# David G. Ashbrook

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## Education & Qualifications

**2011 – 2015, PhD Systems Biology**, The University of Manchester, UK
Thesis title: '*A systems-genetics analysis of complex phenotypes'*
Supervisor: Dr. Reinmar Hager
External examiner: Dr. Darren Logan, Internal examiner: Dr. Kathryn Hentges
Developed methods to investigate the genetics and epigenetics underlying complex traits. This involved extensive behavioural analysis of early life interactions in mice.

**2007 – 2011, BSc (Hons) Neuroscience (Ind), 2:1**, The University of Leeds, UK
Research project: Protein phosphorylation in Myshkin mice, a $Na^+$,$K^+$ ATPase α3 knockout strain, as a model of bipolar disorder.

## Research Experience

**2025 – Current, Baszucki Foundation Chancellor's Fellow,** University of Edinburgh, Edinburgh, UK
Creating rodent model systems that more accurately reflect human populations, to test relationships between metabolism and behaviour

**2025 – Current, Associate Professor,** University of Tennessee Health Science Center, Memphis, Tennessee, USA
Investigating genome-by-environment interactions in rodent models of disease.

**2022 – 2025, Assistant Professor Tenure Track,** University of Tennessee Health Science Center, Memphis, Tennessee, USA
Investigating genome-by-environment interactions in rodent models of disease.

**2020 – 2022, Assistant Professor,** University of Tennessee Health Science Center, Memphis, Tennessee, USA
Investigating genome-by-environment interactions in rodent models of disease.

**2017 – 2020, Postdoctoral Fellow,** University of Tennessee Health Science Center, Memphis, Tennessee, USA
In Prof. Robert W. Williams' group, working on several bioinformatics and behavioural genetics projects, using mouse, rat, and human data.

**2016 – 2017, Postdoctoral Fellow,** University of Toronto, Canada
In the lab of Prof. Patrick O. McGowan, studying the epigenetics of a mouse model of Gulf War Illness, using next-generation sequencing, e.g. RNA-seq, RRBS, and ChIP-seq.

**2009 – 2010, Industrial placement, Molecular Toxicology**, AstraZeneca, UK
Development and characterization of a primary rat kidney cell *in vitro* model.

## Honours and awards

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|---|---|
| 2525 | Elected to International Mammalian Genome Society (IMGS) Nominations and Elections Committee |
| 2023 | LACU Core Advisory Board member at UTHSC |
| 2023 | Guest editor, eLife Special Issue on Systems Genetics |
| 2023 | Elected Secretary of the International Behavioural and Neural Genetics Society (IBANGS) |
| 2023 | Elected Chair of the IMGS Nominations and Elections Committee |
| 2022 | Elected to IMGS Nominations and Elections Committee |
| 2021 | Invited to speak at a Neuroscience 2021 mini-symposium |
| 2020 | Nominated for IMGS Nominations and Elections Committee |

2020 Elected member of IBANGS Membership Committee
2019 International Mammalian Genome Society (IMGC) Scholarship
2018 International Behavioural and Neural Genetics Society (IBANGS) Travel Award
2018 Parental Brain Conference 2018 Invited Speaker, Toronto, Ontario, Canada
2016 Canadian Epigenetics, Environment and Health Research Consortium Travel Award
2015 Medical Research Council (MRC) and the National Institute for Social Care and Health Research (NISCHR) Travel Award

## Grant support

**Current support**

R01AG070913-01 (Williams/Johnson) 02/01/2021 - 8/31/2026 NIH/NIA
Imaging genetics of brain structure and cognitive aging in murine models of Alzheimer's Disease
Role: Co-investigator
Genetic study of the physiological and behavioural features of Alzheimer's and their genetic modifiers, using the BXD recombinant inbred population and AD-BXD population.

R01ES031656-01 (Jones) 04/01/2021 - 6/30/2026 NIH/NIEHS
Genetics of epigenetic response to high circulating glucocorticoids and organophosphorous compounds
Role: Co-investigator
Genetic and epigenetic study of stress and organophosphorous compounds as a model of Gulf War Illness, using the BXD recombinant inbred population.

R01AG075813-01 (**Ashbrook**) 01/01/2022 - 12/31/2026 NIH/NIA
The interaction effects of genetic variants, age, diet, sex and mitochondrial copy number on Alzheimer's disease, ageing-phenotypes and longevity
Role: Principal Investigator
Gene-by-environment study of the effects of age, sex and diet on mitochondrial DNA copy number, and its effects on longevity and Alzheimer's disease related traits.

