HHS Public Access

Author manuscript

Parkinsonism Relat Disord. Author manuscript; available in PMC 2019 August 01.

Published in final edited form as:

Parkinsonism Relat Disord. 2018 August ; 53: 4–9. doi:10.1016/j.parkreldis.2018.04.031.

Genetic variants related to urate and risk of Parkinson's disease

Katherine C. Hughes, ScD[1], **Xiang Gao, MD, PhD**[2], **Eilis J. O'Reilly, ScD**[3,4], **Iris Y. Kim, ScD**[1], **Molin Wang, PhD**[1,5], **Marc G. Weisskopf, PhD, ScD**[1,6], **Michael A. Schwarzschild, MD, PhD**[7], and **Alberto Ascherio, MD, DrPH**[1,3,8]

[1]Department of Epidemiology, Harvard T.H. Chan School of Public Health, Boston, MA, USA [2]Department of Nutritional Health, The Pennsylvania State University, University Park, PA, USA [3]Department of Nutrition, Harvard T.H. Chan School of Public Health, Boston, MA, USA [4]School of Public Health, College of Medicine, University College Cork, Ireland [5]Department of Biostatistics, Harvard T.H. Chan School of Public Health, Boston, MA, USA [6]Department of Environmental Health, Harvard T.H. Chan School of Public Health, Boston, MA, USA [7]MassGeneral Institute for Neurodegenerative Disease, Massachusetts General Hospital, Boston, MA, USA [8]Channing Division of Network Medicine, Department of Medicine, Brigham and Women's Hospital and Harvard Medical School, Boston, MA, USA

Abstract

Introduction—Higher urate concentrations have been associated with a lower risk of developing Parkinson's disease (PD) and with slower rates of clinical decline in PD patients. Whether these associations reflect a neuroprotective effect of urate is unclear. Our objective was to assess

Corresponding author: Katherine C. Hughes, Department of Nutrition, Harvard T. H. Chan School of Public Health, 677 Huntington Ave, Boston MA 02115; Phone: 603-748-1006; Fax: 617-432-2435; kch460@mail.harvard.edu.

Author Contributions

1. Research project. Conception: AA, XG, MAS. Organization: XG, MAS, and AA. Execution: XG, MAS, and AA.
2. Statistical Analysis. Design: KCH, AA. Execution: KCH. Review and Critique: KCH, XG, EJO, IYK, MW, MGW, MAS, and AA.
3. Manuscript Preparation. Writing of the first draft: KCH. Review and Critique: KCH, XG, EJO, IYK, MW, MGW, MAS, and AA.

Disclosures:
Dr. Hughes reports no disclosures.
Dr. Gao has served on committees of the Sleep Research Society, American Academy of Sleep Medicine, and Parkinson Study Group and received funding from the NIH/NINDS.
Dr. O'Reilly reports no disclosures.
Dr. Kim reports no disclosures.
Dr. Wang reports no disclosures.
Dr. Weisskopf reports no disclosures.
Dr. Schwarzschild served on the scientific advisory board for CBD Solutions (foundation), has served as a consultant for New Beta Innovation (company) and Harvard University, and is funded by NIH grants NS090259, NS098746, U13NS103523, Department of Defense W81XWH-11-1-0150, the Michael J. Fox Foundation, the Parkinson's Alliance, the Parkinson's Foundation, Target ALS Foundation.
Dr. Ascherio received a research grant from the Department of Defense related to this work. He has also received research grants from the National Institutes of Health, the Michael J. Fox Foundation, and the National Multiple Sclerosis Society, outside of this work.

whether genetic variants that modify circulating urate levels are also associated with altered PD risk.

Methods—Participants were from three large ongoing cohort studies: the Nurses' Health Study (NHS), the Health Professionals Follow-up Study (HPFS), and the Cancer Prevention Study II Nutrition Cohort (CPS-IIN). We examined associations between single nucleotide polymorphisms (SNPs) in *SLC2A9* and other genes involved in urate transport and PD risk using conditional logistic regression among 1,451 cases and 3,135 matched controls. We assessed associations between SNPs and plasma urate levels in a subset of 1,174 control participants with linear regression models.

Results—We found the expected associations between SNPs in *SLC2A9* and plasma urate levels among men and women; however, SNPs in other genes tended not to be associated with urate. Each SNP in *SLC2A9* explained less than 7% of the variance in plasma urate. We did not find significant associations between the SNPs in *SLC2A9* and PD risk among men or women.

Conclusion—Our results do not support an association between genetic variants associated with circulating urate levels and risk of PD, but larger investigations are needed to determine whether the modest genetic effects on blood urate contribute to predict PD risk.

Keywords

Parkinson's disease; urate

Urate is a powerful antioxidant that circulates at high concentrations in humans and is responsible for most of the antioxidant capacity in human plasma[1]. Because of the proposed role of oxidative stress in the pathology of Parkinson's disease (PD), it has been suggested that high plasma urate levels could be protective against PD[2]. Support for this hypothesis has come from a variety of sources. Laboratory models of PD have demonstrated that urate attenuates MPP+ toxicity in dopaminergic neurons[3] and 6-OHDA toxicity[4], and urate oxidase knock-out mice with increased concentrations of urate in the brain exhibit attenuated toxic effects of 6-OHDA on dopaminergic cells[5]. Several studies have reported that patients with PD have lower urate levels in serum[6, 7] and plasma[8] than individuals without PD. In addition, higher serum and cerebrospinal fluid concentrations of urate have been associated with slower rates of clinical decline in PD patients[9, 10]. Prospective studies have shown that people with lower urate levels have an increased risk of developing PD[11]. However, several of the above studies reported associations only among men[7, 9, 11].

