRK2: The race to discovery
  ○ Autosomal recessive juvenile parkinsonism: PRKN
  ○ GBA: From clinical observation to genetics
● The era of Genome-Wide Association Studies
  ○ PD risk, age at onset and progression
  ○ GWAS in underrepresented populations
  ○ Multi ancestry meta-analyses
● Connecting a global PD community: The GP2 initiative
● Key messages
Conclusions  The similarity in concordance overall indicates that genetic factors do not play a major role in causing typical PD. No genetic component is evident when the disease begins after age 50 years. However, genetic factors appear to be important when disease begins at or before age 50 years.
Brief Communication

Concordance for Parkinson's disease in twins: A 20-year update

Samuel M. Goldman MD, MPH, Kenneth Marek MD, Ruth Ottman PhD, Cheryl Meng MS, Kathleen Comyns MPH, Piu Chan MD, PhD, Jinghong Ma MD, Connie Marras MD, PhD, J. William Langston MD, G. Webster Ross MD, Caroline M. Tanner MD, PhD

During the 1990s, we estimated the genetic contribution to Parkinson's disease risk in a large, population-based twin registry. Because many unaffected twins were still alive, previous concordance estimates were based on incomplete information. Ninety-five percent of twins are now deceased. Here, we update concordance and heritability through 2015 using National Death Index data. In total, we identified 30 concordant and 193 discordant pairs. Proband-wise concordance was 0.20 in monozygotic and 0.13 in dizygotic pairs. Heritability was 0.27 overall, 0.83 in pairs diagnosed ≤50, and 0.19 in pairs diagnosed >50. High concordance in dizygotic twins suggests shared effects of early childhood environment. Ann Neurol 2019;85:600–605
Identification of novel risk loci, causal insights, and heritable risk for Parkinson’s disease: a meta-analysis of genome-wide association studies


Refining heritability estimates and determining extant genetic risk

To quantify how much of the genetic liability we have explained and what direction to take with future PD GWAS we calculated updated heritability estimates and polygenic risk scores (PRS). Using LD score regression (LDSC) on a meta-analysis of all 11 clinically-ascertained datasets from our GWAS and estimated the liability-scale narrow-sense heritability of PD as 0.22 (95% CI 0.18 - 0.26), only slightly lower than a previous estimate derived using GCTA (0.27, 95% CI 0.17 - 0.38)10,13,14. This may be because LDSC is known to be more conservative than GCTA, however, our LDSC heritability estimate does fall within the 95% confidence interval of the GCTA estimate.

Heritability ~ 22%
(⅓ identified by current GWAS)
Family based studies of one SNP
"I have an excel on my computer in the lab" = 1kb of data at one location for one user. Kilobyte sized data.

Earliest GWAS appear
10’s or maybe 100’s of thousands of genotyped SNPs. Some early software like PLINK appears. Laptop compute. Megabyte sized data.

Meta GWAS era
Imputation yields millions of SNPs standardized across studies. Meta-analytic tools to work across silos. Laptop and cluster compute. Gigabyte sized data.

Transitional phase

Centralized research
Bring the user to the data! Software development!

The evolution of Parkinson’s disease genetics
Parkinson’s disease genetics lies on a continuum...

Bandres-Ciga S et al., 2020
A Large Kindred with Autosomal Dominant Parkinson’s Disease

Lawrence I. Golbe, MD,* Giuseppe Di Iorio, MD,† Vincenzo Bonavita, MD,‡ Douglas C. Miller, MD, PhD,‡ and Roger C. Duvoisin, MD*  

We report two large kindreds with Parkinson’s disease (PD) apparently inherited in autosomal dominant fashion. Forty-one persons in four generations have been affected; we have examined 7 of them. The two kindreds originated in a single small town in southern Italy and therefore are probably related. The illness was typical for PD except for early onset at a mean age of 46.5 years and a rapid course that averaged 9.7 years from onset to death. Clinical appearance and response to levodopa were typical for PD. Only one instance of definite nonpenetration is known. Autopsy of 2 patients in one kindred showed the pathological changes typical of PD with Lewy bodies. Disease duration among affected persons who spent most of their lives in Italy was longer than for their affected US relatives, suggesting that exogenous agents may influence the course of this genetic illness. We conclude that what is probably a single gene without an additional environmental insult can cause the pathological changes typical of PD. Our findings therefore enhance the likelihood of a significant genetic component in the cause of sporadic PD. By identifying a toxic gene product, future molecular genetic studies in our kindred(s) may provide insight into the pathogenesis of sporadic PD.