R01CA262112-01 (Makowski) 04/01/2022 - 3/31/2027 NIH/NCI
Determining susceptibility loci in triple negative breast cancer using a novel pre-clinical model
Role: Co-investigator
Genetic study of modifiers of triple negative breast cancer phenotypes using a humanized mouse model, the TNBC-BXD strains.

U01CA272541-01 (Makowski) 09/01/2022 - 08/31/2027 NIH/NCI
Determining the contribution of microbial-derived metabolites to protective immunity in obesity-driven cancer risk
Role: Co-investigator
Gene-by-environment study to identify associations and test mechanisms of mediators of cancer risk in various pre-clinical models along an "obesity-microbes-metabolites- protective immunity" axis.

507021 (Nieman) 04/01/2024-04/01/2029 CIHR
Genetic determinants of radiation-induced brain toxicity in a juvenile mouse model
Role: Co-Applicant
Test genetic effects on long term response to whole brain radiation treatment using the BXD family, identifying loci contributing to resilience and susceptibility

313367/Z/24/Z (Lerch) 10/01/2024-04/01/2026 Wellcome Trust
Sensitising brain MRI to cell type and shape
Role: Key Collaborator
We will develop novel molecular MRI methods to be able to identify brain cell type numbers, shapes and connectivity, using BXD strains as our test cases.

**Completed support**

U01DA047638-01A1 (Chen/Williams) 04/01/2019 - 3/31/2024 NIH/NIDA
Systems genetics of menthol and nicotine addiction
Role: Co-Investigator
Genetic studies of addiction using hybrid rat diversity panel (HRDP) genetic reference population. We are using the HRDP to identify sequence variants that control motivational effects of nicotine with a menthol cue.

2011-2015 1088088 via Systems Biology Doctoral Training Centre BB/G530225/1. *A systems genetics analysis of complex traits in mouse and human model systems.* Role: Award Holder (100% effort).

## Supervisory experience

(2 current staff, 1 current postdoctoral scholar, 2 current PhD students, 4 current PhD committee memberships)

*Staff*

**2022 – Present,** Main supervisor, Researcher 1, Richard Cushing (molecular lab)
**2022 – 2025,** Main supervisor, Research Assistant, Malik Hullette (molecular lab)
**2021 – 2022,** Main supervisor, Research Assistant, Melissa Smith (molecular lab)
**2021 – Present,** Main supervisor, Researcher 1, John Killmar (animal lab)
**2020 – 2023**, Main supervisor, Senior Research Specialist, Jesse Ingles (molecular lab)

*Postdoctoral trainees*

**2023 – Present**, Main supervisor, Postdoctoral Scholar, Mikhail Tiumentsev (UTHSC)

*PhD students*

**2024– Present**, Co-supervisor, Ernestine K Amos-Abanyie (UTHSC)
**2024 – 2025**, Main supervisor, rotation project, Keanna Krist Johnson (UTHSC)
**2022 – Present**, Main supervisor, Joy I. Afolabi (UTHSC)
**2022 – Present**, Member of PhD Committee, Chris Rogers (UTHSC)
**2020 – 2024**, Member of PhD Committee, Andrew B. Stiemke (UTHSC)
**2022 – 2025,** supervisor, rotation project, Flavia Villani (UTHSC)
**2022**, Main supervisor, rotation project, Joseph Andrew Jones (UTHSC)
**2022 – 2025**, Member of PhD Committee, Panjun Kim (UTHSC)
**2021 – 2024**, Member of PhD Committee, Pamela M. Watson (UTHSC)
**2020**, Main supervisor, rotation project, Pamela M. Watson (UTHSC)

*MD students*

**2025,** Main supervisor, rotation project, Daphne Nallamala (UTHSC)
**2023 – 2024,** Main supervisor, rotation project, Zach Fontenot (UTHSC)
**2023,** Main supervisor, rotation project, Matthew Canonico (UTHSC)
**2022,** Main supervisor, rotation project, Wyatt A. Kaiser (UTHSC)
**2021,** Main supervisor, rotation project, Catherine L. Diethelm (UTHSC)

*Undergraduate students*

**2023,** Main Supervisor, Summer project, Saige A. Blanton (Christian Brothers University)
**2021,** Main Supervisor, Summer project, Alisha Chunduri

Mentorship of more junior lab members in Manchester, Toronto, and Tennessee, including four undergraduates, two Masters students, and six PhD students.