Evidence of an association between urate and PD suggests that urate could be a suitable target for neuroprotective therapies, since plasma urate levels can be increased through pharmacologic or dietary interventions. However, despite consistent evidence supporting an association between urate and PD, it is difficult to establish causality due to the inherent limitations of observational studies, particularly confounding and reverse causation. One approach to address these concerns, known as Mendelian randomization, is to take advantage of genetic variants that affect urate levels to investigate causality. Since alleles are assigned randomly during meiosis, genotypes should be unrelated to confounding factors typical of epidemiologic studies. Several genetic loci have been associated with urate

concentration in genome-wide association studies (GWAS), and one locus that has been consistently identified is solute carrier family 2, member 9 (*SLC2A9*)[12–18]. *SLC2A9* encodes glucose transporter 9 (*GLUT9*), which can reabsorb urate in renal tubules[19]. Polymorphisms in *SLC2A9* have been associated with age at onset of PD[20] as well as PD risk when combined with polymorphisms from other genes using a genetic score[21]. However, no association between 12 *SLC2A9* polymorphisms and PD risk was found in a separate study[22].

Therefore, we examined genetic variants that have previously been associated with altered urate levels in relation to PD risk among cases and controls selected from three large prospective cohort studies—the Nurses' Health Study (NHS), Health Professionals Follow-up Study (HPFS), and the Cancer Prevention Study II Nutrition Cohort (CPS-IIN). In addition, as detailed exposure histories have been collected from all members of these cohorts as well as measured plasma urate for a subset of participants, we have a unique ability to assess relationships among genetic variants, plasma urate, and lifestyle factors.

Methods

Study population

The NHS was established in 1976 when 121,700 female registered nurses aged 30–55 years completed a mailed questionnaire regarding their medical histories and baseline health-related exposures. The HPFS was established in 1986 when 51,529 male health professionals aged 40–75 years responded to a similar questionnaire. The CPS-IIN, a sub-cohort of the larger CPS-II, includes 184,190 individuals (86,404 men and 97,786 women) aged 50–74 in 1992 who completed a questionnaire regarding nutrition and other risk factors. For all cohorts, follow-up questionnaires have been sent every two years to update exposure data and disease diagnoses. Follow-up in all cohorts has been approximately 90% or higher. The study was approved by the Human Research Committees at the Harvard T. H. Chan School of Public Health and the Brigham and Women's Hospital.

Case ascertainment and control selection

Procedures for case ascertainment have been described previously[11]. Briefly, cases were first identified through biennial self-report questionnaires. With consent of the participant, we asked the treating neurologist to complete a questionnaire confirming or refuting the PD diagnosis and to send a copy of the medical records, which were reviewed by a neurologist specializing in movement disorders. Cases were confirmed if a diagnosis was considered definite or probable by the treating neurologist, or if the medical record included either a final diagnosis of PD made by a neurologist, or evidence of at least 2 of the 3 cardinal signs (rest tremor, rigidity, bradykinesia) in the absence of features suggesting alternative diagnoses.

For each case, we randomly selected controls who were alive and had not reported PD at the time of the cases' diagnosis. We selected between 2–6 controls per case in the NHS and HPFS and one control per case in the CPS-IIN cohort. Controls were matched to the cases

based on cohort, sex, birth year (+/−1 year), race (white vs. other), fasting status (>8 hours vs. less/unknown), and year, month, and time of blood draw (in two-hour intervals).

Plasma urate assessment

Blood samples were collected from 32,826 members of NHS between 1989–1990, 18,000 members of HPFS between 1993–1995, and 40,000 members of CPS-IIN between 1998–2001. For NHS and HPFS, participants used collection kits provided to them by the studies and returned blood samples via overnight delivery to our lab. More than 95% of samples were delivered within 26 hours of being drawn. Upon arrival, blood samples were centrifuged and blood components were aliquoted into cryotubes and stored in the vapor phase of liquid nitrogen freezers at −130 degrees C or colder until being sent to the laboratory for analysis. For CPS-IIN, participants went to participating hospitals in their communities for blood draws. Hospital staff centrifuged the samples to separate blood components, then shipped samples overnight to a central repository where the samples were aliquoted and frozen in the vapor phase of liquid nitrogen freezers for long-term storage[23]. Samples from cases and controls were handled identically. Concentrations of plasma urate were measured using a colorimetric enzyme assay (Hitachi 911; Roche Diagnostics, Indianapolis, Indiana). Coefficients of variation (CVs) were determined using blinded quality control samples included with the study samples. All reported CVs were <10%.

Genotyping

Participants who had not provided blood samples were invited to provide cheek cell samples. Participants were sent a package contained a small empty cup with a cap and a bottle of mouthwash, and were asked to swish the mouthwash in their mouths and then spit into the cup; samples were mailed back to our lab and processed within a week of receipt. Genotyping using either blood or cheek cells was conducted for 322 confirmed cases and 1337 controls in NHS, 310 confirmed cases and 979 controls in HPFS, and 819 cases and 819 controls in CPS-IIN (the 819 cases in CPS-IIN included 307 individuals whose medical records were incomplete or could not be obtained; these individuals were excluded in sensitivity analyses). Genotyping was carried out through the Harvard Partners Center for Genetics and Genomics at the Harvard Partners Genotyping Facility using the OpenAssay SNP Genotyping System (BioTrove, Woburn, Massachusetts, USA). Our primary gene of interest, *SLC2A9*, has been identified in several genome-wide association studies as the strongest genetic predictor of serum urate levels and gout[12–15, 24]. Although the causal variant has not been identified, we genotyped three SNPs due to their strong associations with urate in previous studies: rs6855911[12, 15, 18, 24], located within intron 7 with minor allele frequency (MAF) of 0.31 (G allele); rs7442295[12, 13, 15, 18], located within intron 6 with a MAF of 0.21 for G allele; and rs16890979[14, 17, 18], a missense mutation in exon 8 with a MAF of 0.22 for T allele (using HapMap data from Utah residents with ancestry from northern and western Europe, abbreviated CEU[25]). These three SNPs are in strong linkage disequilibrium (LD; pairwise r^2 range from 0.68–0.76 from Haploview[26] with HapMap CEU data) and each minor allele of these SNPs has been associated with a 0.30–0.43 mg/dL decrease in serum urate in individuals of European descent[12, 14]. In addition to *SLC2A9*, we selected for analysis other genes of interest due to their role in the transport of urate, including solute carrier family 22, member 12 (*SLC22A12/URAT1)*, ATP-binding cassette