SNCA as a disease-causing Parkinson’s disease gene

Mutation in the α-Synuclein Gene Identified in Families with Parkinson’s Disease


Parkinson’s disease (PD) is a common neurodegenerative disorder with a lifetime incidence of approximately 2 percent. A pattern of familial aggregation has been documented for the disorder, and it was recently reported that a PD susceptibility gene in a large Italian kindred is located on the long arm of human chromosome 4. A mutation was identified in the α-synuclein gene, which codes for a presynaptic protein thought to be involved in neuronal plasticity, in the Italian kindred and in three unrelated families of Greek origin with autosomal dominant inheritance for the PD phenotype. This finding of a specific molecular alteration associated with PD will facilitate the detailed understanding of the pathophysiology of the disorder.
α-Synuclein in Lewy bodies

Maria Grazia Spillantini, Marie Luise Schmidt, Virginia M.-Y. Lee, John Q. Trojanowski, Ross Jakes & Michel Goedert

SNCA point mutations

SNCA described mutations (A53T, E46K, A30P, H50Q, G51D)

Insufficient evidence for pathogenicity of SNCA His50Gln (H50Q) in Parkinson’s disease

Cornelis Blauwendraat1, Demis A. Kia1, Lasse Pihlstrom3, Ziv Gan-Or4,5, Suzanne Lesage6, J. Raphael Gibbs3, Jinhui Ding7, Roy N. Alcalay3,8, Sharon Hassan-Baer9,10,11, Alan M. Pittman4, Janet Brooks1, Connor Edsall1, Sun Ju Chung12, Stefano Goldwurm13,14, Mathias Toft13,15, Claudia Schulte16, International Parkinson’s Disease Genomics Consortium (IPDGC), COURAGE-PD Consortium, Dena Hernandez7, Andrew B. Singleton7, Mike A. Nalls7,17, Alexis Brice8, Sonja W. Scholz14,18, and Nicholas W. Wood2

α-Synucleinopathy associated with G51D SNCA mutation: a link between Parkinson’s disease and multiple system atrophy?

Asife P. Kiely · Yasmine T. Asi · Elena Karka · Patricia Limonina · Helen Ling · Patrick Lewis · Christos Prousalakis · Niall Quinn · Andrew J. Lees · John Hardy · Tamás Revesz · Henry Houlden · Janice L. Holton

The New Mutation, E46K, of α-Synuclein Causes Parkinson and Lewy Body Dementia

Juan J. Zarraonaindia, MD, PhD1, Javier Algozab, MD2, Juan C. Gómez-Esteban, MD, PhD3, Elena Leturzno, PhD3, Raquel Rojo, PhD3, Isabel Aunapo, PhD3, Lidice Villal, PhD3, Janet Hornicka, PhD3, Olga Rodrigo, MD, PhD3, Regula Arrieta, MD, PhD3, Verónica Lórenz, MD3, Estrella González-Torró, MD3, PhD3, Toribio del Ser, MD, PhD3, David G. Munitis, MD, PhD3, and Jesús G. de Yebenes, MD, PhD3,16

Ala30Pro mutation in the gene encoding α-synuclein in Parkinson’s disease

Christos Prousalakis, PhD, MRC
Christopher G. Dudzik, PhD
Timothy Brier, PhD, MBBS
Donna S. MacKay, PhD
J. Mark Cooper, PhD
Glen L. Millhauser, PhD
Henry Houlden, PhD, FRCP
Anthony H. Schapira, MD, DSc, FRCP, FMedSci

A novel α-synuclein missense mutation in Parkinson Disease

α-Synuclein (SNCA) is central to the pathogenesis of Parkinson disease (PD), with 3 missense mutations reported to date. We report a novel mutation (p.H50Q) in a pathologically proven case.

Methods and results. Standard protocol approvals, registrations, and patient consent. Patients had given written informed consent for use of their brains in research. The study was approved by the local ethics committee.

Genetic analysis. We amplified and sequenced SNCAG exons (ENSEMBL transcript ID 394986) in DNA extracted from substantia nigra (SN) of 5 Queen Square PD Brain Bank cases (primers given in table e-1 on the Neurology® Web site at www.neurology.org).