## Teaching experience

**2022 – Present,** University of Tennessee Health Sciences Center, Instructor, **Genetic Epidemiology**
**2020 – Present,** University of Tennessee Health Sciences Center, Instructor, **Medical Genetics**
**2020 – Present,** University of Tennessee Health Sciences Center, Instructor, **Bioinformatics I**
**2017 – Present,** University of Tennessee Health Sciences Center, Instructor, **Integrative Genetics**

**2016 – 2017,** University of Toronto, Sessional Lecturer, **Epigenetics in Health and Disease**
**2014, 2015**, University of Manchester, Teaching Assistant, Africa field course on behaviour and ecology, lecturing and exam marking
**2013 – 2015**, University of Manchester, Teaching Assistant, Undergraduate practical sessions

## Peer-reviewed publications

(37 peer-reviewed journal articles, Google Scholar > 2100 citations, h-index: 18)
(23 preprint deposits on BioRxiv; 16 peer-reviewed and published)

**Peer-reviewed manuscripts**

37. Rajan, J. R. S., Gill, K., Chow, E., Ashbrook, D. G., Williams, R. W., Zwicker, J. G., et al. (2025). *Investigating motor coordination using BXD recombinant inbred mice to model the genetic underpinnings of developmental coordination disorder.* **Genes, brain, and behavior**, 24, e70014. doi:10.1111/gbb.70014.
36. Garrison, E., Guarracino, A., Heumos, S., Villani, F., Bao, Z., …Ashbrook, D.G.,…Tattini, L. (2024). *Building pangenome graphs.* **Nature Methods** 21, 2008–2012. doi:10.1038/s41592-024-02430-3.
35. Ball, R. L., Bogue, M. A., Liang, H., Srivastava, A., Ashbrook, D. G., Lamoureux, A., et al. (2024). *GenomeMUSter mouse genetic variation service enables multitrait, multipopulation data integration and analysis.* **Genome Research**, 34, 145–159. doi:10.1101/gr.278157.123.
34. Sullivan, K. A., Chapman, C., Lu, L., Ashbrook, D. G., Wang, Y., Alduraibi, F. K., et al. (2023). *Increased development of T-bet+CD11c+ B cells predisposes to lupus in females: Analysis in BXD2 mouse and genetic crosses.* **Clinical immunology,** 257, 109842. doi:10.1016/j.clim.2023.109842.
33. Johnson, G. A., Tian, Y., Ashbrook, D. G., Cofer, G. P., Cook, J. J., Gee, J. C., et al. (2023). *Merged magnetic resonance and light sheet microscopy of the whole mouse brain.* **Proceedings of the National Academy of Sciences of the United States of America**, 120, e2218617120. doi:10.1073/pnas.2218617120.
32. Maksimov, M. O., Wu, C., Ashbrook, D. G., Villani, F., Colonna, V., Mousavi, N., et al. (2023). *A novel quantitative trait locus implicates Msh3 in the propensity for genome-wide short tandem repeat expansions in mice.* **Genome Research**, 33, 689–702. doi:10.1101/gr.277576.122.
31. Meade, R. K., Long, J. E., Jinich, A., Rhee, K. Y., Ashbrook, D. G., Williams, R. W., et al. (2023). *Genome-wide screen identifies host loci that modulate M. tuberculosis fitness in immunodivergent mice.* **Genes|Genomes|Genetics** (Bethesda). doi:10.1093/g3journal/jkad147.
30. Gu, Q., Orgil, B.-O., Bajpai, A. K., Chen, Y., Ashbrook, D. G., Starlard-Davenport, A., et al. (2023). *Expression levels of the Tnni3k gene in the heart are highly associated with cardiac and glucose metabolism-related phenotypes and functional pathways.* **International journal of molecular sciences**. 24, 12759. doi:10.3390/ijms241612759.
29. Gill, K., Rajan Soundara Rajan, J., Chow, E., Ashbrook, D. G., Williams, R. W., Zwicker, J. G., Goldowitz, D. (2023). *Developmental Coordination Disorder: What can we learn from recombinant inbred mice using motor learning tasks and quantitative trait locus analysis.* **Genes, Brain and Behavior**. doi: 10.1111/gbb.12859.
28. Mozhui, K., O'Callaghan, J. P., Ashbrook, D. G., Prins, P., Zhao, W., Lu, L., et al. (2023). *Epigenetic analysis in a murine genetic model of Gulf War illness.* **Frontiers in Toxicology**, 5, 1162749. doi:10.3389/ftox.2023.1162749.
27. Noël, A., Ashbrook, D. G., Xu, F., Cormier, S. A., Lu, L., O'Callaghan, J. P., et al. (2022). *Genomic basis for individual differences in susceptibility to the neurotoxic effects of diesel exhaust.* **International Journal of Molecular Sciences**, 23, 12461. doi:10.3390/ijms232012461.
26. Wang, X., Bajpai, A. K., Gu, Q., Ashbrook, D. G., Starlard-Davenport, A., and Lu, L. (2023). *Weighted gene co-expression network analysis identifies key hub genes and pathways in acute myeloid leukemia.* **Frontiers in Genetics,** 14, 1009462. doi:10.3389/fgene.2023.1009462.
25. Sasani, T. A., Ashbrook, D. G., Beichman, A. C., Lu, L., Palmer, A. A., Williams, R. W., et al.

