Sang Hong Lee, Ph.D.

Curriculum Vitae

Associate Professor in Statistical Genetics, Australian Centre for Precision Health (ACPrecH),
UniSA Allied Health and Human Performance, University of South Australia.

Tel: +61 8 8302 1882
Email: hong.lee@unisa.edu.au
Address: Level 8, South Australia Health and Medical Research Institute (SAHMRI) building, City West Campus, School of Health Sciences, University of South Australia, Adelaide, 5000, Australia
Updated in July, 2021

Executive Summary

Dr Lee has introduced paradigm-shifting concepts and tools in the context of complex trait analyses that have had a significant impact on the field, evidenced by the number of citations, 26,000 (Google Scholar) for his publications (h-index = 55). The number of citations counted since 2016 is around 20,000. The number of his peer-reviewed publications is 109 (Scopus ID 26643600700). Dr Lee has been awarded two ARC Fellowships, two ARC Discovery Projects, one ARC Linkage Infrastructure, Equipment and Facilities Grant and three NHMRC Project Grants since 2013, totaling around $4.3M. Dr Lee has established a research group in ACPrecH and has worked on multiple projects. He has also been collaborating with many world-leading scientists. Dr Lee has vigorously planned future research projects aligned with the national priority.

1. Education

Date of award: April, 2006
Degree: Doctor of Philosophy at the University of New England
Title: Fine mapping of quantitative trait loci: Statistical development and application in livestock

Date of award: February, 2002
Degree: Master of Agriculture at the University of New England

Date of award: February, 1998
Degree: Bachelor of Agriculture at DONG-A University, Pusan, Korea

2. Employment

Date: Jan, 2019 – present
Institute: The University of South Australia
Position: Associate Professor (level D)
Duty: Scientific research and teaching

Date: Sep, 2017 – Dec, 2018
Institute: The University of South Australia
Position: Senior Lecturer (level C)
Duty: Scientific research and teaching

Date: Mar, 2015 – Aug, 2017

Institute: The University of New England
Position: Senior Research Fellow (level C)
Duty: Scientific research and teaching

Date: Jan, 2012 – Feb, 2015
Institute: Queensland Brain Institute, The University of Queensland
Position: Research Fellow (level B)
Duty: Scientific research

Date: Feb, 2009 – Dec, 2011
Institute: Queensland Institute of Medical Research
Position: Post-doctoral research fellow (level A)
Duty: Scientific research

Date: Feb, 2008 – Feb, 2009
Institute: Korean National Institute of Animal Science
Position: Government officer
Duty: Extension, farmer education, related agricultural research and administration

Date: April, 2006 – Feb, 2008
Institute: The University of New England
Position: Post-doctoral research fellow (level A)
Duty: Scientific research

Date: March, 2005 – April, 2006:
Institute: The University of New England
Position: Research Assistant
Duty: Scientific data analysis

3. Awards and appointments

Finalist in the Australian Museum Eureka Prizes in the category of Scientific Research (2012)
Finalist in the Australia Society of Medical Research Queensland Health and Medical Senior Researcher Award (2014)
Adjunct Senior Lecturer in University of New England (2017 – 2019)
Adjunct Senior Lecturer in University of Queensland (2015 – 2020)
A Faculty Appointment at the South Australian Health and Medical Research Institute (SAHMRI) (2018 – 2021)

4. Research support

I have been successful in obtaining multiple research grants from various funding bodies including Australian Research Council and National Health and Medical Research Council, totaling around $4.6M.

MRFF Research Grant (MRF2007431) (2021 – 2025), $1,260K, CIC
Cooperative Research Program for Agriculture Science and Technology Development (PJ0160992021) (2021 – 2022), $330K, CIA
ARC Discovery project grant (DP190100766) (2019 – 2022), $410K, CIA
NHMRC Project Grant (GNT1157281) (2019 – 2021), $440K, CIC
ARC Future Fellowship (FT160100229) (2017-2020), $720K, CIA
ARC Linkage Infrastructure, Equipment and Facilities (LE170100032) (2017), $900K, Co-investigator
ARC Discovery project grant (DP160102126) (2016 – 2018), $330K, CIA
NHMRC project grant (APP1087889) (2015 – 2019), $700K, CIB
NHMRC project grant (APP1080157) (2015 – 2017), $344K, CIA
NHMRC project grant (APP1047956) (2013 – 2015), $560K, CIB
Discovery Early Career Research Award (DE130100614) (2013 – 2015), $375K, CIA
University of New England Research Assistantship (UNERA) (2003 - 2005)

5. Contribution to the field

As evidence of my engagement and national and international standing, I am regularly invited to provide peer review for high quality journals in the discipline and for esteemed funding agencies, and to join key professional bodies and to organise significant events in the field. These include:

Editorial Board
Associate Editor in Frontiers in Genetics, Frontiers in Plant Science, Frontiers in Ecology and Evolution, International Journal of Genomics.

Referee for peer-reviewed journals
Nature Genetics, Nature Communications, American Journal of Human Genetics, PLoS Genetics, Human Molecular, Genetics, Genetics, Current Genomics, PLoS One, BMC Genetics, Genetics Selection Evolution, Gene and many others.

Referee for funding agencies
NHMRC, ARC and Wellcome Trust/DBT India Alliance.

Referee for PhD/Honours thesis
University of Sydney, University of Queensland and University of New England

Organising conference and workshop
The sole organiser for the Brisbane Statistical Human Genetics Forum (October 2013) and member of the organizing committee for the summer school in animal genetics and breeding in Armidale in Feb/2005, Feb/2006 and Feb/2007.

Consulting and other forms of knowledge exchange
I regularly participate scientific discussions via email, media and online forum, e.g. a few hundreds time per year. I have released software that helps students and researchers solve their problems in their data analyses, addressing their (numerous) demands to implement functions and methods that are necessary for them. In the process, I have also disseminated novel knowledge about specific algorithms and models. I have documented some essential components from these discussions and made available to public (MTG2 manual including 13 chapters).

Resource managements

In the genomic era, there are a number of genotype and phenotype data publicly available as a form of "big data". For example, I have managed to have access to multiple data sets from Wellcome Trust Case Control Consortium (WTCCC), therosclerosis Risk in Communities (ARIC), Framingham Heart Study (FHS), Genetic Epidemiology Research on Adult Health and Aging (GERA), Database of Genotype and Phenotype (dbGaP), UK10K and UK Biobank. I have made these data sets available to other researchers within the centre and university (following the data agreement policy, which is a part of data management). This will help enhance research capacity of the centre and university.

I also regularly contribute computing facility to the institute so that other researchers in the institute can use the facility for free. For example, I contributed a computer server (~ $30,000) in 2013, two blade servers (~ $50,000) in 2015 and plan to purchase a blade server (~ $50,000) in this year.

6. Invited Speaker/Lecturer

(Travel/accommodation expenses covered by the host)

1. The efficiency of designs for fine mapping of quantitative trait loci using combined linkage disequilibrium and linkage. **Lee, S. H.** and van der Werf, J. H. J. Bioinformatics Symposium, 1-2nd September 2003, Sydney University, Biological Informatics and Technology Centre, Australia.

2. Regional Training Course on Selective Breeding Gene Technologies (Korea), organized by FAO/IAEA, 3–7 April 2006.

3. Fine-mapping of quantitative trait loci using combined linkage disequilibrium and linkage with general pedigrees. **Lee, S. H.** and Van der Werf, J. H. J. (2007) The Association for the Advancement of Animal Breeding and Genetics 17: 376-382.