Reiko Krüger1,2, Wilfried Kuhn1, Thomas Müller1, Dirk Woitalla1, Manuel Graeber1, Sigfried Kösel1, Horst Przuntek1, Jörg T. Eppenstein2, Ludger Schöls1 & Olaf Riess2
1Neurological University Hospital and 2Department of Molecular Human Genetics, Ruhr-University, 44780 Bochum, Germany.
3Department of Neuromorphology, Max-Planck-Institute for Psychiatry, 81377 Munich, Germany. *Correspondence should be addressed to O.R. e-mail: olaf.riess@ruhr-uni-bochum.de
Gene dosage mutations in SNCA cause Parkinson’s disease

α-Synuclein Locus Triplication Causes Parkinson’s Disease

A. B. Singleton,†† M. Farrer,† J. J. Johnson,† A. Singleton,‡ S. Hague,† J. Kachergus,§ M. Hulihan,‡ T. Peuralinna,∥ A. Dutra,∥ R. Nussbaum,‡ S. Lincoln,§ A. Crawley,‡ M. Hanson,†
D. Maraganore,§ C. Adler,∥ M. R. Cookson,† M. Muenter,∥ M. Baptista,† D. Miller,† J. Blanchat,∥ J. Hardy,† K. Gwinn-Hardy‡
Dementia as a *SNCA* Triplication Phenotype

Gwinn et al., 2011
L-dopa slows the progression of familial parkinsonism

Katrina Gwinn-Hardy, Virgilio Gerald H Evidente, Cheryl Waters, Manfred D Muenter, John Hardy

A: Kaplan-Meier mortality for all patients
B: Hoehn and Yahr staging for each of the patients
Solid lines illustrate treated patients and dotted lines, untreated patients. Hoehn and Yahr staging was not possible on all patients. Only those for whom three of more staging points were possible were included.
Clinical analysis of 17 patients in 12 Japanese families with autosomal-recessive type juvenile parkinsonism

Atsushi Ishikawa, MD, and Shoji Tsuji, MD

Article abstract—We present the clinical features of 17 patients from 12 Japanese families with familial juvenile parkinsonism suggesting autosomal-recessive inheritance (AR-JP). Because the marriages of the parents in all but one family were consanguineous and all patients were only first generation, an autosomal-recessive trait was strongly suspected. Analysis of the clinical features showed female predominance, mean age at onset 27.8 years, and slow progression. The symptoms of the parkinsonian triad (tremor, rigidity, and bradykinesia) were mild, but gait freezing, hyperreflexia, foot dystonia, and retropulsion were relatively prominent. A characteristic finding was amelioration of parkinsonian symptoms after sleep in all patients. Response to levodopa was satisfactory, but dopa-induced choreic limb dyskinesia and wearing-off phenomenon occurred frequently. Juvenile parkinsonism is a syndrome that encompasses several clinical entities. The similarity of clinical findings in these patients, and the differences from other types of parkinsonism, indicates that AR-JP is a distinct clinical entity.

NEUROLOGY 1996;47:160–166
PRKN as a disease-causing Parkinson’s disease gene

Found by homozygosity mapping and in cases with exon deletions

Mutations in the *parkin* gene cause autosomal recessive juvenile parkinsonism

Tohru Kitada, Shuichi Asakawa, Nobutaka Hattori, Hiroto Matsumine, Yasuhiro Yamamura, Shinsei Minoshima, Masayuki Yokochi, Yoshikuni Mizuno & Nobuyoshi Shimizu
No Lewy Bodies!!!

So is it a different disease?

Parkin Disease

A Clinicopathologic Entity?

Karen M. Doherty, MRCP; Laura Silveira-Moriyama, PhD; Laura Parkkinen, PhD; Daniel G. Healy, PhD; Michael Farrell, FRCP; Niccolo E. Mencacci, MD; Zeshan Ahmed, PhD; Francesca M. Brett, FRCP; John Hardy, PhD; Niall Quinn, MD; Timothy J. Counihan, FRCP; Timothy Lynch, FRCP; Zoe V. Fox, PhD; Tamas Revesz, FRCP; Andrew J. Lees, MD; Janice L. Holton, FRCP
PARK-8: The race to discovery

Funayama et al., 2002
LRRK2 as a disease-causing Parkinson’s disease gene

Mutations in LRRK2 Cause Autosomal-Dominant Parkinsonism with Pleomorphic Pathology

Cloning of the Gene Containing Mutations that Cause PARK8-Linked Parkinson’s Disease