(2022). *A natural mutator allele shapes mutation spectrum variation in mice.* **Nature**, 2021.03.12.435196. doi:10.1038/s41586-022-04701-5.

24. Chunduri, A., Watson, P. M., and Ashbrook, D. G. (2022). *New insights on gene by environmental effects of drugs of abuse in animal models using GeneNetwork.* **Genes** (Basel). 13, 614. doi:10.3390/genes13040614.
23. Dietrich, P., Alli, S., Mulligan, M. K., Cox, R., Ashbrook, D. G., Williams, R. W., et al. (2022). *Identification of cyclin D1 as a major modulator of 3-nitropropionic acid-induced striatal neurodegeneration.* **Neurobiology of disease,** 162, 105581. doi:10.1016/j.nbd.2021.105581.
22. Roy, S., Sleiman, M. B., Jha, P., Ingels, J.F., Chapman, C.J.,…Ashbrook, D.G.,…Williams, R.W. (2021). *Gene-by-environmental modulation of lifespan and weight gain in the murine BXD family.* **Nature Metabolism**, 3, 1217–1227. doi:10.1038/s42255-021-00449-w.
21. Lauby, S. C., Ashbrook, D. G., Malik, H. R., Chatterjee, D., Pan, P., Fleming, A. S., et al. (2021). *The role of interindividual licking received and dopamine genotype on later-life licking provisioning in female rat offspring.* **Brain and Behavior**, e02069. doi:10.1002/brb3.2069.
20. Ashbrook, D. G., Arends, D., Prins, P., Mulligan, M. K., Roy, S., Williams, E. G., et al. (2021). *A platform for experimental precision medicine: The extended BXD mouse family.* **Cell Systems** doi:10.1016/j.cels.2020.12.002.
19. Xu, F., Gao, J., Bergman, S., Sims, A. C., Ashbrook, D. G., Baric, R. S., et al. (2020). *Genetic dissection of the regulatory mechanisms of Ace2 in the infected mouse lung.* **Frontiers Immunology** doi:10.3389/fimmu.2020.607314.
18. Sandoval-Sierra, J. V., Helbing, A. H. B., Williams, E. G., Ashbrook, D. G., Roy, S., Williams, R. W., et al. (2020). *Body weight and high-fat diet are associated with epigenetic aging in female members of the BXD murine family.* **Aging Cell**, e13207. doi:10.1111/acel.13207.
17. Wang, N., Anderson, R. J., Ashbrook, D. G., Gopalakrishnan, V., Park, Y., Priebe, C. E., et al. (2020). *Variability and heritability of mouse brain structure: Microscopic MRI atlases and connectomes for diverse strains.* **Neuroimage** 222, 117274. doi:10.1016/j.neuroimage.2020.117274.
16. Xu, F., Ashbrook, D. G., Gao, J., Starlard-Davenport, A., Zhao, W., Miller, D. B., et al. (2020). *Genome-wide transcriptome architecture in a mouse model of Gulf War Illness.* **Brain, Behavior, and Immunity** doi:10.1016/j.bbi.2020.06.018.
15. Jones, B. C., Miller, D. B., Lu, L., Zhao, W., Ashbrook, D. G., Xu, F., et al. (2020). *Modeling the genetic basis of individual differences in susceptibility to Gulf War Illness.* **Brain sciences** 10, 143. doi:10.3390/brainsci10030143.
14. Ashbrook, D. G., Cahill, S., and Hager, R. (2019*). A cross-species systems genetics analysis links APBB1IP as a candidate for schizophrenia and prepulse inhibition.* **Frontiers in behavioral neuroscience** 13. doi:10.3389/fnbeh.2019.00266.
13. Potter, H. G., Ashbrook, D. G., and Hager, R. (2018). *Offspring genetic effects on maternal care.* **Frontiers in neuroendocrinology***,* doi:10.1016/j.yfrne.2018.12.004.
12. Herrera, S., de Vega, W. C., Ashbrook, D., Vernon, S. D., and McGowan, P. O. (2018). *Genome-epigenome interactions associated with Myalgic Encephalomyelitis/Chronic Fatigue Syndrome*. **Epigenetics***,* 13, 1174–1190. doi:10.1080/15592294.2018.1549769.
11. Ashbrook, D. G., Roy, S., Clifford, B. G., Riede, T., Scattoni, M. L., Heck, D. H., et al. (2018). *Born to cry: A genetic dissection of infant vocalization.* **Frontiers in behavioral neuroscience**, 12, 250. doi:10.3389/fnbeh.2018.00250.
10. Ashbrook, D. G., Hing, B., Michalovicz, L. T., Kelly, K. A., Miller, J. V, de Vega, W. C., et al. (2018). *Epigenetic impacts of stress priming of the neuroinflammatory response to sarin surrogate in mice: a model of Gulf War illness*. **Journal of neuroinflammation***,* 15, 86. doi:10.1186/s12974-018-1113-9.
9. Ashbrook, D. G., Mulligan, M. K., and Williams, R. W. (2017). *Post-genomic behavioral genetics: From revolution to routine.* **Genes, brain, and behavior***,* e12441. doi:10.1111/gbb.12441.
8. Ashbrook, D.G., Sharmin, N., Hager, R., (2017). *Offspring genes indirectly influence sibling and maternal behavioural strategies over resource share.* **Proceedings of the Royal Society. B, Biological sciences***,* 284, 20171059. doi:10.1098/rspb.2017.1059