4. Statistical analysis and application for animal breeding using genomic information. **Lee, S.H.**, Kim, S., Lee, S.H., Choi, S.B., Cho, Y.M., Park, E.W., Choi, Y.L. and Lee, S.C. (2008) The 8th Congress of the Korean Society of Animal Science and Technologies 1: 139-150.

5. Estimating genetic variances for disease liability explained by all SNPs from case-control GWAS. **Lee, S. H.,** Wray, N. R., Goddard, M. E., Visscher, P. M. (2010) Queensland Workshop Frontiers in Statistical Genetics and Genomics; Resolving complex traits through coancestry and the shared inheritance of genome (Brisbane, Australia).

6. Summer Institute in Statistical Genetics, Seattle, USA (2010) (Tutor)

7. Summer Institute in Statistical Genetics, Seattle, USA (2011) (Tutor)

8. **Lee, S. H.** (2012) Genomic Partitioning by Functional Annotation of variance and Covariance Explained by SNPs. XXth World Congress of Psychiatric Genetics; Confounding the Complexity of Brain and Behavior (Hamburg, Germany).

9. **Lee, S. H.** (2013) Estimation of SNP-heritability from dense genotype data. Brisbane Statistical Human Genetics Forum (Brisbane, Australia)

10. **Lee, S. H.** (2014) Joint analysis of psychiatric disorders increases accuracy of risk prediction for schizophrenia. XXIInd World Congress of Psychiatric Genetics; Pathways to Therapy and Prevention (Copenhagen, Denmark).

11. Quantitative, Population and Statistical Genetics. The 1st Winter Workshop, Chung-Nam National University, South Korea 22-24 Feb 2016.

12. Investigating the Genetic Architecture of Complex Traits & Prediction of Phenotype from Genome-wide SNPs, Armidale Summer Course 2016, Armidale, Australia

13. Genotype by environment interaction in breeding programs, Armidale Summer Course 2017, Armidale, Australia

14. **Lee, S. H.** (2018) Genomic prediction, The Korean society of animal breeding and genomics, Chung-Nam National University, South Korea, 5 – 7 July 2018.

15. **Lee, S. H.** (2021) Novel statistical methods for genetic evaluations, The Korean society of animal breeding and genomics, Daejeon Convention Centre, South Korea, 1-2 July 2021.

16. **Lee, S. H.** (2021) Population analysis using statistical tools, Data science in human disease symposium, Seoul, South Korea, 24 Aug 2021.

The quality of my presentation and contribution is evidenced by highly positive feedbacks from the audiences, e.g. Figure 1.

The Korean Society of Animal Breeding & Genetics

Questionnaire for the 1st Genetic Workshop of Animal Breeding and Genomics

- Date: 2016. 22. Feb (Mon) ~ 24. Feb (Wed)
- Venue: College of Agriculture and Life Science, Chungnam National University
- Attendance: Research Scientist and Postgraduate Students (50 persons)
- Lecturer: Dr. Sang Hong Lee, University of New England, Australia

Q1. The course contributed to my understanding of the subject materials

Very Good	Good	Normal	Bad	Worse
35	13	1		

Q2. The lecturer was well prepared for each lecture

Very Good	Good	Normal	Bad	Worse
30	15	5		

Q3. The lecturer's explanations were clear and understandable

Very Good	Good	Normal	Bad	Worse
32	17	1		

Q4. The course materials (textbook, handouts, readings, etc.) were helpful

Very Good	Good	Normal	Bad	Worse
40	10			

Q5. The lecturer has expertise in the content of the lecture

Very Good	Good	Normal	Bad	Worse
45	5			

Q6. I am satisfied with this course

Very Good	Good	Normal	Bad	Worse
50				

- Overall Evaluation: This course was very helpful for attendee to improve knowledge of quantitative genetic theory and practical things with genome data. All of the attendee evaluated that Dr. Hong Lee's lecture was very clear and qualified so that they would like to take this course again in near future.

Professor Chang Hee Do

President of Korean Society of Animal Breeding and Genetics

The Korean Society of Animal Breeding & Genetics

Figure 1. Averaged evaluation score of 77% at the highest rate "very good" from a statistical genetics course

7. Teaching Experience

I teach novel concepts, designs and tools that can essentially improve students' capacity to analyse and characterise complex traits in the population based on genomic information in the context of Statistical Genetics. I have coordinated and taught a number of regular university courses including Statistical Learning, Biomedical Science, Quantitative, Population and Statistical Genetics and Health Data Sources and Management (Big Genomic data).

Date: 2012 (trimesters 3)
Role: Tutor
Course: Biomedical Science (BIOM3), University of Queensland

Date: Mar, 2016 – Jul, 2017 (weekly)
Role: Lecturer
Course: Quantitative, Population and Statistical Genetics (for postgraduate students)

Date: 2017 (trimesters 1)
Role: Coordinator
Course: Statistical learning (STAT330), University of New England

Date: 2018 (trimesters 2)
Role: Lecturer
Course: Health Data Sources and Management (HLTH 5190), University of South Australia

8. Supervision Experience

From the supervisions of 6 research students and 6 junior researchers, there were 12 publications in high-profile journals (including JAMA Psych (impact factor (IF) 15), Mol Psych (IF 13), Am J Hum Genet (IF 9) and PLoS Genet (IF 6)). There are currently 8 manuscripts in preparation.

Table 1. Summary of (co)supervisions and outcomes.

Postdoctoral Fellow/Student Name	Years Involved	Supervisory Role	Postdoctoral Fellow/Student's Degree/Course/Training/ Study	Status	Trainee status	Outcomes
Mr Seung Whan Lee	2006-2008	Co-supervision	PhD at Animal Genetics, the University of New England	Completed	Assistant Professor at Chungnam National University, South Korea	Three papers (Co-author)[2-4]
Ms Aimee Hanson	2012	Co-supervision	Winter Research Scholarship Program at the University of Queensland	Completed	PhD in UQ	
Mr Wouter Peyrot	2013	Co-supervision	Visiting student	Completed	Postdoctoral fellow at VU University Medical Center	One paper (Co-author)[12]
Ms Cara Nolan	2014	Supervision	Associate Researcher	Completed	Master in UC Berkeley	
Mr Robert Maier	2014-2015	Co-supervision	PhD at Queensland Brain Institute, University of Queensland	Completed	Postdoctoral fellow at Broad Institute, USA	Two papers (Corresponding and co-author)[7, 8]
Dr Divya Mehta	2014-2016	Co-supervision	Postdoctoral Fellow	Completed	Senior Research Fellow at Queensland University Technology	One paper (Corresponding author)[9]
Dr Gerhard Moser	2015-2016	Supervision	Data analyst and consultant	Completed	Senior Research Scientist at Australian Agriculture Company	Two papers (Co-author)[1, 10]
Ms Shalanee Weerasinghe	2016	Supervision	Associate Researcher	Completed	Research Scientist at Agricultural Business Research Institute	Two papers (Corresponding author)[5, 6]
Mr Mohammad Zaher al Kalaldeh	2017-2018	Co-supervision	PhD at Animal Genetics, University of New England	Submitted	Postdoctoral Fellow at University of New England	Two papers (Co-author)[15,16]
Dr Guiyan Ni	2016-2019	Supervision	Postdoctoral Fellow	Completed	Postdoctoral Fellow at University of Queensalnd	Four papers (Corresponding author)[11,13,17,18]
Dr Azmeraw Amare	2018	Supervision	Research Associate	Completed	Research Associate at SAHMRI	One paper (Corresponding author)[17]
Dr Gopal Gowane	2018-2019	Co-supervision	Visiting scholar	Completed	Research Scientist at ICAR in India	One paper (Co-author)[14]
Mr Buu Turong	2019	Supervision	Research Associate	Completed	MD degree to be finished in Jul/2021	One manuscript (Corresponding author)
Ms Yoonji Jung	2019	Supervision	Visiting student (Master)	On-going	Master at Chung Nam University in S. Korea	One manuscript (Corresponding author)
Ms Sohyoung Won	2019	Supervisor	Visiting student (Master)	Completed	PhD in Seoul University	
Dr Xuan Zhou	2017-2018	Supervision	Research Associate	On-going	Research Associate at University of South Australia	Two manuscripts (Corresponding author)
Dr Cheonglong Yu	2018-2020	Supervision	Research Fellow	On-going	Research Fellow at University of South Australia	One manuscript (Corresponding author)
Ms Jisu Shin	2019-2021	Supervision	Master	On-going		
Mr Muktar Ahmed	2019-2022	Co-supervision	PhD	On-going		

