

Title	Using microbiomes to predict methane emissions in sheep
Project Timeframe	Aug 2017 – Sep 2020
Countries Involved	New Zealand (AgResearch, PGgRc) Australia (University of New South Wales)
Aim	To understand whether the microbial community that is hosted in the forestomach of the sheep in symbiotic relationship could be sampled and described sufficiently to test whether the composition 1) varied between individual sheep and 2) could be used to predict how much methane a sheep might emit during digestion.
Research Highlights	<ul style="list-style-type: none"> • Part 1 of the project focused on the development of a method to sequence ~1% of the microbial genomes sampled from each sheep's gut using a simple stomach tubing method. • Part 2 of the project developed a bioinformatics pipeline to visualise and describe the microbial composition of 4000 samples taken from 1100 animals as lambs and adults grazing grass and eating Lucerne pellets, fully measured for health, production, reproduction, methane emissions and feed intake. • Results showed that the data was affected by feeding regime and grouping of animals but that this could be successfully adjusted for in order to make individual samples comparable. • A combination of host and microbial genomes was very successful in ranking sheep for methane and feed efficiency. • The project has developed laboratory capability to process thousands of samples and a very accomplished postdoctoral scientist. • International collaboration was established with the Department of Agriculture in New South Wales (Australia)
Future Work	<ul style="list-style-type: none"> • The sequencing and prediction methods currently in use can be improved further, while there is much more to learn about the ruminant gut. • The next step is to develop these predictors for further testing in cattle. • These tools will be applied within new GRA projects such as the Grass to Gas and the Cattle fermentation flagship



**Key
Research
Output(s)**

Journal article(s)

Hess, M., Hodgkinson, H., Hess, A., Zetouni, L., Budel, J., Henry, H., Van Stijn, T., Kirk, M., Dodds, K., Brauning, R., McCulloch, A., Hickey, S., Johnson, T., Jonker, A., Morton, N., Hendy, S., Janssen, P., McEwan, J., Rowe, S. (In Prep.) Population analysis of sheep rumen metagenome profiles captured by restriction enzyme reduced representation sequencing reveals individual profiles are influenced by environment, age and genetics of the host.

Hess, M., Johnson, T., Brauning, R., McCulloch, A., Hickey, S., Henry, H., Van Stijn, T., Dodds, K., Hess, A., Jonker, A., Janssen, P., McEwan, J., Rowe, S. (In Prep.) A New Frontier: Combining Host and Rumen Metagenome Profiling for Selection in Sheep: Prediction of Production, Health and Environmentally Important Traits.

Hess, M., Rowe, S., Van Stijn, T., Henry, H., Hickey, S., Brauning, R., McCulloch, A., Hess, A., Kirk, M., Kumar, S., Pinares-Patino, C., Kittelmann, S., Wood, G., Janssen, P., McEwan, J. (2020) A restriction enzyme reduced representation sequencing approach for low-cost, high-throughput metagenome profiling. *Plos One*, 15(4): e0219882

Conference proceedings/presentations

Hess, M., Zetouni, L., Budel, J., Van Stijn, T.C., Henry, H.M., Kirk, M.R., Brauning, R., McCulloch, A.F., Dodds, K., Hess, A.S., Wood, G., Hickey, S.M., Jonker, A., Johnson, T., Oddy, V., Camara, M., Janssen, P.H., McEwan, J.C., Rowe, S.J. Metagenomics for selection of environmentally friendly ruminants. *6th International Conference on Quantitative Genetics*, Brisbane. 2-12 November 2020.

Hess, M., Zetouni, L., Budel, J., Van Stijn, T.C., Henry, H.M., Kirk, M.R., Brauning, R., McCulloch, A.F., Hess, A.S., Wood, G., Hickey, S.M., Jonker, A., Johnson, T., Janssen, P.H., McEwan, J.C., Rowe, S.J. Restriction Enzyme Reduced Representation Sequencing of rumen microbiomes for selection of sheep with reduced methane emissions. *New Zealand Microbial Ecology Consortium*, Auckland. 20-21 February 2020.