7. Franke, B., Stein, J. L., Ripke, S., Anttila, V., Hibar, D. P., van Hulzen, K. J. E.,…Ashbrook, D.G., Hager, R., et al. (2016). *Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept*. **Nature Neuroscience** 19, 420–431. doi:10.1038/nn.4228
6. Ashbrook, D. G., Gini, B., and Hager, R. (2015). *Genetic variation in offspring indirectly influences the quality of maternal behaviour in mice*. **Elife***,* 4. doi:10.7554/eLife.11814.
5. Ashbrook, D. G., Williams, R. W., Lu, L., and Hager, R. (2015). *A cross-species genetic analysis identifies candidate genes for mouse anxiety and human bipolar disorder*. **Frontiers in behavioral neuroscience***,* 9, 171. doi:10.3389/fnbeh.2015.00171.
4. Hibar, D. P., Stein, J. L., Renteria, M. E., Arias-Vasquez, A., Desrivières, S., Jahanshad, N., Toro, R., Wittfeld, K., Abramovic, L., Andersson, M.,…Ashbrook, D.G., Hager, R., et al. (2015). *Common genetic variants influence human subcortical brain structures*. **Nature***,* 520, 224–229. doi:10.1038/nature14101.
3. Ashbrook, D. G., Delprato, A., Grellmann, C., Klein, M., Wetzel, R., Overall, R. W., and Badea, A. (2014). *Transcript co-variance with Nestin in two mouse genetic reference populations identifies Lef1 as a novel candidate regulator of neural precursor cell proliferation in the adult hippocampus*. **Frontiers in neuroscience***,* 8, 418. doi:10.3389/fnins.2014.00418.
2. Ashbrook, D. G., Williams, R. W., Lu, L., Stein, J. L., Hibar, D. P., Nichols, T. E., Medland, S. E., Thompson, P. M., and Hager, R. (2014). *Joint genetic analysis of hippocampal size in mouse and human identifies a novel gene linked to neurodegenerative disease*. **BMC Genomics***,* 15, 850. doi:10.1186/1471-2164-15-850.
1. Ashbrook, D. G., and Hager, R. (2013). *Empirical testing of hypotheses about the evolution of genomic imprinting in mammals*. **Frontiers in neuroanatomy***,* 7, 6. doi:10.3389/fnana.2013.00006.