sub-family G member 2 *(ABCG2)*, and solute carrier family 17, member 3 *(SLC17A3/NPT4)*.

Covariate assessment

Data on covariates, including age, body mass index (BMI), smoking, and usual diet, including coffee and alcohol intake, were collected via self-report questionnaires every two years, as previously described[27].

Statistical analyses

Basic characteristics of the study population were assessed using means for continuous variables and percentages for discrete variables. Given previously reported sex differences for the association between urate and PD risk[11] and different ranges, we performed analyses separately in men and women. We used histograms and q-q plots to check for normality and then examined associations between individual SNPS and urate using linear regression under an additive genetic model for individuals with measured urate. We used R^2 as a measure of the proportion of the variation in plasma urate explained by each SNP. Because only SNPs located within *SLC2A9* demonstrated statistically significant associations with urate, we also created a genetic score by summing the number of *SLC2A9* alleles that have been associated with lowered urate in previous GWAS. Finally we explored possible modification of the association between the genetic score and urate by factors associated with altered urate levels, including BMI, alcohol, fructose, vitamin C in all three cohorts, and additionally dairy protein and the dietary urate index in the NHS and HPFS, by including cross-product terms between these variables (higher vs. lower, based on the median values) and the genetic score.[27, 28] We then conducted analyses of the genetic score and urate within levels of variables identified as effect modifiers through testing of the interaction terms.

We then assessed the association between each SNP and PD risk under an additive genetic model using conditional logistic regression. In a second model we additionally adjusted for smoking status, coffee intake, BMI, and alcohol consumption. Covariates were obtained from the questionnaire preceding blood draw. In addition to the individual SNPs, we also examined the association between the genetic score and PD using conditional logistic regression. We performed analyses first separately by study and gender, and then used a random meta-analysis approach to pool results and assess potential heterogeneity. Finally, we estimated the association between genetically determined plasma urate and PD risk using the two-stage regression described below. First we fit a linear regression model within the subset of controls with measured urate and SNPs, with plasma urate as the dependent variable and the three *SLC2A9* SNPs as independent variables, and obtained fitted urate levels. Fitted urate levels for cases and controls without measured urate were obtained by substituting their genotypes into the first-stage regression model. Then we used the fitted urate levels as a continuous independent variable in a conditional logistic regression model for PD. In sensitivity analyses, we repeated analyses after excluding cases without confirmation from medical records and those who were diagnosed with PD after age 80.

Results

Baseline characteristics are presented in Table 1. A total of 1,451 cases and 3,135 controls were included. We examined associations between SNPs and urate in a subset of 1,174 controls with measured urate. As expected, urate levels were higher among men than women. In both men and women across all three cohorts, we found statistically significant associations between all three *SLC2A9* SNPs and urate (figure), with each explaining 3.93–5.79% of the overall variance in plasma urate among female controls and 1.45–6.43% among male controls. RS6855911 exhibited the strongest associations with plasma urate among women--a one-allele increment was associated with a 0.47 mg/dL decrease in urate levels (95% CI −0.62, −0.33). Among men, rs7442295 was most strongly associated with plasma urate, and a one-allele increment was associated with a 0.42 mg/dL decrease in urate levels (95% CI −0.60, −0.23). Associations were similar in men and women. The genetic score consisting of all three SLC2A9 SNPs explained 5.22% of the variation in urate levels in women and 3.97% in men. SNPs from other genes were not associated with urate levels (Supplementary Table) and did not contribute to explaining more of the variation—for example, an alternative genetic score that included all measured SNPs explained 3.06% of the variation in urate levels in women and 2.34% in men.

We then examined associations between each SNP and risk of PD. Only one SNP (rs1165202) within the *SLC17A3* gene was significantly associated with PD (pooled RR 0.87, 95% CI 0.79–0.96). Results from minimally and fully adjusted models did not show significant associations with PD risk for other SNPs in men or women (Table 2); pooled, multivariable-adjusted relative risks ranged from 0.92–1.08. The genetic score including the three SNPs within *SLC2A9* was not associated with PD risk: the pooled RR was 1.01 (95% CI: 0.97, 1.05). Results were similar after additional adjustment for diuretic and aspirin use (results not shown). Finally, we performed a two-stage regression to examine the association between genetically-predicted urate and PD risk. Consistent with the results above, we did not find significant associations for men (pooled RR for a 1mg/dL higher urate=1.00, 95% CI 0.69–1.45) or women (pooled RR for a 1mg/dL higher urate 1.09, 95% CI 0.76–1.57). Results did not change after excluding cases without confirmation from medical records or after excluding individuals whose PD was diagnosed after age 80.