Publications from my supervisions (annotated in Table 1)

1. Chen, G.-B., Lee, S.H., Montgomery, G.W. et al. 2017. Performance of risk prediction for inflammatory bowel disease based on genotyping platform and genomic risk score method. BMC Medical Genetics 18(1) 94.
2. Lee, S., Cho, Y., Lee, S. et al. 2008. Identification of marbling-related candidate genes in M-longissimus dorsi of high- and low marbled Hanwoo (Korean Native Cattle) steers. BMB Reports 41(12) 846-851.
3. Lee, S., van der Werf, J., Lee, S. et al. 2010. Genetic polymorphisms of the bovine Fatty acid binding protein 4 gene are significantly associated with marbling and carcass weight in Hanwoo (Korean Cattle). *Animal Genetics* 41(4) 442-444.
4. Lee, S.H., van der Werf, J.H.J., Kim, N.K. et al. 2011. QTL and gene expression analyses identify genes affecting carcass weight and marbling on BTA14 in Hanwoo (Korean Cattle). *Mammalian Genome* 22(9-10) 589-601.
5. Lee, S.H., Weerasinghe, W.M.S.P. and van der Werf, J.H.J. 2017. Genotype-environment interaction on human cognitive function conditioned on the status of breastfeeding and maternal smoking around birth. *Scientific Reports* 7 6087. (**Corresponding author**)
6. Lee, S.H., Weerasinghe, W.M.S.P., Wray, N. et al. 2017. Using information of relatives in genomic prediction to apply effective stratified medicine. *Scientific Reports* 7 4209. (**Corresponding author**)
7. Maier, R., Moser, G., Chen, G.-B. et al. 2015. Joint analysis of psychiatric disorders increases accuracy of risk prediction for schizophrenia, bipolar disorder and major depression disorder. *Am J Hum Genet* 96 283-294. (**Corresponding author**) **(Impact Factor 10)**
8. Maier, R.M., Zhu, Z., Lee, S.H. et al. 2018. Improving genetic prediction by leveraging genetic correlations among human diseases and traits. *Nat Commun* 9(1) 989. **(Impact Factor 12)**
9. Mehta, D., Tropf, F.C., Graten, J. et al. 2016. Evidence for genetic overlap between schizophrenia and age at first birth in women. *JAMA Psych* 73 497-505. (**Corresponding author**) **(Impact Factor 15)**
10. Moser, G., Lee, S.H., Hayes, B.J. et al. 2015. Simultaneous discovery, estimation and prediction analysis of complex traits using a Bayesian mixture model. *PLoS Genet* 11 e1004969. **(Impact Factor 6)**
11. Ni, G., Moser, G., Schizophrenia Working Group of the Psychiatric Genomics Consortium et al. 2018. Estimation of genetic correlation using linkage disequilibrium score regression and genomic restricted maximum likelihood. *Am J Hum Genet* 102 1185-1194. (**Corresponding author**) **(Impact Factor 10)**
12. Peyrot, W.J., Lee, S.H., Milaneschi, Y. et al. 2015. The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25,000 subjects. *Mol Psychiatry* 20(6) 735-743. **(Impact Factor 13)**
13. Ni, G., van der Werf, J., Zhou, X., Hyppönen, E., Wray, N.R., and **Lee, S.H**. Genotype–covariate correlation and interaction disentangled by a whole-genome multivariate reaction norm model. *Nature communications* 10, 2239 (2019)
14. Gowane, G.R., **Lee, S.H**., Clark, S., Moghaddar, N., Al-Mamun, H.A., and van der Werf, J.H.J. Effect of selection and selective genotyping for creation of reference on bias and accuracy of genomic prediction. *J Anim Breed Genet* (2019)
15. Al Kalaldeh M, Gibson J, **Lee SH**, Gondro C, van der Werf JHJ. Detection of genomic regions underlying resistance to gastrointestinal parasites in Australian sheep. Genetics Selection Evolution. 2019;51(1):37. doi: 10.1186/s12711-019-0479-1

16. Al Kalaldeh M, Gibson J, Duijvesteijn N, Daetwyler HD, MacLeod I, Moghaddar N, et al. Using imputed whole-genome sequence data to improve the accuracy of genomic prediction for parasite resistance in Australian sheep. Genetics Selection Evolution. 2019;51(1):32. doi: 10.1186/s12711-019-0476-4
17. Ni, G., Amare, A.T., Zhou, X. …, **Lee SH.** 2019. The genetic relationship between female reproductive traits and six psychiatric disorders. *Scientific Reports* 9(1) 12041
18. Ni, G., Gratten, J., Wray, N.R. & **Lee, S.H**. Age at first birth in women is genetically associated with increased risk of schizophrenia. *Sci Rep* **8**, 10168 (2018).

9. Publications

Book Chapters

1. **Lee, S. H**., Sapkota, Y., Fung, J., Montgomery, G. W. Genetic Biomarkers for Endometriosis: Biomarkers for Endometriosis. Edited by T. M. D'Hooghe (Springer) (2017) pp 83–93.
2. Yang, J., **Lee, S. H.,** Goddard, M. E., Visscher, P. M. Genome-Wide Complex Trait Analysis (GCTA): Methods, Data Analyses, and Interpretations Genome-Wide Association Studies and Genomic Prediction. 1019, 215-236 (2013).