Mutations in LRRK2 Cause Autosomal-Dominant Parkinsonism with Pleomorphic Pathology

Cloning of the Gene Containing Mutations that Cause PARK8-Linked Parkinson’s Disease


Coro Paisán-Ruiz, Shushant Jain, E. Whitney Evans, William P. Gilks, Javier Simón, Marcel van der Brug, Adolfo López de Munain, Silvia Aparicio, Angel Martinez Gil, Naheed Khan, Janel Johnson, Javier Ruiz Martinez, David Nicholl, Itxaso Martí Carrera, Amets Saenz Peña, Rohan de Silva, Andrew Lees, José Félix Martí-Massó, Jordi Pérez-Tur, Nick W. Wood, and Andrew B. Singleton
Hereditary Early-Onset Parkinson’s Disease Caused by Mutations in PINK1

Enza Maria Valente,1,2* Patrick M. Abou-Sleiman,2* Viviana Caputo,1,3* Miratul M. K. Muqit,2,4† Kirsten Harvey,5 Suzana Gispert,6 Zeeshan Ali,6 Domenico Del Turco,7 Anna Rita Bentivoglio,8 Daniel G Healy,9 Alberto Albanese,10 Robert Nussbaum,11 Rafael González-Maldonado,12 Thomas Deller,7 Sergio Salvi,1 Pietro Cortelli,13 William P. Gilks,2 David S. Latchman,4,14 Robert J. Harvey,5 Bruno Dallapiccola,1,3 Georg Aebburger,15 Nicholas W. Wood2,*

Parkinson’s disease (PD) is a neurodegenerative disorder characterized by degeneration of dopaminergic neurons in the substantia nigra. We previously mapped a locus for a rare familial form of PD to chromosome 1p36 (PARK6). Here we show that mutations in PINK1 (PTEN-induced kinase 1) are associated with PARK6. We have identified two homozygous mutations affecting the PINK1 kinase domain in three consanguineous PARK6 families: a truncating nonsense mutation and a missense mutation at a highly conserved amino acid. Cell culture studies suggest that PINK1 is mitochondrially located and may exert a protective effect on the cell that is abrogated by the mutations, resulting in increased susceptibility to cellular stress. These data provide a direct molecular link between mitochondria and the pathogenesis of PD.

Mutations in the DJ-1 Gene Associated with Autosomal Recessive Early-Onset Parkinsonism

Vincenzo Bonifati,1,2* Patrizia Rizzu,1 Marijke J. van Baren,1 Onno Schaap,1 Guido J. Breedveld,1 Elmar Krieger,3 Marieke C. J. Dekker,1 Ferdinando Squitieri,4 Pablo Ibanez,5 Marijke Joosse,1 Jeroen W. van Dongen,1 Nicola Vanacore,2,6 John C. van Swieten,7 Alexis Brice,5 Giuseppe Meco,2 Cornelia M. van Duijn,1 Ben A. Oostra,1 Peter Heutink1*

Genome-wide Linkage Analysis of a Parkinsonian-Pyramidal Syndrome Pedigree by 500 K SNP Arrays

Seyyedehdi Shojaeie,1 Farzad Sina,4 Setareh Sadat Banihosseini,5 Mohammad Hossein Kazemi,5 Reza Kalhor,6 Gholam-Ali Shahidi,4 Hossein Fakhrai-Rad,7 Mostafa Ronaghi,7 and Elahe Elahi2,3,*
Heterozygous GBA mutations predispose to Parkinson’s disease