In exploratory analyses, we investigated the association between SNPs and urate stratified by body mass index and the dietary urate index and its components. We found an interaction between BMI and *SLC2A9* variants (pooled *p* for interaction=0.0006), where the association between additional risk variants and lowered urate was stronger for men and women with BMI below the median. For those with BMI above the median level, each additional risk allele was associated with 0.12 mg/dL lowered urate (95% CI −0.21, −0.03), while for those with BMI below the median each additional risk allele was associated with 0.17 mg/DL lowered urate (95% CI −0.22, −0.12). No other significant interactions were found ($p>0.05$ for all). However, *SLC2A9* risk variants were not associated with PD risk after stratifying by BMI (RR for BMI below the median=1.02, 95% CI 0.95–1.10; RR for BMI above the median: 1.00, 95% CI 0.92–1.09).

Discussion

Previous research has demonstrated an association between urate and lowered PD risk; however, whether this association reflects a neuroprotective effect of urate is difficult to confirm in observational studies because of the possibility of unmeasured confounding. Since polymorphisms should be minimally confounded by other factors, studying the association between genetic determinants of urate levels and PD risk could provide important insights into the relationship between urate and PD. In this analysis, we found the expected associations between variants in *SLC2A9* and urate levels among both men and women in three cohorts; however, we did not find associations between these genetic variants and PD risk.

One explanation of our results is that the relatively small proportion of the variation in urate levels explained by the SNPs in our participants mean that the association between urate and PD could not be detected using these variants. Since the effects of individual variants on phenotypes are often small, this is a common drawback to Mendelian randomization studies.[29] Since the *SLC2A9* score only accounted for 5.22% of the variation in urate concentrations in women and 3.97% in men, genetic factors other than the common variants assessed in this analysis may contribute more to between-person differences in circulating urate levels. In a recent analysis in these cohorts, we found approximately a 40% reduced risk of PD among men in the highest quartile of plasma urate (6.3–9.0 mg/dL) compared to men in the lowest quartile (<4.9 mg/dL)[11]. Based on data from our cohorts, we estimated that the approximately 0.80mg/dL decrease in plasma urate associated with having two copies of the risk allele compared to having none for one of the SNPs in *SLC2A9* would predict a 10.5% increase in PD risk, assuming a linear association. Power of our study may thus have been insufficient to detect this relatively modest difference in genetically determined PD risk.

Another possible explanation of our results is that plasma urate does not have a causal effect on PD. While possible, these findings should be weighed against the evidence from a variety of sources supporting the hypothesis that urate is neuroprotective. Higher urate levels have been associated with decreased risk of PD in prospective studies[11] and with slower rates of clinical decline in PD patients[9, 10]. Dietary determinants of urate have also been associated with altered PD risk[27]. Of note, a recent analysis using the same *SLC2A9* variants found a hazard ratio for disease progression of 1.27 for a 0.5mg/dL genetically conferred decrease in serum urate[30], which may suggest that urate is a stronger predictor of PD progression than risk. Further, it is possible that genetic determinants of plasma urate differ from genetic determinants of CNS urate. While cerebrospinal fluid, brain, or neuronal urate may be neuroprotective, as plasma urate does not directly determine urate levels in the immediate environment of the degenerating neurons, it may be unrelated or only weakly related to PD risk. This explanation could be supported by our finding of a significant association between rs1165202 and PD risk. While the T allele at this locus was associated with lowered serum urate and with gout in white participants[14] and was not associated with plasma urate in our study, it has been associated with significantly higher cerebrospinal fluid urate levels.[31]

The strengths of our study include the availability of genetic data as well as plasma urate measurements and data on diet and lifestyle factors, as well as the relatively large sample size. A previous study examining associations between variants in *SLC2A9* and risk of PD also found no association, yet had roughly half the number of cases compared to our study[22]; taken together, the agreement between these studies lends more confidence to the results. One weakness is that the participants are almost exclusively of European descent, limiting the generalizability of our findings. However, restricting our analysis to individuals of European descent also minimizes the potential for confounding by population stratification. In addition, for *SLC2A9* in particular, associations with urate levels have been found in many different populations[12–18].

In conclusion, our results do not support an association between genetic variants associated with circulating urate levels and risk of PD, but larger investigations are needed to determine whether the modest genetic effects on blood urate contribute to predict PD risk.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

Study funding: This study was supported by NIH grants UM1 CA186107, UM1 CA167552, and R01 NS061858, and by Department of Defense grant W81XWH-14-0131.

References

1. Yeum KJ, Russell RM, Krinsky NI, Aldini G. Biomarkers of antioxidant capacity in the hydrophilic and lipophilic compartments of human plasma. Arch Biochem Biophys. 2004; 430(1):97–103. [PubMed: 15325916]
2. Cipriani S, Chen X, Schwarzschild MA. Urate: a novel biomarker of Parkinson's disease risk, diagnosis and prognosis. Biomark Med. 2010; 4(5):701–12. [PubMed: 20945982]
3. Cipriani S, Desjardins CA, Burdett TC, Xu Y, Xu K, Schwarzschild MA. Urate and its transgenic depletion modulate neuronal vulnerability in a cellular model of Parkinson's disease. PLoS One. 2012; 7(5):e37331. [PubMed: 22606360]
4. Gong L, Zhang QL, Zhang N, Hua WY, Huang YX, Di PW, Huang T, Xu XS, Liu CF, Hu LF, Luo WF. Neuroprotection by urate on 6-OHDA-lesioned rat model of Parkinson's disease: linking to Akt/GSK3beta signaling pathway. J Neurochem. 2012; 123(5):876–85. [PubMed: 23094836]
5. Chen X, Burdett TC, Desjardins CA, Logan R, Cipriani S, Xu Y, Schwarzschild MA. Disrupted and transgenic urate oxidase alter urate and dopaminergic neurodegeneration. Proc Natl Acad Sci U S A. 2013; 110(1):300–5. [PubMed: 23248282]
6. Winquist A, Steenland K, Shankar A. Higher serum uric acid associated with decreased Parkinson's disease prevalence in a large community-based survey. Mov Disord. 2010; 25(7):932–6. [PubMed: 20310031]
7. Andreadou E, Nikolaou C, Gournaras F, Rentzos M, Boufidou F, Tsoutsou A, Zournas C, Zissimopoulos V, Vassilopoulos D. Serum uric acid levels in patients with Parkinson's disease: their relationship to treatment and disease duration. Clin Neurol Neurosurg. 2009; 111(9):724–8. [PubMed: 19632030]
8. Annanmaki T, Muuronen A, Murros K. Low plasma uric acid level in Parkinson's disease. Mov Disord. 2007; 22(8):1133–7. [PubMed: 17443703]
9. Schwarzschild MA, Schwid SR, Marek K, Watts A, Lang AE, Oakes D, Shoulson I, Ascherio A, Hyson C, Gorbold E, Rudolph A, Kieburtz K, Fahn S, Gauger L, Goetz C, Seibyl J, Forrest M,