Peer-reviewed Journal Article

Q= **Quartile** and denotes the journals relative impact within their category, *e.g.* **Q1** = the 'best' 25 % of journals in the SCI Subject Category, from Journal Citation Reports; **IF**= 2016 Impact Factor; **Cited**= from Google Scholar, Feb 2018

3. Ahmed, M., Gebremichael, A., **Lee, S.H**., et al. (2021) Adiposity and Cancer: A Mendelian Randomization Analysis in the UK Biobank. International Journal of Obesity. Accepted.
4. Yang, Z., Wu, H., Lee, P.H., Tsetsos, F., Davis, L.K., Yu, D., **Lee, S.H.** et al. (2021) Investigating shared genetic basis across Tourette Syndrome and comorbid neurodevelopmental disorders along the impulsivity-compulsivity spectrum. Biological Psychiatry. In press. https://doi.org/10.1016/j.biopsych.2020.12.028
5. Zhou, D., Yu, D., Scharf, J.M., Mathews, C.A., McGrath, L., Cook, E., **Lee, S.H.** et al. (2021) Contextualizing genetic risk score for disease screening and rare variant discovery. Nature Communications **12**, 4418.
6. Gershon, E.S.*, **Lee, S.H.*** et al. (2021) An opportunity for primary prevention research in psychotic disorders. Schizophrenia Research (*Joint first author). In press. https://doi.org/10.1016/j.schres.2021.07.001
7. Shin, J., and **Lee, S.H.** (2021). GxEsum: a novel approach to estimate the phenotypic variance explained by genome-wide GxE interaction based on GWAS summary statistics for biobank-scale data. Genome Biology **22**: 183.
8. Zhou, X., Im, H.K., and **Lee, S.H.** (2020). CORE GREML for estimating covariance between random effects in linear mixed models for complex trait analyses. Nat Comm **11**, 4208
9. Zhou, X., van der Werf, J., Carson-Chahhoud, K., Ni, G., McGrath, J., Hyppönen, E., and **Lee, S.H.** Whole-Genome Approach Discovers Novel Genetic and Nongenetic Variance Components Modulated by Lifestyle for Cardiovascular Health. J Am Heart Assoc **9**, e015661 (2020).
10. Yu, C., Ni, G., van der Werf, J. & **Lee, S.H.** Detecting Genotype-Population Interaction Effects by Ancestry Principal Components. *Frontiers in Genetics* **11**, 379 (2020)
11. Truong, B., Zhou, X., Shin, J., Li, J., van der Werf, J.H.J., Le, T.D., and **Lee, S.H.** Efficient polygenic risk scores for biobank scale data by exploiting phenotypes from inferred relatives. Nature communications **11**, 3074 (2020)
12. Lam, M., Awasthi, S., Watson, H.J., Goldstein, J., Panagiotaropoulou, G., Trubetskoy, V., Karlsson, R., Frei, O., Fan, C.-C., De Witte, W., et al. RICOPILI: Rapid Imputation for COnsortias PIpeLIne. Bioinformatics **36**, 930-933 (2020).
13. Ni, G., van der Werf, J., Zhou, X., Hyppönen, E., Wray, N.R., and **Lee, S.H**. Genotype–covariate correlation and interaction disentangled by a whole-genome multivariate reaction norm model. *Nature communications* 10, 2239 (2019)

14. Ni, G., Amare, A.T., Zhou, X. …, **Lee SH.** The genetic relationship between female reproductive traits and six psychiatric disorders. *Scientific Reports* 9: 12041 (2019)
15. Mulder, H.A., **Lee, S.H**., Clark, S., Hayes, B.J., and van der Werf, J.H. The Impact of Genomic and Traditional Selection on the Contribution of Mutational Variance to Long-Term Selection Response and Genetic Variance. Genetics (In press) (2019)
16. Van Rheenen, W., Peyrot, W.J., Schork, A.J., **Lee, S.H**., and Wray, N.R. Genetic correlations of polygenic disease traits: from theory to practice. *Nature Reviews Genetics* **20**: 567-581 (2019)
17. Gowane, G.R., **Lee, S.H**., Clark, S., Moghaddar, N., Al-Mamun, H.A., and van der Werf, J.H.J. Effect of selection and selective genotyping for creation of reference on bias and accuracy of genomic prediction. *J Anim Breed Genet* (2019)
18. Al Kalaldeh M, Gibson J, **Lee SH**, Gondro C, van der Werf JHJ. Detection of genomic regions underlying resistance to gastrointestinal parasites in Australian sheep. Genetics Selection Evolution. 2019;51(1):37. doi: 10.1186/s12711-019-0479-1
19. Al Kalaldeh M, Gibson J, Duijvesteijn N, Daetwyler HD, MacLeod I, Moghaddar N, et al. Using imputed whole-genome sequence data to improve the accuracy of genomic prediction for parasite resistance in Australian sheep. Genetics Selection Evolution. 2019;51(1):32. doi: 10.1186/s12711-019-0476-4
20. Ni, G., Moser, G., Schizophrenia Working Group of the Psychiatric Genomics Consortium, Wray, N.R. & **Lee, S.H**. Estimation of genetic correlation using linkage disequilibrium score regression and genomic restricted maximum likelihood. *Am J Hum Genet* **102**, 1185-1194 (2018).
21. Ni, G., Gratten, J., Wray, N.R. & **Lee, S.H**. Age at first birth in women is genetically associated with increased risk of schizophrenia. *Sci Rep* **8**, 10168 (2018).
22. Bipolar Disorder and Schizophrenia Working Group of the Psychiatric Genomics Consortium. Genomic dissection of bipolar disorder and schizophrenia, including 28 subphenotypes. *Cell* **173**, 1705-1715 (2018).
23. Maier, R., Zhu, Z., **Lee, S.H.,** Trzaskowski, M., Rudefer, D.M., Stahl, E.A., Ripke, S., Wray, N.R., Yang, J., Visscher, P., *et al.* Improving genetic prediction by leveraging genetic correlations among human diseases and traits. *Nature Communications* **9**, 989 (2018). [**Q1**; IF 12.12, Cited **0**].
24. Martin, J., Walters, R.K., Demontis, D., Mattheisen, M., **Lee, S.H.,** Robinson, E., Brikell, I., Ghirardi, L., Larsson, H., Lichtenstein, P., *et al.* A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. *Biological Psychiatry*. 83(12):1044-1053 (2018). [**Q1**; IF 11.41, Cited **1**].
25. Tropf, F.C., **Lee, S.H.,** Verweij, R.M., Stulp, G., van der Most, P.J., de Vlaming, R., Bakshi, A., Briley, D.A., Rahal, C., Hellpap, R., *et al.* Hidden heritability due to heterogeneity across seven populations. *Nature Human Behaviour* **1**, 757-765 (2017). [Cited **1**].
26. Power, R.A., Tansey, K.E., Buttenschøn, H.N., Cohen-Woods, S., Bigdeli, T., Hall, L.S., Kutalik, Z., **Lee, S.H**., Ripke, S., Steinberg, S., *et al.* Genome-wide Association for Major Depression Through Age at Onset Stratification: Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. *Biological Psychiatry* **81**, 325-335 (2017). [**Q1**; IF 11.41, Cited **40**].
27. **Lee, S.H.,** Weerasinghe, W.M.S.P., Wray, N., Goddard, M., and Van der Werf, J. Using information of relatives in genomic prediction to apply effective stratified medicine. *Scientific Reports* **7**, 42091 (2017). [**Q1**; IF 4.26, Cited **12**].