Multicenter Analysis of Glucocerebrosidase Mutations in Parkinson’s Disease


A Multicenter Study of Glucocerebrosidase Mutations in Dementia With Lewy Bodies

Michael A. Nalls, PhD; Raquel Duran, PhD; Grisel Lopez, MD; Marzena Kurzawa-Akanbi, PhD; Ian G. McKeel, FMedSci; Patrick F. Chimney, PhD; Christopher M. Morris, PhD; Jessie Theuns, PhD; David Cross, MD; PhD; Patrick Crus, MD, PhD; Sebastiaan Engelborghs, MD, PhD; Peter Paul De Deyn, MD, PhD; Christine Van Broeckhoven, PhD, DSc; David M. A. Mann, PhD; Julie Snowden, PhD; Stewart Pickering-Brown, PhD; Nicola Halliwell, BSc; Yvonne Davidson, MSc; Linda Gibbons, MSc; Jenny Harris, BSc; Una-Marie Sheerin, MD; Jose Bras, PhD; John Hardy, PhD; Lorraine Clark, PhD; Karen Marder, MD, MPh; Lawrence S. Honig, MD, PhD; Daniela Berg, MD; Walter Maetzler, MD; Kathrin Brockmann, MD; Thomas Gasser, MD; Fabiana Novellino, MD; Aldo Quattrone, MD; Grazia Ainesi, PhD; Elvira Valeria De Marco, PhD; Ekaterina Rogaeva, PhD; Mario Manelli, MD, PhD; Sandra E. Black, MD; Juan M. Bilbao, MD; Tatiana Foroud, PhD; Bernardino Ghetti, MD; William C. Nichols, PhD; Nathan Panzer, PhD; Glenda Halliday, PhD; Suzanne Lesage, PhD; Stephan Klebe, MD, PhD; Alexandra Durr, MD, PhD; Charles Daychouets, MD, PhD; Alexis Brice, MD; Benoit I. Giasson, PhD; John Q. Trojanowski, MD, PhD; Howard I. Hurtig, MD; Nahid Taybi, PhD; Claudia Landazábal, Melanie A. Knight, PhD; Margaux Keller, BA; Andrew B. Singleton, PhD, Tyra G. Wolfsberg, PhD; Ellen Sidransky, MD
The GWAS era in Parkinson’s disease

- Historically, only familial sequencing and small-scale genotyping studies were possible.
- Now, technology allows for cheap high-throughput sequencing of thousands of samples.
The GWAS era in Parkinson’s disease

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

Wataru Satake1,3, Yuko Nakabayashi1,2, Ikuko Mizuta1,2, Yushi Hirota1,2, Chiyomi Ito1,2, Michiaki Kubo1, Takahisa Kawaguchi4, Tatsuhiko Tsunoda4, Masahiko Watanabe5, Atsushi Takeda5, Hiroyuki Tomiyama7, Kenji Nakashima6, Kazuko Hasegawa6, Fumiya Obata10, Takeo Yoshikawa11, Hideshi Kawakami12, Saburo Sakoda3, Mitsutoshi Yamamoto13, Nobutaka Hattori1, Miho Murata14, Yusuke Nakamura14,15 & Tatsushi Toda1,2

Genome-wide association study reveals genetic risk underlying Parkinson’s disease

Javier Simón-Sánchez1,2,22, Claudia Schulte3,22, Jose M Bras1,22, Manu Sharma5,22, J Raphael Gibbs1,3, Daniela Berg1, Coro Paisan-Ruiz2, Peter Lichtner5, Sonja W Scholz1,5, Dena G Hernandez1,5, Reijo Krutger3, Monica Federoff1, Christine Klein7, Alison Goate6, Joel Perlmutter6, Michael Bonin9, Michael A Nalls1, Thomas Illig10, Christian Gieger19, Henry Houlden3, Michael Steffen11, Michael S Okun12, Brad A Racette5, Mark R Cookson4, Kelly D Foote32, Hubert F Hernandez12, Bryan J Traynor1, Stefan Schreiber13, Sampath Arepalli1, Ryan Zonoz1, Katrina Gwinn15, Marcel van der Brugg11,15, Grisel Lopez16, Stephen J Chao32, Arthur Schatzkin17, Yukyung Park17, Albert Hollenbeck18, Jianjun Gao19, Xuewei Hua9, Nick W Wood5, Delia Lorenzi21, Günther Deuschl21, Honglei Chen19, Olaf Riess9, John A Hardy5, Andrew B Singleton1 & Thomas Gasser3

2,000 Asians
SNCA and BST1

2,000 Europeans
SNCA and MAPT
Common genetic variation in the HLA region is associated with late-onset sporadic Parkinson’s disease

Taye H Hamza1, Cyrus P Zabetian1,2, Albert Tenesa4, Alain Laederach1, Jennifer Montimurro1, Dora Yearout1,3, Denise M Kay1, Kimberly F Doheny5, Justin Paschall6, Elizabeth Pugh5, Victoria I Kusel1, Randall Collura1, John Roberts2, Alida Griffith3, Ali Samii2,3, William K Scott9, John Nutt10, Stewart A Factor11 & Haydeh Payami1

Imputation of sequence variants for identification of genetic risks for Parkinson’s disease: a meta-analysis of genome-wide association studies

International Parkinson Disease Genomics Consortium*

A Two-Stage Meta-Analysis Identifies Several New Loci for Parkinson’s Disease

International Parkinson’s Disease Genomics Consortium (IPDGC), Wellcome Trust Case Control Consortium 2 (WTCCC2)
The first Parkinson’s disease GWAS...