Ondrasik J. Serum urate as a predictor of clinical and radiographic progression in Parkinson disease. Arch Neurol. 2008; 65(6):716–23. [PubMed: 18413464]

10. Ascherio A, LeWitt PA, Xu K, Eberly S, Watts A, Matson WR, Marras C, Kieburtz K, Rudolph A, Bogdanov MB, Schwid SR, Tennis M, Tanner CM, Beal MF, Lang AE, Oakes D, Fahn S, Shoulson I, Schwarzschild MA. Urate as a predictor of the rate of clinical decline in Parkinson disease. Arch Neurol. 2009; 66(12):1460–8. [PubMed: 19822770]
11. Gao X, O'Reilly EJ, Schwarzschild MA, Ascherio A. Prospective study of plasma urate and risk of Parkinson disease in men and women. Neurology. 2016
12. Li S, Sanna S, Maschio A, Busonero F, Usala G, Mulas A, Lai S, Dei M, Orru M, Albai G, Bandinelli S, Schlessinger D, Lakatta E, Scuteri A, Najjar SS, Guralnik J, Naitza S, Crisponi L, Cao A, Abecasis G, Ferrucci L, Uda M, Chen WM, Nagaraja R. The GLUT9 gene is associated with serum uric acid levels in Sardinia and Chianti cohorts. PLoS Genet. 2007; 3(11):e194. [PubMed: 17997608]
13. Wallace C, Newhouse SJ, Braund P, Zhang F, Tobin M, Falchi M, Ahmadi K, Dobson RJ, Marcano AC, Hajat C, Burton P, Deloukas P, Brown M, Connell JM, Dominiczak A, Lathrop GM, Webster J, Farrall M, Spector T, Samani NJ, Caulfield MJ, Munroe PB. Genome-wide association study identifies genes for biomarkers of cardiovascular disease: serum urate and dyslipidemia. Am J Hum Genet. 2008; 82(1):139–49. [PubMed: 18179892]
14. Dehghan A, Kottgen A, Yang Q, Hwang SJ, Kao WL, Rivadeneira F, Boerwinkle E, Levy D, Hofman A, Astor BC, Benjamin EJ, van Duijn CM, Witteman JC, Coresh J, Fox CS. Association of three genetic loci with uric acid concentration and risk of gout: a genome-wide association study. Lancet. 2008; 372(9654):1953–61. [PubMed: 18834626]
15. Doring A, Gieger C, Mehta D, Gohlke H, Prokisch H, Coassin S, Fischer G, Henke K, Klopp N, Kronenberg F, Paulweber B, Pfeufer A, Rosskopf D, Volzke H, Illig T, Meitinger T, Wichmann HE, Meisinger C. SLC2A9 influences uric acid concentrations with pronounced sex-specific effects. Nat Genet. 2008; 40(4):430–6. [PubMed: 18327256]
16. Kamatani Y, Matsuda K, Okada Y, Kubo M, Hosono N, Daigo Y, Nakamura Y, Kamatani N. Genome-wide association study of hematological and biochemical traits in a Japanese population. Nat Genet. 2010; 42(3):210–5. [PubMed: 20139978]
17. Karns R, Zhang G, Sun G, Rao Indugula S, Cheng H, Havas-Augustin D, Novokmet N, Rudan D, Durakovic Z, Missoni S, Chakraborty R, Rudan P, Deka R. Genome-wide association of serum uric acid concentration: replication of sequence variants in an island population of the Adriatic coast of Croatia. Ann Hum Genet. 2012; 76(2):121–7. [PubMed: 22229870]
18. Kottgen A, Albrecht E, Teumer A, Vitart V, Krumsiek J, Hundertmark C, Pistis G, Ruggiero D, O'Seaghdha CM, Haller T, Yang Q, Tanaka T, Johnson AD, Kutalik Z, Smith AV, Shi J, Struchalin M, Middelberg RP, Brown MJ, Gaffo AL, Pirastu N, Li G, Hayward C, Zemunik T, Huffman J, Yengo L, Zhao JH, Demirkan A, Feitosa MF, Liu X, Malerba G, Lopez LM, van der Harst P, Li X, Kleber ME, Hicks AA, Nolte IM, Johansson A, Murgia F, Wild SH, Bakker SJ, Peden JF, Dehghan A, Steri M, Tenesa A, Lagou V, Salo P, Mangino M, Rose LM, Lehtimaki T, Woodward OM, Okada Y, Tin A, Muller C, Oldmeadow C, Putku M, Czamara D, Kraft P, Frogheri L, Thun GA, Grotevendt A, Gislason GK, Harris TB, Launer LJ, McArdle P, Shuldiner AR, Boerwinkle E, Coresh J, Schmidt H, Schallert M, Martin NG, Montgomery GW, Kubo M, Nakamura Y, Tanaka T, Munroe PB, Samani NJ, Jacobs DR Jr, Liu K, D'Adamo P, Ulivi S, Rotter JI, Psaty BM, Vollenweider P, Waeber G, Campbell S, Devuyst O, Navarro P, Kolcic I, Hastie N, Balkau B, Froguel P, Esko T, Salumets A, Khaw KT, Langenberg C, Wareham NJ, Isaacs A, Kraja A, Zhang Q, Wild PS, Scott RJ, Holliday EG, Org E, Viigimaa M, Bandinelli S, Metter JE, Lupo A, Trabetti E, Sorice R, Doring A, Lattka E, Strauch K, Theis F, Waldenberger M, Wichmann HE, Davies G, Gow AJ, Bruinenberg M, Stolk RP, Kooner JS, Zhang W, Winkelmann BR, Boehm BO, Lucae S, Penninx BW, Smit JH, Curhan G, Mudgal P, Plenge RM, Portas L, Persico I, Kirin M, Wilson JF, Mateo Leach I, van Gilst WH, Goel A, Ongen H, Hofman A, Rivadeneira F, Uitterlinden AG, Imboden M, von Eckardstein A, Cucca F, Nagaraja R, Piras MG, Nauck M, Schurmann C, Budde K, Ernst F, Farrington SM, Theodoratou E, Prokopenko I, Stumvoll M, Jula A, Perola M, Salomaa V, Shin SY, Spector TD, Sala C, Ridker PM, Kahonen M, Viikari J, Hengstenberg C, Nelson CP, Meschia JF, Nalls MA, Sharma P, Singleton AB, Kamatani N, Zeller T, Burnier M, Attia J, Laan M, Klopp N, Hillege HL, Kloiber S, Choi H, Pirastu M, Tore S, Probst-Hensch NM, Volzke H, Gudnason V, Parsa A, Schmidt R, Whitfield JB, Fornage M, Gasparini P, Siscovick DS, Polasek O,