28. **Lee, S.H.,** Weerasinghe, W.M.S.P., and van der Werf, J.H.J. Genotype-environment interaction on human cognitive function conditioned on the status of breastfeeding and maternal smoking around birth. *Scientific Reports* **7**, 6087 (2017). [**Q1**; IF 4.26, Cited **0**].
29. **Lee, S.H.,** Clark, S., and van der Werf, J.H.J. Estimation of genomic prediction accuracy from reference populations with varying degrees of relationship. *PLOS ONE* **12**, e0189775 (2017). [**Q1**; IF 2.81, Cited **1**].
30. CNV and Schizophrenia Working Groups of the Psychiatric Genomics Consortium. Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. *Nature Genetics* **49**, 27-35 (2017). [**Q1**; IF 27.96, Cited **47**].
31. Chen, G.-B., Lee, S.H., Montgomery, G.W., Wray, N.R., Visscher, P.M., Gearry, R.B., Lawrance, I.C., Andrews, J.M., Bampton, P., Mahy, G., et al. Performance of risk prediction for inflammatory bowel disease based on genotyping platform and genomic risk score method. *BMC Medical Genetics* **18**, 94 (2017). [**Q1**; IF 2.20, Cited **1**].
32. Yang, J., **Lee, S.H**., Wray, N.R., Goddard, M.E., and Visscher, P.M. GCTA-GREML accounts for linkage disequilibrium when estimating genetic variance from genome-wide SNPs. *Proceedings of the National Academy of Sciences* **113**, E4579-E4580 (2016). [**Q1**; IF **9.67**, Cited **8**].
33. Mehta, D., Tropf, F.C., Graten, J., Bakshi, A., Zhu, Z., Bacanu, S.A., Hemani, G., Magnusson, P.K., Barban, N., Esko, T., …, **Lee, S.H.** Evidence for genetic overlap between schizophrenia and age at first birth in women. *JAMA Psychiatry* **73**, 497-505 (2016). [**Q1**; IF **15.31**, Cited **13**] (**Last author**)
34. **Lee, S.H**., & van der Werf, J.H.J. MTG2: An efficient algorithm for multivariate linear mixed model analysis based on genomic information. *Bioinformatics* **32**, 1420-1422 (2016). [**Q1**; IF **7.31**, Cited **23**]
35. Chen, G.B., **Lee, S.H.,** Zhu, Z.X., Benyamin, B., and Robinson, M.R. EigenGWAS: finding loci under selection through genome-wide association studies of eigenvectors in structured populations. *Heredity* **117**, 51-61 (2016). [**Q1**; IF **3.80**, Cited **16**]
36. Chen, G.-B., Lee, S.H., Robinson, M.R., Trzaskowski, M., Zhu, Z.-X., Winkler, T.W., Day, F.R., Croteau-Chonka, D.C., Wood, A.R., Locke, A.E., *et al.* Across-cohort QC analyses of GWAS summary statistics from complex traits. *European Journal of Human Genetics* **25**, 137-146 (2016). [**Q1**; IF **4.35**, Cited **4**]
37. Bigdeli, T.B., Ripke, S., Bacanu, S-A., **Lee, S.H**., Wray, N.R., Gejman, P.V., Rietschel, M., Cichon, S., Clair, D., Corvin, A., *et al.* Genome-wide association study reveals greater polygenic loading for schizophrenia in cases with a family history of illness. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics* **171**, 276-289 (2016). [**Q1**; IF **3.42**, Cited **9**]
38. Loh, P-R., Bhatia, G., Gusev, A., Finucane, H.K., Bulik-Sullivan, B.K., Pollack, S.J., de Candia, T.R., **Lee, S.H**., Wray, N.R., *et al.* Contrasting genetic architectures of schizophrenia and other complex diseases using fast variance-components analysis. *Nature Genetics* **47**, 1385-1392 (2015). [**Q1**; IF **27.96**, Cited **92**].
39. **Lee, S.H.** Implications of simplified linkage equilibrium SNP simulation. *Proceedings of the National Academy of Sciences* **112**, E5449-E5451 (2015). [**Q1**; IF **9.67**, Cited **2**].
40. Yang, J., Bakshi, A., Zhu, Z., Hemani, G., Vinkhuyzen, A.A.E., **Lee, S.H**., Robinson, M.R., Perry, J.R.B., Nolte, I.M., van Vliet-Ostaptchouk, J.V., *et al.* Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. *Nature Genetics* **47**, 1114–1120 (2015). [**Q1**; IF **27.96**, Cited **175**].
41. **Lee, S.H**., Byrne, E.M., Hultman, C.M., Kähler, A., Vinkhuyzen, A.A., Ripke, S., Andreassen, O.A., Frisell, T., Gusev, A., Hu, X., *et al.* New data and an old puzzle: the negative association

between schizophrenia and rheumatoid arthritis. *International Journal of Epidemiology* **44**, 1706-1721 (2015). [**Q1**; IF **9.18**, Cited **24**].
42. The Network Pathway Analysis Subgroup of the Psychiatric Genomics. Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. *Nature Neuroscience* **18**, 199-209 (2015). [**Q1**; IF **17.84**, Cited **68**].
43. Bérénos, C., Ellis, P.A., Pilkington, J.G., **Lee, S.H**., Graten, J. & Pemberton, J.M. Heterogeneity of genetic architecture of body size traits in a free-living population. *Molecular Ecology* **24**, 1810-1830 (2015). [**Q1**; IF **6.09**, Cited **19**].
44. Peyrot WJ, **Lee SH**, Milaneschi Y, *et al.* The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25000 subjects. *Molecular Psychiatry* **20**, 735-743 (2015). [**Q1**; IF **13.2**, Cited **15**]
45. Zhu, Z., Bakshi, A., Vinkhuyzen, A.A.E., Hemani, G., **Lee, S.H**., Nolte, I.M., van Vliet-Ostaptchouk, J.V., Snieder, H., Esko, T., Milani, L. et al. Dominance Genetic Variation Contributes Little to the Missing Heritability for Human Complex Traits. *The American Journal of Human Genetics* **96**, 377-385 (2015). [**Q1**; IF **9.03**, Cited **56**]
46. Moser, G., **Lee, S.H**., Hayes, B.J., Goddard, M.E., Wray, N.R. & Visscher, P.M. Simultaneous discovery, estimation and prediction analysis of complex traits using a Bayesian mixture model. *PLoS Genetics* **11**, e1004969 (2015). [**Q1**; IF **6.1**, Cited **92**]
47. Maier, R., Moser, G., Chen, G.-B., Ripke, S., Cross disorder Working group of the Psychiatric Genomics Consortium, Coryell, W., Potash, J.B., Scheftner, W.A., Shi, J., Weissman, M.M., …, **Lee, S.H.** Joint analysis of psychiatric disorders increases accuracy of risk prediction for schizophrenia, bipolar disorder and major depression disorder. *The American Journal of Human Genetics* **96**, 283-294 (2015). [**Q1**; IF **9.03**, Cited **74**] (**Last author**)
48. Wray, N.R., **Lee, S.H**., Mehta, D., Vinkhuyzen, A.A.E., Dudbridge, F. & Middeldorp, C.M. Research Review: Polygenic methods and their application to psychiatric traits. *Journal of Child Psychology and Psychiatry* **55**, 1068-1087 (2014). [**Q1**; IF **6.46**, Cited **177**]
49. Visscher, P.M., Hemani, G., Vinkhuyzen, A.A.E., Chen, G.-B., **Lee, S.H**., Wray, N.R., Goddard, M.E. & Yang, J. Statistical Power to Detect Genetic (Co)Variance of Complex Traits Using SNP Data in Unrelated Samples. *PLoS Genetics* **10**, e1004269 (2014). [**Q1**; IF **6.1**, Cited **133**]
50. Schizophrenia Working Group of the Psychiatric Genomics Consortium. Biological insights from 108 schizophrenia-associated genetic loci. *Nature* **511**, 421-427 (2014). [**Q1**; IF **40.14**, Cited **1995**]
51. Gusev, A., **Lee, S.H**., Trynka, G., Finucane, H., Vilhjalmsson, B.J., Xu, H., Zang, C., Ripke, S., Bulik-Sullivan, B., Stahl, E. *et al.* Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. *The American Journal of Human Genetics* **95**, 535-552 (2014). [**Q1**; IF **9.03**, Cited **234**]
52. Chen, G.-B., **Lee, S.H**., Brion, M.-J.A., Montgomery, G.W., Wray, N.R., Radford-Smith, G.L., Visscher, P.M. & The International IBD Genetics Consortium. Estimation and partitioning of (co)heritability of inflammatory bowel disease from GWAS and immunochip data. *Human Molecular Genetics* **23**, 4710-4720 (2014). [**Q1**; IF **5.99**, Cited **50**]
53. Yang, L., Neale, B.M., Liu, L., **Lee, S.H**., Wray, N.R., Ji, N., Li, H., Qian, Q., Wang, D., Li, J. *et al.* Polygenic transmission and complex neuro developmental network for attention deficit hyperactivity disorder: genome-wide association study of both common and rare variants. *American Journal of Medical Genetics B Neuropsychiatric Genetics* **162B**, 419-430 (2013). [**Q1**; IF **3.42**, Cited **103**]
54. Ripke, S., O'Dushlaine, C., Chambert, K., Moran, J.L., Kahler, A.K., Akterin, S., Bergen, S.E., Collins, A.L., Crowley, J.J., Fromer, M., Kim, Y., **Lee, S.H.** *et al.* Genome-wide association