*In preprint*

11. Arends, D., Ashbrook, D. G., Roy, S., Lu, L., Sloan, Z. A., Centeno, A. G., et al. (2025). *Genetic modulation of lifespan: Dynamic effects, sex differences, and body weight trade-offs.* **bioRxiv**, 2025.04.27.649857. doi:10.1101/2025.04.27.649857.
10. Johnson, G. A., Tian, Y., Hornburg, K., Cook, J. J., Qi, Y., White, L. E., Killmar, J. T., Kaczorowski, C., Ashbrook D. G., Williams R. W. (2025) *Global dissection of the impact of Alzheimer's disease on brain architecture and behavior: High resolution MRH resolves robust regional effects*. **bioRxiv** 2025.01.08.632011 doi:10.1101/2025.01.08.632011
9. Villani, F., Sasani, T., Maksimov, M., Hakan Gunturkun, M., Ma, N., Ren, Y., … Ashbrook, D. G. (2025). *Deep sequencing of a large family of isogenic mice enables complex variants discovery and accurate phenotype mapping*. **bioRxiv**, 2022.04.21.489063. doi:10.1101/2022.04.21.489063.
8. Darnell, S. S., Overall, R. W., Guarracino, A., Colonna, V., Villani, F., Garrison, E., et al. (2024). *Creating a biomedical knowledge base by addressing GPT inaccurate responses and benchmarking context*. **bioRxiv**, 2024.10.16.618663. doi:10.1101/2024.10.16.618663.
7. Jones, B. C., O'Callaghan, J. P., Ashbrook, D. G., Lu, L., Prins, P., Zhao, W., et al. (2024). *Epigenetic study of the long-term effects of Gulf War illness*. **bioRxiv**, 2024.11.29.626040. doi:10.1101/2024.11.29.626040.
6. Simon, S. E., Simmons, B. W., Kim, M., Joseph, S. C., Korba, E.,… Sipe, L. M., Ashbrook, D. G., Makowski, L. (2024) *Determining susceptibility loci in triple negative breast cancer using a novel pre-clinical model*. **bioRxiv** 2024.02.08.579359 doi:10.1101/2024.02.08.579359
5. Gómez-Pascual, A., Glikman, D. M., Ng, H. X., Tomkins, J. E., Lu, L., Xu, Y., Ashbrook, D. G., et al. (2023). *Polyglucosan body density in the aged mouse hippocampus is controlled by a novel modifier locus on chromosome 1*. **bioRxiv**, 2023.11.22.567373. doi:10.1101/2023.11.22.567373
4. Willcox, J. A. L., Telpoukhovskaia, M. A., Hadad, N., Boas, S. M., Dunn, A., Saul, M. C., Ashbrook, D.G. et al. (2023). *RNA Strain-Match: A tool for matching single-nucleus, single-cell, or bulk RNA-sequencing alignment data to its corresponding genotype*. **bioRxiv**, 2023.07.14.548847. doi:10.1101/2023.07.14.548847.
3. Gunturkun, M. H., Villani, F., Colonna, V., Ashbrook, D. G., Williams, R. W., and Chen, H. (2021). *SVJAM: Joint analysis of structural variants using linked read sequencing data.*

**bioRxiv**, 2021.11.02.467006. doi:10.1101/2021.11.02.467006.

2. Watson, P. M., and Ashbrook, D. G. (2020). *GeneNetwork: a continuously updated tool for systems genetics analyses*. **bioRxiv**, 2020.12.23.424047. doi:10.1101/2020.12.23.424047.
1. Lemen, P. M., Hatoum, A. S., Dickson, P. E., Mittleman, G., Agrawal, A., Reiner, B. C., et al. (2022). *Opiate responses are controlled by interactions of Oprm1 and Fgf12 loci in the murine BXD family: Correspondence to human GWAS finding*. **bioRxiv**, 2022.03.11.483993. doi:10.1101/2022.03.11.483993.

**Book Chapters**

1. Ashbrook, D. G. (2023). "*Experimental precision medicine: Mouse models in which to test precision medicine*" in **Reference Module in Biomedical Sciences** (Elsevier). doi:10.1016/B978-0-12-824010-6.00057-5.
    - Invited chapter
2. Ashbrook, D. G., and Lu, L (2021) "*Recombinant inbred mice as models for medicine and biology*" in **Animal Models in Medicine and Biology** (IntechOpen), ed. E Purevjav (London), ISBN 978-1-83968-805-8. doi: 10.5772/intechopen.96173
3. Ashbrook, D. G., and Hager, R. (2017). "*Social interactions and indirect genetic effects on complex juvenile and adult traits*" in ***Methods in Molecular Biology*** (Clifton, N.J.), eds. K. Schughart and R. W. Williams (New York: Springer New York), 499–517. doi:10.1007/978-1-4939-6427-7_24.
    - Invited chapter

## Conferences and selected presentations

34. **38th International Mammalian Genome Society Conference, Glasgow, Scotland, UK**, 6-9 April 2025
    - Talk: 'Genetic modulation of neuroanatomy, mitochondrial function, and behaviour in the AD-BXD mouse model of Alzheimer's Disease'
33. **School of Biomedical Sciences Seminar Series, University of Leeds, Leeds, UK**, 27 March 2025
    - Invited speaker, 'The effects of genetic background on Alzheimer's related traits in a mouse model'
32. **21st annual meeting of the Complex Trait Community in collaboration with the Rat Genomics Community**, **Medical College of Wisconsin, Milwaukee, WI, USA**, 2-5 October 2024
    - Poster, 'Mouse Longevity App – an ongoing project to collect and make available mouse lifespan data'
31. **Integrative Physiology Colloquium, University of Colorado Boulder, Boulder, CO, USA,** 8 April 2024
    - Invited speaker, 'The importance of genetic background for model organism genetics'
30. **The Allied Genetics Conference, Gaylord National Resort & Convention Center, Metro Washington, DC, USA**, 6-10 March 2024
    - PhD student poster, 'Machine learning for quantification of behavior in rodent models of aging and Alzheimer's disease'
    - Postdoctoral trainee poster, 'Mitochondrial phenotypes in BXD models of aging and Alzheimer's disease'
29. **20th Annual Meeting of the Complex Trait Community (CTC) and the Rat Genomics & Models Community, University of Tennessee Health Science Center, Memphis, TN, USA**, 7-12 October 2023
    - Co-host and organizer
    - Session chair, 'Machine learning for rodent behavior'
28. **International Mouse Phenotyping Consortium** (**IMPC) Annual International Conference, The Power of Mouse Genetics: Opportunities for Genomic and Precision Medicine, Keble College, Oxford, UK**, 9-11 July 2023
    - Poster: 'Massive diallel crosses (DAX) as a tool for investigating gene-by-gene-by-