Campbell H, Rudan I, Bouatia-Naji N, Metspalu A, Loos RJ, van Duijn CM, Borecki IB, Ferrucci L, Gambaro G, Deary IJ, Wolffenbuttel BH, Chambers JC, Marz W, Pramstaller PP, Snieder H, Gyllensten U, Wright AF, Navis G, Watkins H, Witteman JC, Sanna S, Schipf S, Dunlop MG, Tonjes A, Ripatti S, Soranzo N, Toniolo D, Chasman DI, Raitakari O, Kao WH, Ciullo M, Fox CS, Caulfield M, Bochud M, Gieger C. Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nat Genet. 2013; 45(2):145–54. [PubMed: 23263486]

19. Taniguchi A, Kamatani N. Control of renal uric acid excretion and gout. Curr Opin Rheumatol. 2008; 20(2):192–7. [PubMed: 18349750]
20. Facheris MF, Hicks AA, Minelli C, Hagenah JM, Kostic V, Campbell S, Hayward C, Volpato CB, Pattaro C, Vitart V, Wright A, Campbell H, Klein C, Pramstaller PP. Variation in the uric acid transporter gene SLC2A9 and its association with AAO of Parkinson's disease. J Mol Neurosci. 2011; 43(3):246–50. [PubMed: 20589538]
21. Gonzalez-Aramburu I, Sanchez-Juan P, Jesus S, Gorostidi A, Fernandez-Juan E, Carrillo F, Sierra M, Gomez-Garre P, Caceres-Redondo MT, Berciano J, Ruiz-Martinez J, Combarros O, Mir P, Infante J. Genetic variability related to serum uric acid concentration and risk of Parkinson's disease. Mov Disord. 2013; 28(12):1737–40. [PubMed: 23712608]
22. Gao J, Xu H, Huang X, Chen H. Short communication: genetic variations of SLC2A9 in relation to Parkinson's disease. Transl Neurodegener. 2013; 2(1):5. [PubMed: 23422251]
23. Calle EE, Rodriguez C, Jacobs EJ, Almon ML, Chao A, McCullough ML, Feigelson HS, Thun MJ. The American Cancer Society Cancer Prevention Study II Nutrition Cohort: rationale, study design, and baseline characteristics. Cancer. 2002; 94(9):2490–501. [PubMed: 12015775]
24. Stark K, Reinhard W, Neureuther K, Wiedmann S, Sedlacek K, Baessler A, Fischer M, Weber S, Kaess B, Erdmann J, Schunkert H, Hengstenberg C. Association of common polymorphisms in GLUT9 gene with gout but not with coronary artery disease in a large case-control study. PLoS One. 2008; 3(4):e1948. [PubMed: 18398472]
25. The International HapMap Project. Nature. 2003; 426(6968):789–96. [PubMed: 14685227]
26. Barrett JC, Fry B, Maller J, Daly MJ. Haploview: analysis and visualization of LD and haplotype maps. Bioinformatics. 2005; 21(2):263–5. [PubMed: 15297300]
27. Gao X, Chen H, Choi HK, Curhan G, Schwarzschild MA, Ascherio A. Diet, urate, and Parkinson's disease risk in men. Am J Epidemiol. 2008; 167(7):831–8. [PubMed: 18326873]
28. Huffman JE, Albrecht E, Teumer A, Mangino M, Kapur K, Johnson T, Kutalik Z, Pirastu N, Pistis G, Lopez LM, Haller T, Salo P, Goel A, Li M, Tanaka T, Dehghan A, Ruggiero D, Malerba G, Smith AV, Nolte IM, Portas L, Phipps-Green A, Boteva L, Navarro P, Johansson A, Hicks AA, Polasek O, Esko T, Peden JF, Harris SE, Murgia F, Wild SH, Tenesa A, Tin A, Mihailov E, Grotevendt A, Gislason GK, Coresh J, D'Adamo P, Ulivi S, Vollenweider P, Waeber G, Campbell S, Kolcic I, Fisher K, Viigimaa M, Metter JE, Masciullo C, Trabetti E, Bombieri C, Sorice R, Doring A, Reischl E, Strauch K, Hofman A, Uitterlinden AG, Waldenberger M, Wichmann HE, Davies G, Gow AJ, Dalbeth N, Stamp L, Smit JH, Kirin M, Nagaraja R, Nauck M, Schurmann C, Budde K, Farrington SM, Theodoratou E, Jula A, Salomaa V, Sala C, Hengstenberg C, Burnier M, Magi R, Klopp N, Kloiber S, Schipf S, Ripatti S, Cabras S, Soranzo N, Homuth G, Nutile T, Munroe PB, Hastie N, Campbell H, Rudan I, Cabrera C, Haley C, Franco OH, Merriman TR, Gudnason V, Pirastu M, Penninx BW, Snieder H, Metspalu A, Ciullo M, Pramstaller PP, van Duijn CM, Ferrucci L, Gambaro G, Deary IJ, Dunlop MG, Wilson JF, Gasparini P, Gyllensten U, Spector TD, Wright AF, Hayward C, Watkins H, Perola M, Bochud M, Kao WH, Caulfield M, Toniolo D, Volzke H, Gieger C, Kottgen A, Vitart V. Modulation of genetic associations with serum urate levels by body-mass-index in humans. PLoS One. 2015; 10(3):e0119752. [PubMed: 25811787]
29. Pierce BL, Ahsan H, Vanderweele TJ. Power and instrument strength requirements for Mendelian randomization studies using multiple genetic variants. Int J Epidemiol. 2011; 40(3):740–52. [PubMed: 20813862]
30. Simon KC, Eberly S, Gao X, Oakes D, Tanner CM, Shoulson I, Fahn S, Schwarzschild MA, Ascherio A. Mendelian randomization of serum urate and parkinson disease progression. Ann Neurol. 2014; 76(6):862–8. [PubMed: 25257975]
31. Maetzler W, Stapf AK, Schulte C, Hauser AK, Lerche S, Wurster I, Schleicher E, Melms A, Berg D. Serum and cerebrospinal fluid uric acid levels in lewy body disorders: associations with disease