analysis identifies 13 new risk loci for schizophrenia. *Nature Genetics* **45**, 1150-1159 (2013). [**Q1**; IF **27.96**, Cited **918**]
55. Rietveld, C.A., Medland, S.E., Derringer, J., Yang, J., Esko, T., Martin, N.W., Westra, H.-J., Shakhbazov, K., Abdellaoui, A., Agrawal, A. *et al.* GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. *Science* **340**, 1467-1471 (2013). [**Q1**; IF **37.21**, Cited **417**]
56. **Lee, S.H**., Yang, J., Chen, G.-B., Ripke, S., Stahl, E.A., Hultman, C.M., Sklar, P., Visscher, P.M., Sullivan, P.F., Goddard, M.E. *et al.* Estimation of SNP heritability from dense genotype data. *The American Journal of Human Genetics* **93**, 1151-5 (2013). [**Q1**; IF **9.03**, Cited **52**]
57. **Lee, S.H**. & Wray, N.R. Novel genetic analysis for case-control genome-wide association studies: quantification of power and genomic prediction accuracy. *PLOS ONE* **8**, e71494 (2013). [**Q1**; IF **2.81**, Cited **27**]
58. **Lee, S.H**., Ripke, S., Neale, B.M., Faraone, S.V., Purcell, S.M., Perlis, R.H., Mowry, B.J., Thapar, A., Goddard, M.E., Witte, J.S. *et al.* Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. *Nature Genetics* **45**, 984-994 (2013). [**Q1**; IF **27.96**, Cited **983**]
59. **Lee, S.H**., Harold, D., Nyholt, D.R., Goddard, M.E., Zondervan, K.T., Williams, J., Montgomery, G.W., Wray, N.R., Visscher, P.M., Consortium, A. *et al.* Estimation and partitioning of polygenic variation captured by common SNPs for Alzheimer's disease, multiple sclerosis and endometriosis. *Human Molecular Genetics* **22**, 832-841 (2013). [**Q1**; IF **5.99**, Cited **108**]
60. de Candia, T.R., **Lee, S.H**., Yang, J., Browning, B.L., Gejman, P.V., Levinson, D.F., Mowry, B.J., Hewitt, J.K., Goddard, M.E., O'Donovan, M.C. *et al.* Additive genetic variation in schizophrenia risk is shared by populations of African and European descent. *The American Journal of Human Genetics* **93**, 463-470 (2013). [**Q1**; IF **9.03**, Cited **35**]
61. Davis, L.K., Yu, D., Keenan, C.L., Gamazon, E.R., Konkashbaev, A.I., Derks, E.M., Neale, B.M., Yang, J., **Lee, S.H**., Evans, P. *et al.* Partitioning the heritability of tourette syndrome and obsessive compulsive disorder reveals differences in genetic architecture. *PLoS Genetics* **9**, e1003864 (2013). [**Q1**; IF **6.1**, Cited **156**]
62. Berndt, S.I., Gustafsson, S., Magi, R., Ganna, A., Wheeler, E., Feitosa, M.F., Justice, A.E., Monda, K.L., Croteau-Chonka, D.C., Day, F.R. *et al.* Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics* **45**, 501-12 (2013). [**Q1**; IF **27.96**, Cited **332**]
63. Wray, N.R., **Lee, S.H**. & Kendler, K.S. Impact of diagnostic misclassification on estimation of genetic correlations using genome-wide genotypes. *European Journal of Human Genetics* **20**, 668-674 (2012). [**Q1**; IF **4.35**, Cited **43**]
64. Vinkhuyzen, A.A.E., Pedersen, N.L., Yang, J., **Lee, S.H**., Magnusson, P.K.E., Iacono, W.G., McGue, M., Madden, P.A.F., Heath, A.C., Luciano, M. *et al.* Common SNPs explain some of the variation in the personality dimensions of neuroticism and extraversion. *Translational Psychiatry* **2** (2012). [**Q1**; IF **5.62**, Cited **141**]
65. **Lee, S.H**., Yang, J., Goddard, M.E., Visscher, P.M. & Wray, N.R. Estimation of pleiotropy between complex diseases using single-nucleotide polymorphism-derived genomic relationships and restricted maximum likelihood. *Bioinformatics* **28**, 2540-2542 (2012). [**Q1**; IF **7.31**, Cited **265**]
66. **Lee, S.H**., Goddard, M.E., Wray, N.R. & Visscher, P.M. A better coefficient of determination for genetic profile analysis. *Genetic Epidemiology* **36**, 214-224 (2012). [**Q1**; IF **2.60**, Cited **57**]
67. **Lee, S.H**., DeCandia, T.R., Ripke, S., Yang, J., PGC-SCZ, ISC, MGS, Sullivan, P.F., Goddard, M.E., Keller, M.C. *et al.* Estimating the proportion of variation in susceptibility to