environment interactions, genetic background effects, and experimental precision medicine'

27. **Genes, Brain, and Behavior Meeting 2023, University of Galway, Galway, Ireland**, 22-25 May 2023
    - Poster: 'Imaging genetics of brain structure and connectome in murine models of aging'
    - Program committee member
26. **National Institute on Drug Abuse** (**NIDA) Genetics and Epigenetics Meeting 2023, National Institutes of Health (NIH), Bethesda, USA**, 16-17 May 2023
    - Poster: 'Good wine and old data get better with age: New insights on gene-by-environment effects of drugs of abuse in mice using GeneNetwork.org'
25. **19th Annual Meeting of the Complex Trait Community (CTC) and the Rat Genomics & Models Community, University of Colorado Anschutz Medical Campus, Aurora, USA,** 29-30 September 2022
    - Talk: 'A novel pre-clinical model identifies genetic modifiers of triple negative breast cancer risk and progression'
24. **Genes, Brain, and Behavior Meeting 2022, Memphis, USA**, 23-27 May 2022
    - Symposium: 'Revolutionary genomics: Third-generation sequencing and pangenome approaches to understanding genes and behavior'
    - Local organizing committee member
23. **Center for In Vivo Microscopy (CIVM) Seminar Series, Duke University, Durham, USA**, **virtual,** 4 March 2022
    - Talk: 'The importance of genetic background for model organism genetics, using the AD-BXD Alzheimer's disease model'
    - Invited talk to about our collaboration with Duke, and the background to it
22. **UTHSC Center for Cancer Research Symposium, Memphis, USA**, 3 December 2021
    - Talk: 'Including genetic complexity in models of disease'
    - Invited talk to cancer research community on how and why to include genetics in their rodent models
21. **Neuroscience 2021, Society for Neuroscience meeting 2021, virtual,** 8-11 November 2021
    - Talk: 'GeneNetwork.org: genetic analysis for all neuroscientists'
    - Invited talk at a minisymposium on 'Highlights From the Era of Open Source Online Tools — From Genes to Neurons, Circuits, Behaviors, and Whole Brain Data'
20. **Cardiff School of Biosciences, Cardiff University, virtual,** 11 August 2021
    - Talk: 'Complexity and connectivity: Genes, environment and the brain'
19. **Genes, Brain, and Behavior Meeting 2021, virtual,** 12-15 May 2021
    - Talk: 'Massive Diallel Crosses (DAX) as a tool for gene-by-environment interactions, epistasis, and experimental precision medicine'
18. **International Behavioural & Neural Genetics Society Virtual Trainee Symposium**, 23 September 2020
    - Talk: 'The interaction effects of genetic variants, diet, and mitochondrial copy number on aging and longevity in the BXD family'
17. **Systems Genetics: From Genomes to Complex Traits, EMBL, Heidelberg, Germany,** 29 September – 2 October 2019
    - Talk: 'Sequencing the BXD family, a cohort for experimental systems genetics and precision medicine'
16. **33rd International Mammalian Genome Society Conference, Strasbourg, France,** 25-28 September 2019
    - Talk: 'Sequencing the BXD family, a cohort for experimental systems genetics and precision medicine'
    - Received IMGS Scholarship to attend
15. **Complex Traits Consortium / Rat Genomics 17th Annual Meeting, La Jolla, CA, USA,** 8-11 June 2019
    - Talk: 'Sequencing the BXD family, a cohort for experimental systems genetics and

precision medicine'

