#### DMPUTATIONAL BIOLOGIST

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Computational biologist with experience in integrative population and functional genomics.

## **Education**

PhD in Infection Biology 2018 - 2024

University College Dublin

Dublin, Ireland

• Thesis: Integrative population and functional genomics of trypanotolerance in hybrid African cattle, published in *Heredity* (doi:10.1038/s41437-024-00734-w) and *PLOS Neglected Tropical Diseases* (doi:10.1371/journal.pntd.0012882), with the final experimental chapter available as a preprint on bioRxiv (doi:10.1101/2025.07.30.667693).

### **MSc in Evolutionary Biology**

2015 - 2016

University College Dublin

Dublin, Ireland

• Thesis: A population genomics analysis of the endangered Galway sheep breed, published in *Frontiers in Genetics* (doi: 10.3389/fgene.2019.00927).

### BA (Mod) in Natural Sciences (Zoology)

2011 - 2015

TRINITY COLLEGE DUBLIN

Dublin, Ireland

• Thesis: Mytilus edulis as a bioindicator of water pollution: Potential histopathology biomarkers in Dublin Bay and Newquay, Co. Clare.

# **Publications**.

McHugo, G. P., Ward, J. A., Browne, J. A., O'Gorman, G. M., Meade, K. G., Hill, E. W., Hall, T. J., & MacHugh, D. E. (2025). Functional genomics of trypanotolerant and trypanosusceptible cattle infected with Trypanosoma congolense across multiple time points and tissues. *PLOS Neglected Tropical Diseases*, 19(8), e0012882. doi:10.1371/journal.pntd.0012882.

O'Grady, J. F., McHugo, G. P., Ward, J. A., Hall, T. J., Faherty O'Donnell, S. L., Correia, C. N., Browne, J. A., McDonald, M., Gormley, E., Riggio, V., Prendergast, J. G. D., Clark, E. L., Pausch, H., Meade, K. G., Gormley, I. C., Gordon, S. V., & MacHugh, D. E. (2025). Integrative genomics sheds light on the immunogenetics of tuberculosis in cattle. *Communications Biology*, 8(1), 479. doi:10.3929/ethz-b-000728420.

O'Grady, J. F., McHugo, G. P., Ward, J. A., Hall, T. J., Faherty O'Donnell, S. L., Correia, C. N., Browne, J. A., McDonald, M., Gormley, E., Riggio, V., Prendergast, J. G. D., Clark, E. L., Pausch, H., Meade, K. G., Gormley, I. C., Gordon, S. V., & MacHugh, D. E. (2025). Integrative genomics sheds light on the immunogenetics of tuberculosis in cattle. *Communications Biology*, 8(1), 479. doi:10.1038/s42003-025-07846-x.

McHugo, G. P., Ward, J. A., Ng'ang'a, S. I., Frantz, L. A. F., Salter-Townshend, M., Hill, E. W., O'Gorman, G. M., Meade, K. G., Hall, T. J., & MacHugh, D. E. (2025). Genome-wide local ancestry and the functional consequences of admixture in African and European cattle populations. *Heredity*, 134(1), 49–63. doi:10.1038/s41437-024-00734-w.

Hall, T. J., McHugo, G. P., Mullen, M. P., Ward, J. A., Killick, K. E., Browne, J. A., Gordon, S. V., & MacHugh, D. E. (2024). Integrative and comparative genomic analyses of mammalian macrophage responses to intracellular mycobacterial pathogens. *Tuberculosis*, 147, 102453. doi:10.1016/j.tube.2023.102453.

Kelly, P. A., McHugo, G. P., Scaife, C., Peters, S., Stevenson, M. L., McKay, J. S., MacHugh, D. E., Saez, I. L., & Breathnach, R. (2024). Unveiling the role of endoplasmic reticulum stress pathways in canine demodicosis. *Parasite Immunology*, 46(4), e13033. doi:10.1111/pim.13033.

Ward, J. A., Ng'ang'a, S. I., Randhawa, I. A. S., McHugo, G. P., O'Grady, J. F., Flórez, J. M., Browne, J. A., Pérez O'Brien, A. M., Landaeta-Hernández, A. J., Garcia, J. F., Sonstegard, T. S., Frantz, L. A. F., Salter-Townshend, M., & MacHugh, D. E. (2024). Genomic insights into the population history and adaptive traits of Latin American Criollo cattle. *Royal Society Open Science*, *11*(3), 231388. doi:10.1098/rsos.231388.

Bhat, S. A., Elnaggar, M., Hall, T. J., McHugo, G. P., Reid, C., MacHugh, D. E., & Meade, K. G. (2023). Preferential differential gene expression within the WC1.1+γδT cell compartment in cattle naturally infected with Mycobacterium bovis. *Frontiers in Immunology*, *14*, 1265038. doi:10.3389/fimmu.2023.1265038.

Correia, C. N., McHugo, G. P., Browne, J. A., McLoughlin, K. E., Nalpas, N. C., Magee, D. A., Whelan, A. O., Villarreal-Ramos, B., Vordermeier, H. M., Gormley, E., Gordon, S. V., & MacHugh, D. E. (2022). High-resolution transcriptomics of bovine purified protein derivative-stimulated peripheral blood from cattle infected with Mycobacterium bovis across an experimental time course. *Tuberculosis*, 136, 102235. doi:10.1016/j.tube.2022.102235.

Ward, J. A., McHugo, G. P., Dover, M. J., Hall, T. J., Ng'ang'a, S. I., Sonstegard, T. S., Bradley, D. G., Frantz, L. A. F., Salter-Townshend, M., & MacHugh, D. E. (2022). Genome-wide local ancestry and evidence for mitonuclear coadaptation in African hybrid cattle populations. *iScience*, *25*(7), 104672. doi:10.1016/j.isci.2022.104672.

Hall, T. J., Mullen, M. P., McHugo, G. P., Killick, K. E., Ring, S. C., Berry, D. P., Correia, C. N., Browne, J. A., Gordon, S. V., & MacHugh, D. E. (2021). Integrative genomics of the mammalian alveolar macrophage response to intracellular mycobacteria. *BMC Genomics*, 22, 343. doi:10.1186/s12864-021-07643-w.

McHugo, G. P., Dover, M. J., & MacHugh, D. E. (2019). Unlocking the origins and biology of domestic animals using ancient DNA and paleogenomics. *BMC Biology*, *17*, 98. doi:10.1186/s12915-019-0724-7.

McHugo, G. P., Browett, S., Randhawa, I. A. S., Howard, D. J., Mullen, M. P., Richardson, I. W., Park, S. D. E., Magee, D. A., Scraggs, E., Dover, M. J., Correia, C. N., Hanrahan, J. P., & MacHugh, D. E. (2019). A population genomics analysis of the native Irish Galway sheep breed. *Frontiers in Genetics*, *10*, 927. doi:10.3389/fgene.2019.00927.

Browett, S., McHugo, G., Richardson, I. W., Magee, D. A., Park, S. D. E., Fahey, A. G., Kearney, J. F., Correia, C. N., Randhawa, I. A. S., & MacHugh, D. E. (2018). Genomic characterisation of the indigenous Irish Kerry cattle breed. *Frontiers in Genetics*, *9*, 51. doi:10.3389/fgene.2018.00051.