schizophrenia captured by common SNPs. *Nature Genetics* **44**, 247-250 (2012). [**Q1**; IF **27.96**, Cited **438**]
68. Keller, M.C., Simonson, M.A., Ripke, S., Neale, B.M., Gejman, P.V., Howrigan, D.P., **Lee, S.H**., Lencz, T., Levinson, D.F., Sullivan, P.F. *et al.* Runs of Homozygosity Implicate Autozygosity as a Schizophrenia Risk Factor. *PLoS Genetics* **8**, 425-435 (2012). [**Q1**; IF **6.1**, Cited **78**]
69. Calvin, C.M., Deary, I.J., Webbink, D., Smith, P., Fernandes, C., **Lee, S.H**., Luciano, M. & Visscher, P.M. Multivariate genetic analyses of cognition and academic achievement from two population samples of 174,000 and 166,000 school children. *Behavior Genetics* **42**, 699-710 (2012). [**Q2**; IF **3.09**, Cited **40**]
70. Yang, J., **Lee, S.H**., Goddard, M. & Visscher, P. GCTA: A tool for genome-wide complex trait analysis. *The American Journal of Human Genetics* **88**, 76-82 (2011). [**Q1**; IF **9.03**, Cited **1833**]
71. Painter, J., Anderson, C., Nyholt, D., Macgregor, S., Lin, J., **Lee, S.H**., Lambert, A., Zhao, Z., Roseman, F., Guo, Q. *et al.* Genome-wide association study identifies a locus at 7p15.2 associated with endometriosis. *Nature Genetics* **43**, 51-U69 (2011). [**Q1**; IF **27.96**, Cited **242**]
72. Martin, N.W., Medland, S.E., Verweij, K.J.H., **Lee, S.H**., Nyholt, D.R., Madden, P.A., Heath, A.C., Montgomery, G.W., Wright, M.J. & Martin, N.G. Educational Attainment: A Genome Wide Association Study in 9538 Australians. *PLoS ONE* **6** (2011). [**Q1**; IF **2.81**, Cited **21**]
73. Lee, S.H., van der Werf, J.H.J., Kim, N.K., **Lee, S.H**., Gondro, C., Park, E.W., Oh, S.J., Gibson, J.P. & Thompson, J.M. QTL and gene expression analyses identify genes affecting carcass weight and marbling on BTA14 in Hanwoo (Korean Cattle). *Mammalian Genome* **22**, 589-601 (2011). [**Q2**; IF **2.60**, Cited **11**]
74. **Lee, S.H**., Wray, N., Goddard, M. & Visscher, P. Estimating Missing Heritability for Disease from Genome-wide Association Studies. *The American Journal of Human Genetics* **88**, 294-305 (2011). [**Q1**; IF **9.03**, Cited **595**]
75. Goddard, M.E., **Lee, S.H**., Yang, J., Wray, N.R. & Visscher, P.M. Population Structure Can Inflate SNP-Based Heritability Estimates (Response). *The American Journal of Human Genetics* **89**, 193-195 (2011). [**Q1**; IF **9.03**, Cited **9**]
76. Lee, S.H., van der Werf, J., **Lee, S.H**., Park, E., Oh, S., Gibson, J. & Thompson, J. Genetic polymorphisms of the bovine Fatty acid binding protein 4 gene are significantly associated with marbling and carcass weight in Hanwoo (Korean Cattle). *Animal Genetics* **41**, 442-444 (2010). [**Q1**; IF **2.68**, Cited **44**]
77. **Lee, S.H**., Nyholt, D., Macgregor, S., Henders, A., Zondervan, K., Montgomery, G. & Visscher, P. A Simple and Fast Two-Locus Quality Control Test to Detect False Positives Due to Batch Effects in Genome-Wide Association Studies. *Genetic Epidemiology* **34**, 854-862 (2010). [**Q1**; IF **2.60**, Cited **15**]
78. **Lee, S.H**., Goddard, M., Visscher, P. & van der Werf, J. Using the realized relationship matrix to disentangle confounding factors for the estimation of genetic variance components of complex traits. *Genetics Selection Evolution* **42** (2010). [**Q1**; IF **2.96**, Cited **46**]
79. Idaghdour, Y., Czika, W., Shianna, K., **Lee, S.H**., Visscher, P., Martin, H., Miclaus, K., Jadallah, S., Goldstein, D., Wolfinger, R. *et al.* Geographical genomics of human leukocyte gene expression variation in southern Morocco. *Nature Genetics* **42**, 62-67 (2010). [**Q1**; IF **27.96**, Cited **129**]
80. Marshall, K., Maddox, J., **Lee, S.H**., Zhang, Y., Kahn, L., Graser, H., Gondro, C., Walkden-Brown, S. & van der Werf, J. Genetic mapping of quantitative trait loci for resistance to Haemonchus contortus in sheep. *Animal Genetics* **40**, 262-272 (2009). [**Q1**; IF **2.68**, Cited **52**]
81. **Lee, S.H**., Van der Werf, J. & Kinghorn, B. Using an evolutionary algorithm and parallel computing for haplotyping in a general complex pedigree with multiple marker loci. *BMC Bioinformatics* **9** (2008). [**Q1**; IF **3.49**, Cited **5**]

82. **Lee, S.H.**, van der Werf, J., Hayes, B., Goddard, M. & Visscher, P. Predicting unobserved phenotypes for complex traits from whole-genome SNP data. *PLoS Genetics* **4**, e1000231 (2008). [**Q1**; IF **6.1**, Cited **169**]
83. **Lee, S.H**. & van der Werf, J. Simultaneous fine mapping of closely linked epistatic quantitative trait loci using combined linkage disequilibrium and linkage with a general pedigree. *Genetics Selection Evolution* **40**, 265-278 (2008). [**Q1**; IF **2.96**, Cited **6**]
84. Lee, S.H., Cho, Y., **Lee, S.H**., Kim, B., Kim, N., Choy, Y., Kim, K., Yoon, D., Im, S., Oh, S. & Park, E. Identification of marbling-related candidate genes in M-longissimus dorsi of high- and low marbled Hanwoo (Korean Native Cattle) steers. *BMB Reports* **41**, 846-851 (2008). [**Q3**; IF **1.95**, Cited **34**]
85. van der Werf, J., Marshall, K. & **Lee, S.H**. Methods and experimental designs for detection of QTL in sheep and goats. *Small Ruminant Research* **70**, 21-31 (2007). [**Q2**; IF **1.34**, Cited **27**]
86. Kijas, J., McCulloch, R., Edwards, J., Oddy, V., **Lee, S.H**. & van der Werf, J. Evidence for multiple alleles effecting muscling and fatness at the Ovine GDF8 locus. *BMC Genetics* **8** (2007). [**Q3**; IF **2.81**, Cited **87**]
87. **Lee, S. H**. & van der Werf, J. H. Fine mapping of multiple interacting quantitative trait loci using combined linkage disequilibrium and linkage information. *Journal of Zhejiang Universicty Science B* (2007) 8: 787-791. [**Q3**; IF **1.42**, Cited **3**]
88. **Lee, S. H**. & Van der Werf, J. Using dominance relationship coefficients based on linkage disequilibrium and linkage with a general complex pedigree to increase mapping resolution. *Genetics* **174**, 1009-1016 (2006). [**Q1**; IF **4.56**, Cited **21**]
89. **Lee, S. H**. & Van der Werf, J. H. J. Simultaneous fine mapping of multiple closely linked quantitative trait loci using combined linkage disequilibrium and linkage with a general pedigree. *Genetics* 173: 2329-2337 (2006). [**Q1**; IF **4.56**, Cited **21**]
90. **Lee, S. H**. & Van der Werf, J. H. J. An efficient variance component approach implementing an average information REML suitable for combined LD and linkage mapping with a general complex pedigree. *Genetics Selection Evolution* 38: 25-43 (2006). [**Q1**; IF **2.96**, Cited **43**]
91. **Lee, S. H**. & Van der Werf, J. & Tier, B. Combining the meiosis Gibbs sampler with the random walk approach for linkage and association studies with a general complex pedigree and multimarker loci. *Genetics* **171**, 2063-2072 (2005). [**Q1**; IF **4.56**, Cited **14**]
92. **Lee, S. H**. & Van der Werf, J. The role of pedigree information in combined linkage disequilibrium and linkage mapping of quantitative trait loci in a general complex pedigree. *Genetics* **169**, 455-466 (2005). [**Q1**; IF **4.56**, Cited **30**]
93. **Lee, S. H**. & Van der Werf, J. H. J. The efficiency of designs for fine-mapping of quantitative trait loci using combined linkage disequilibrium and linkage *Genetics Selection Evolution* **36,** 145-161 (2004). [**Q1**; IF **2.96**, Cited **42**]

Refereed Conference Papers

94. **Lee, S. H.,** Clark, S. A., & van der Werf, J. H. J. Estimation of genomic prediction accuracy based on population structure. 20th *World Congress Genetics Applied Livestock Production*. (2018)
95. Mulder, H.A., **Lee, S.H.,** Clark, S., Hayes, B. J., & van der Werf, J.H.J. The fate of new mutations: genomic selection exploits new mutation variance to a much smaller degree than traditional selection. 20th *World Congress Genetics Applied Livestock Production*, vol. Genetic Gain - Breeding Strategies 1, p. 415 (2018)
96. G. Gowane, **Lee, S. Hong**, Clark, S., Moghaddar, N., A Hawlader, A. - M., and van der Werf, J. H. J., "Optimising bias and accuracy in genomic prediction of breeding values", *Proceedings of*

the World Congress on Genetics Applied to Livestock Production, vol. Electronic Poster Session - Method and Tools - Prediction 1, p. 117 (2018).