PD-code meta-analysis 01.13.2009, lambda = 1.035441

Simon-Sanchez et al., 2009
The latest Parkinson’s disease GWAS...

Nalls et al., 2019
Identification of novel risk loci, causal insights, and heritable risk for Parkinson's disease: a meta-analysis of genome-wide association studies by Nalls et al., 2019

What was done?
- GWAS looking at 57K cases and proxy cases against 1.4M controls

What was found?
- Identified 90 independent genome-wide significant risk signals across 78 genomic regions
And... what is next??

Projection of the number of GWAS loci with the increase of Parkinson’s disease cases

Blauwendraat et al., 2020
What has come out of GWAS versus PD risk?

Bandres-Ciga et al., 2019
“Multi-omic” refers to the ability to leverage human genetic and molecular profiles in our search for deeper understanding of disease.

This involves:

- Data harmonization
  - aligning study data to high-quality reference panels
- Intelligent storage of data as cohorts continue to grow in size and scope
- Standardization of processes and data for fast processing and automation of analyses
GWAS versus Parkinson’s disease age at onset

Blauwendraat et al., 2019
GWAS versus Parkinson’s disease progression

**FIG. 4.** Manhattan plot for the variant-based GWAS of cognitive progression. The red dashed line indicates the genome-wide significance threshold, \( P = 5 \times 10^{-8} \). The top genes from the MAGMA gene-based analysis and \( P \) values are shown on the right. [Color figure can be viewed at wileyonlinelibrary.com]
GWAS versus Parkinson’s disease progression

- SLC44A1 was associated with reaching Hoehn and Yahr stage 3
- Rs61863020(G>A), an intergenic variant and expression quantitative trait loci for ADRA2A-encoded alpha2 adrenoreceptor was associated with a lower prevalence of insomnia at baseline
GWAS versus Parkinson’s disease progression

- Discovery of a potential novel genome-wide signal within the RIMS2 locus, putatively associated with PDD. The RIMS2 variant was highlighted as a stronger predictor of PDD than GBA and APOE, which, surprisingly, did not reach genome-wide significance.

Liu et al., 2021
GWAS in non-European populations

- Working towards conducting GWAS in different populations and sub-populations
  → Already underway!
  - **Han Chinese** (Foo et al., 2020)
  - **Latin America** (Loesch et al., 2020)

Foo et al., 2020

Loesch et al., 2020
Multi-ancestry GWAS meta-analyses

Kim et al., 2022

- 11 new risk loci!
The Global Parkinson’s Genetics Program

Total Global Data

57
Unique Locations

130
Cohorts

161,578
Samples Expected

8,645
Samples Completed

https://parkinsonsroadmap.org/#
Black and African American Connections to Parkinson's Disease

WHAT IS GENETIC RESEARCH?
Research helps answer questions about health and disease. Studying genes can help us learn more about diseases and develop treatments.

WHAT DO I NEED TO KNOW?
There are risks and benefits to joining a study. You will be asked to donate blood or saliva one time. Your information will be kept private and secure. You will get a $25 gift card.

HOW CAN I HELP?
Black and African American people are valuable partners in research. Joining a study can help us learn more about what causes disease or protects health in your community.

WHY IS PARKINSON'S RESEARCH IMPORTANT?
The number of people with Parkinson's disease is growing. This research is part of a global project to better understand how genes cause Parkinson's and impact the disease.

Letters: New Observation | Open Access | 

Black and African American Connections to Parkinson's Disease Study: Addressing Missing Diversity in Parkinson's Disease Genetics

Sara Bandres-Ciga PhD on behalf of the Black and African American Connections to Parkinson's Disease (BLAAC PD) Study Group
Key messages

- Until two decades ago, PD was considered the archetypal example of a non-genetic disease.
- The identification of disease-causing genetic mutations in SNCA marked the starting point for PD genetics.
- Genetics has been key at informing biological pathways involved in disease etiology.
- In the GWAS era, great advances have been made in identifying many loci linked to PD risk, age at onset and progression (mostly in European populations).
- Success in the new era of PD genetics requires extensive scientific collaboration and will not progress without teamwork in an open scientific environment.
Thanks for having me!