occurrence and amyloid-beta pathway. J Alzheimers Dis. 2011; 27(1):119–26. [PubMed: 21765209]

Highlights

- SNPs in *SLC2A9* were associated with plasma urate levels in both men and women.
- SNPs in other genes involved in urate transport were not associated with plasma urate in our cohorts.
- *SLC2A9* SNPs were not associated with risk of Parkinson's disease.

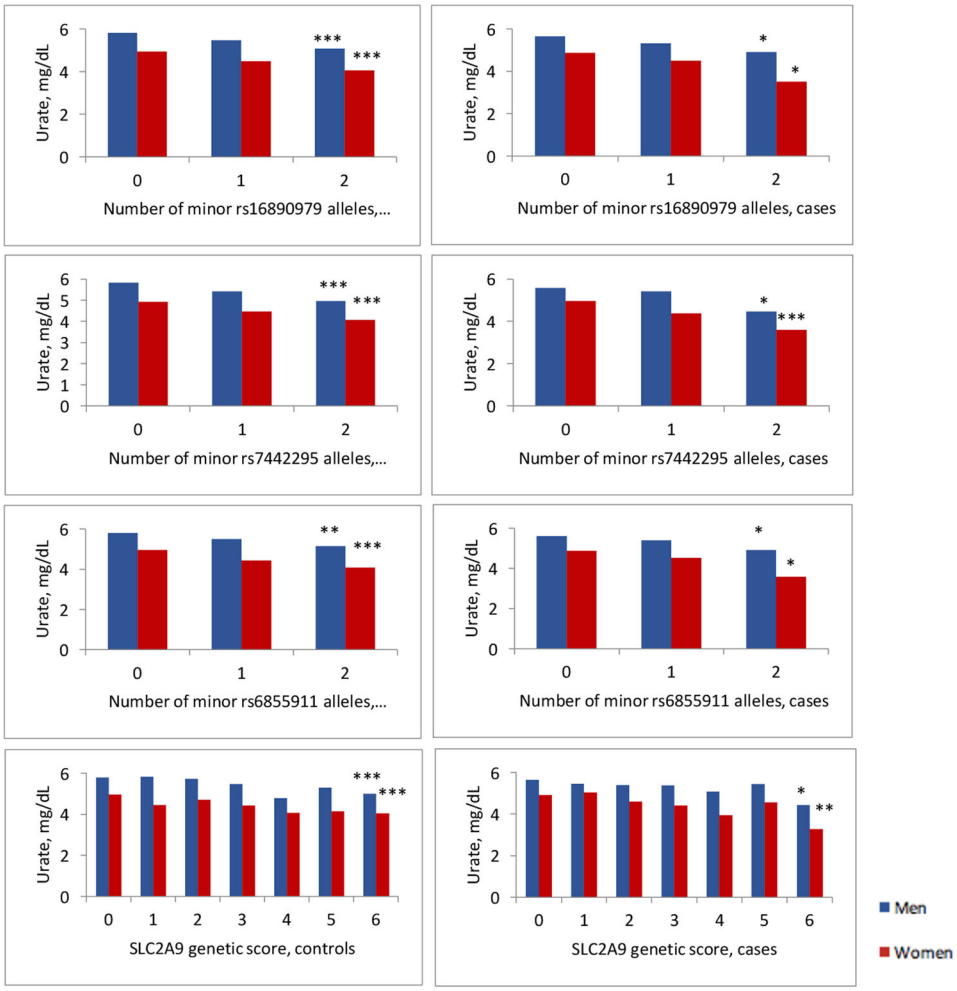

Figure 1.