97. Clark, S. A., **Lee, S. H.,** & van der Werf, J. H. J. Using genomic information to estiamte genotype by environment interactions. *Proceedings of the Association for the Advancement of Animal Breeding and Genetics* 21: 137-140 (2015).
98. van der Werf, J. H. J., Clark, S. A., & **Lee, S. H.** Predicting genomic selection accuracy from hetergeneous sources. *Proceedings of the Association for the Advancement of Animal Breeding and Genetics* 21: 161-164 (2015).
99. Marshall, K., **Lee, S. H.** & van der Werf, J. H. J. Information sources in linkage disequilibrium – linkage mapping using half-sib designs. *8th World Congress Genetics Applied Livestock Production*. Communication 21-09 (2006).
100. **Lee, S. H.** & van der Werf, J. H. J. Fine mapping of multiple QTL using a reversible jump MCMC. *8th World Congress Genetics Applied Livestock Production*. Communication 21-08 (2006).
101. **Lee, S. H**., van der Werf, J. H. J. & Tier, B. Combining two Markov chain Monte Carlo approaches for linkage and association studies with a complex pedigree and multi marker loci. *Proceedings of the Association for the Advancement of Animal Breeding and Genetics* 16: 107-110 (2005).

Preparations

Zhou, X., … & Lee, S.H. (2021) ERM (submitted).
Jisu Shin, …..,. Lee SH (2021) GxE for type II diabetes (submitted)
Turong, B., … & Lee, S.H. (2021) GECIM (in preparation).
Muktar Ahmed, …, Lee SH (2021) GxE for cancer (in preparation)
Momin Moksedul, …, Lee SH (2021) Cross-ethnicity genetic correlation (in preparation)
Momin Moksedul, …, Lee SH (2021) Cross-breed analysis using Hanwoo (in preparation)
Nashat, M., Zhou, X., … & Lee, S.H. (2021) Cancer using ERM approach (in preparation).
Pabres., P., … & Lee, S.H. (2021) Genome-transcriptome using GTEx (in preparation).
Nashat, M., … & Lee, S.H. (2021) ssGBLUP (in preparation).

10. Ten career-best research output

Citations are from Google Scholar, Feb 2018

1. **Lee, S. H**.; Van der Werf, J. H. J. An efficient variance component approach implementing an average information REML suitable for combined LD and linkage mapping with a general complex pedigree. *Genetics Selection Evolution* 38: 25-43 (2006). [1st author; **43** citations]

   In this work, I developed an efficient and robust genomic residual maximum likelihood (GREML) method and the direct average information (AI) algorithm that has been used to tackle important problems in complex traits over the last 10 years.

2. **Lee, S.H.**, van der Werf, J., Hayes, B., Goddard, M. & Visscher, P. Predicting unobserved phenotypes for complex traits from whole-genome SNP data. *PLoS Genetics* **4**, e1000231 (2008). [1st author; **171** citations]

A pioneering study that predicts future phenotypes using a cutting-edge method, featured in the Nov 2008 issue of Nature Review Genetics.

3. Yang, J., **Lee, S.H**., Goddard, M. & Visscher, P. GCTA: A tool for genome-wide complex trait analysis. *The American Journal of Human Genetics* **88**, 76-82 (2011). [2nd author; **1833** citations]

   One of most widely used software in complex traits analysis that has implemented the direct AI algorithm developed in #1.

4. **Lee, S.H**., Wray, N., Goddard, M. & Visscher, P. Estimating Missing Heritability for Disease from Genome-wide Association Studies. *The American Journal of Human Genetics* **88**, 294-305 (2011). [1st author; **595** citations]

   A breakthrough theory study that generalised Robertson transformation in the liability threshold model. This method has been implemented in GCTA software developed in #3.

5. **Lee, S.H**., DeCandia, T.R., Ripke, S., Yang, J., PGC-SCZ, ISC, MGS, Sullivan, P.F., Goddard, M.E., Keller, M.C., Visscher, P.M. & Wray, N.R. Estimating the proportion of variation in susceptibility to schizophrenia captured by common SNPs. *Nature Genetics* **44**, 247-250 (2012). [1st author; **438** citations]

   This paper is the first to dissect the genetic architecture of schizophrenia based on genome-wide SNPs using our method developed in #1, #3 and #4.

6. **Lee, S.H**., Yang, J., Goddard, M.E., Visscher, P.M. & Wray, N.R. Estimation of pleiotropy between complex diseases using single-nucleotide polymorphism-derived genomic relationships and restricted maximum likelihood. *Bioinformatics* **28**, 2540-2542 (2012). [1st author; **265** citations]

   A cutting-edge method was developed to estimate genetic corelation between two independent groups. This method has contributed to a breakthorough study to show evidence of shared genetic architecture of complex tratis (#8).

7. Ripke, S. *et al.* Genome-wide association analysis identifies 13 new risk loci for schizophrenia. *Nature Genetics* **45**, 1150-1159 (2013). [12th author; **918** citations]

   A comprehensive study that find novel causal variatns for schizophrenia. We contributed substantially to this study using the statistical models for complex traits developed in #1, #3 and #4.

8. **Lee, S.H**. *et al.* Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. *Nature Genetics* **45**, 984-994 (2013). [1st author; **983** citations] (Funded by ARC grant DE130100614)

   A breakthrough study that dissects shared genetic architecture between complex traits using the statistical methods developed in #1, #3, #4, #6, which has attracted outstanding media attention (Altmetric score 313 ranked 1st out of 66 tracked articles of a similar age in Nature Genetics).

9. Ripke, S. *et al.* Biological insights from 108 schizophrenia-associated genetic loci. *Nature* **511**, 421-427 (2014). [118th author ; **1995** citations]

A landmark study in psychiatric genetics to which we contributed substantailly, e.g. analyses of prediction measures in validation data sets, using the statistical methods developed in #4 and in this study.

10. Maier, R., Moser, G., Chen, G.-B., Ripke, S., Cross disorder Working group of the Psychiatric Genomics Consortium, Coryell, W., Potash, J.B., Scheftner, W.A., Shi, J., Weissman, M.M., Hultman, C.M., Landén, M., Levinson, D.F., Kendler, K.S., Smoller, J.W., Wray, N.R., & **Lee, S.H.** Joint analysis of psychiatric disorders increases accuracy of risk prediction for schizophrenia, bipolar disorder and major depression disorder. *The American Journal of Human Genetics* **96**, 283-294 (2015). [Last author; **74** citations] (Funded by ARC grant DE130100614)

    In this study we developed an efficient multivariate model for estimation and prediction that has been implemented in software, MTG2, a multivariate version of GCTA (#3).