14. **21st Annual Genes, Brain & Behavior Meeting, Edinburgh, UK,** 10-14 May, 2019
    - Talk: 'Sequencing the BXD family, a cohort for experimental systems genetics and precision medicine'
13. **Parental Brain Conference 2018, Toronto, Ontario, Canada**, 13-14 July, 2018
    - Talk: 'Indirect genetic effects of, and on, maternal care'
    - Invited speaker
12. **16th Annual Meeting of the Complex Trait Community meeting, Glasgow, UK,** 20-22 June 2018
    - Talk: 'Sequencing the BXD family, a cohort for experimental systems genetics and precision medicine'
11. **20th Annual Genes, Brain & Behavior Meeting, Rochester, MN, USA**, 17-21 May 2018
    - Talk: 'Sequencing the BXD family, a cohort for experimental systems genetics and precision medicine'
    - Awarded IBANGS Young Investigator Travel Award to attend
10. **15th Annual Meeting of The MidSouth Computational Biology and Bioinformatics Society, Starkville, MS, USA**, 29-31 March 2018
    - Talk: 'Sequencing the BXD family, a cohort for experimental systems genetics and precision medicine'
9. **11th Annual Canadian Neuroscience Meeting, Montreal**, **Québec, Canada**, 28-31 May 2017
    - Poster: 'Epigenetic impacts of stress priming of the neuroinflammatory response to sarin surrogate in mice: a model of Gulf War Illness'
8. **The Canadian Epigenetics, Environment and Health Research Consortium Network Annual Meeting, "Epigenomics in Development and Disease", Estérel, Québec, Canada**, 18-21 September 2016
    - Awarded a CEEHRC Travel Award to attend
7. **MRC Centre for Neuropsychiatric Genetics and Genomics 6th Annual Summer School in Brain Disorder Research, Cardiff, UK**, 6th - 9th July 2015
    - Attendance award by MRC and NISCHR
6. **2015 Complex Trait Community 14th Annual Meeting, Portland, OR, USA**, 8th - 11th June 2015
    - Talk: 'Indirect genetic effects influence sibling and maternal behaviour in mice'
5. **From functional genomics to systems biology, EMBO Conference Series, Heidelberg, Germany**, 8th - 11th November 2014
    - Poster: 'Joint genetic analysis of hippocampal size in mouse and human identifies a novel gene linked to neurodegenerative disease'
4. **2014 PhD Conference, Manchester, UK**, 9th May 2014
    - Talk: 'Joint genetic analysis of hippocampal volume in mouse and human identifies novel genes linked to neurodegenerative disease'
    - Prize for Best Talk
3. **INCF Course on Neuroinformatics, Neurogenomics and Brain Disease, Fraueninsel, Germany**, 14th - 20th September 2013
    - Resulted in a paper (Ashbrook et al. 2014)
2. **Systems Biology Graduate Conference 2012, Oxford, UK**, 26th - 27th June 2012
    - Poster: 'Investigating parent-of-origin and imprinting effects in BXD using bioinformatics tools'
1. **The Dynamics of Disease - a Workshop in Medical Systems Biology, Manchester, UK**, 28th Nov - 2nd Dec 2011

## Society Memberships

British Neuroscience Association, Complex Trait Community, Federation of European Neuroscience Societies, International Mammalian Genome Society, International Behavioural and Neural Genetics Society (Society Secretary, Member of Membership Committee)

## Research Summary

My primary research interest is the interplay between the genome and the environment, and integrating levels of biology, from genes, to transcription, epigenetics, and finally complex behaviours and diseases. My previous work has involved extensive use of rodent populations, both generating my own data, and reanalysing the broad phenome already available for these populations.

Work in my lab is making use of the BXD mouse family, and the AD-BXD – a model of familial Alzheimer's disease that takes advantage of genetic diversity. This has particularly focused on age as an environmental effect and gene-by-gene effects on phenotypes relating to normal cognitive ageing and neurodegeneration. We have a project currently underway involving behavioural characterization of ~40 strains of the AD-BXD family along with deep MRI imaging, and a second grant looking at the relationship between genetics, age, sex, diet, mitochondria, ageing and longevity. We have been able to identify independent loci altering behavioral, physiological and anatomical phenotypes in the transgenic littermates, and not in their non-transgenic controls.

In a similar project, we have identified loci modulating different aspects of breast cancer, including age of onset and multiplicity, in a genetic model of breast cancer. This approach has resulted in two funded grants, and a preprint of results from the first of these is in preparation for submission.

During my first postdoctoral fellowship in Toronto, I investigated the transcriptomic and epigenomic effects of corticosterone combined with diisopropyl fluorophosphate, as a mouse model of Gulf War Illness – a neuroinflammatory disease resulting in sickness behaviour. This gave me experience in analyzing the interactions between 'omics datasets and experimental environmental perturbations.

Other aspects of my work include the examination of indirect genetic effects and parent-of-origin effects on early life behaviour and developmental disorders, and the joint-analysis of phenotypes collected across species.