Plasma urate level by number of *SLC2A9* minor alleles in PD cases and controls

Table 1

Age-adjusted characteristics of the study population

	Women		Men	
	Controls (n=1631)	**Cases (n=616)**	**Controls (n=1504)**	**Cases (n=835)**
Age, years*	61.2(7.0)	63.9(7.7)	68.0(7.4)	69.0(6.7)
UA	4.8(1.1)	4.7(1.2)	5.6(1.1)	5.5(1.0)
Body mass index, kg/m	25.8(4.1)	25.5(3.9)	26.1(3.3)	26.2(3.4)
Current smoker, %	8.2	3.1	4.9	1.8
Past smoker, %	38.9	34.9	51.6	49.5
Caucasian, %	98.8	98.5	99.5	95.8
Alcohol, g/day	4.8(8.0)	4.1(7.6)	8.7(13.2)	7.4(10.1)
Coffee, servings/day	1.6(1.5)	1.7(1.6)	1.8(1.7)	1.9(1.7)
Fructose intake, gm	21.0(10.4)	20.3(10.4)	22.6(12.6)	22.1(10.3)
Vitamin C intake, mg	271.8(281.1)	217.3(229.9)	215.8(256.4)	170.2(163.7)
High blood pressure, %	29.3	30.8	28.9	33.4
Use of diuretics, %	16.5	15.1	7.3	10.7

Values are means(SD) or percentages and are standardized to the age distribution of the study population.

*Value is not age adjusted

Parkinsonism Relat Disord. Author manuscript; available in PMC 2019 August 01.

Table 2

Associations between urate transporter-related SNPs and risk of Parkinson's disease

		Women		Men		Pooled
N cases, controls		**616, 1631**		**835, 1504**		
	EA/NEA[1]	**RR (95% CI)[2]**	**RR (95% CI), fully adjusted[3]**	**RR (95% CI)**	**RR (95% CI), fully adjusted[3]**	**RR (95% CI), fully adjusted[3]**
SLC2A9						
rs16890979	(C,T)	0.97 (0.82, 1.14)	1.00 (0.85, 1.19)	1.03 (0.90, 1.19)	1.04 (0.89, 1.20)	1.02 (0.91, 1.14)
rs7442295	(A,G)	0.99 (0.83, 1.17)	1.01 (0.85, 1.21)	0.99 (0.85, 1.14)	0.98 (0.85, 1.14)	1.00 (0.89, 1.12)
rs6855911	(A,G)	0.97 (0.83, 1.14)	1.00 (0.84, 1.18)	1.04 (0.91, 1.19)	1.04 (0.91, 1.20)	1.02 (0.92, 1.14)
SNP score[4]		0.99 (0.93, 1.05)	1.00 (0.94, 1.06)	1.01 (0.96, 1.06)	1.01 (0.96, 1.06)	1.01 (0.97, 1.05)
URAT1						
rs11231825	(T,C)	1.04 (0.90, 1.21)	1.07 (0.91, 1.24)	1.05 (0.72, 1.54)	1.07 (0.76, 1.51)	1.06 (0.91, 1.25)
rs11602903	(A,T)	0.98 (0.85, 1.14)	1.00 (0.86, 1.18)	1.08 (0.79, 1.46)	1.09 (0.83, 1.44)	1.05 (0.92, 1.20)
rs3825016	(C,T)	1.01 (0.87, 1.17)	1.03 (0.88, 1.20)	1.06 (0.77, 1.46)	1.08 (0.81, 1.45)	1.06 (0.92, 1.21)
rs3825018	(A,G)	0.96 (0.82, 1.12)	0.94 (0.78, 1.13)	0.95 (0.73, 1.25)	0.94 (0.73, 1.20)	0.94 (0.83, 1.07)
rs475688	(C,T)	0.97 (0.80, 1.18)	0.94 (0.75, 1.18)	0.93 (0.72, 1.21)	0.92 (0.74, 1.14)	0.92 (0.81, 1.05)
rs476037	(A,G)	1.01 (0.76, 1.34)	1.05 (0.76, 1.45)	1.09 (0.70, 1.69)	1.09 (0.73, 1.64)	1.08 (0.87, 1.33)
rs7932775	(C,T)	1.08 (0.91, 1.29)	1.06 (0.82, 1.36)	1.02 (0.87, 1.20)	1.02 (0.86, 1.21)	1.05 (0.93, 1.18)
rs893006	(A,C)	0.98 (0.84, 1.14)	0.96 (0.82, 1.13)	0.94 (0.75, 1.19)	0.93 (0.77, 1.13)	0.94 (0.85, 1.05)
ABCG2						
rs2231142	(G,T)	0.81 (0.64, 1.02)	0.76 (0.60, 0.97)	1.23 (0.98, 1.56)	1.21 (0.96, 1.53)	0.97 (0.73, 1.28)
SLC17A3						
rs1165205	(A,T)	0.90 (0.76, 1.06)	0.86 (0.67, 1.12)	0.87 (0.76, 0.99)	0.86 (0.75, 0.98)	0.87 (0.79, 0.96)

[1] Effect allele/noneffect allele

[2] Results from conditional logistic regression model

[3] Results from conditional logistic regression model with additional adjustment for BMI (<25, 25 to <30, ≥30), alcohol intake in grams per day (none, <5, 5 to <10, 10 to <15, ≥15 for women and none, <10, 10 to <20, 20 to <30, and ≥30 for men), coffee intake in servings per day (none, <1, 1, 2, ≥3), and smoking status (never, past, current)

[4] Sum of *SLC2A9* effect alleles (0–6)