Hess, M., Zetouni, L., Budel, J., Van Stijn, T.C., Henry, H.M., Kirk, M.R., Brauning, R., McCulloch, A.F., Hess, A.S., Wood, G., Hickey, S.M., Jonker, A., Johnson, T., Oddy, V., Camara, M., Janssen, P.H., McEwan, J.C., Rowe, S.J. Metagenomic profiling of thousands of samples to aid selection of environmentally friendly ruminants. *Plant and Animal Genomes Conference*, San Diego. 11-15 January 2020.

Hess, M., Zetouni, L., Budel, J., Van Stijn, T.C., Henry, H.M., Brauning, R., McCulloch, A.F., Hickey, S.M., Hess, A.S., Kirk, M.R., Wood, G., Janssen, P.H., McEwan, J.C., Rowe, S.J. Metagenome profiling of thousands of New Zealand sheep rumen samples. *MapNet 2019*, 18-19 November 2019.

Hess, M.K., Johnson, P.L., Knowler, K., Hickey, S.M., Hess, A.S., McEwan, J.C., Rowe, S.J. GWAS for methane yield, residual feed intake and liveweight in New Zealand sheep. *Proceedings of the 23rd Conference of the Association for the Advancement of Animal Breeding and Genetics*, Armidale. 27 October – 1 November 2019.

Rowe, S.J., Hickey, S.M., Jonker, A., Hess, M.K., Janssen, P., Johnson, T., Bryson, B., Knowler, K., Pinares-Patiño, C., Bain, W., Elmes, S., Young, E., Wing, J., Waller, E., Pickering, N., McEwan, J. Selection for divergent methane yield in New Zealand sheep – a ten-year perspective. *Proceedings of the 23rd Conference of the Association for the Advancement of Animal Breeding and Genetics*, Armidale. 27 October – 1 November 2019.

Hess, M., Zetouni, L., Budel, J., Van Stijn, T.C., Henry, H.M., Brauning, R., McCulloch, A.F., Hickey, S.M., Hess, A.S., Kirk, M.R., Kumar, S., Morton, N., Flay, H., Kittelmann, S., Henderson, G., Hendy, S., Wood, G., Attwood, G., Janssen, P.H., McEwan, J.C., Rowe, S.J. High-throughput metagenome sequencing for prediction of quantitative traits. *37th International Society for Animal Genetics Conference*, Lleida. 7-15 July 2019.

Hess, M., Rowe, S., Van Stijn, T., Brauning, R., Hess, A., Kirk, M., Kumar, S., Attwood, G., Janssen, P., McEwan, J. High-throughput sequencing of metagenomes for large-scale prediction of quantitative traits. *Gordon Research Conference in Quantitative Genetics*, Barga. 10-15 February 2019.



- Hess, M., Rowe, S., Van Stijn, T., Brauning, R., Hess, A., Kirk, M., Kumar, S., Attwood, G., Janssen, P., McEwan, J. High-throughput sequencing pipeline for metagenome profiling. *MapNet 2018*, Dunedin. 20-21 November 2018.
- Hess, M., Rowe, S., Van Stijn, T., Brauning, R., Hess, A., Kirk, M., Kumar, S., Attwood, G., Janssen, P., McEwan, J. Restriction Enzyme Reduced Representation Sequencing for high-throughput metagenome profiling. *7th International Symposium on Animal Functional Genomics*, Adelaide. 12-15 November 2018.
- Hess, M., Rowe, S., Van Stijn, T., Brauning, R., Hess, A., Kirk, M., Kumar, S., Attwood, G., Janssen, P., McEwan, J. (2018) High-throughput metagenome sequencing pipeline using either a reference-based or reference-free approach. *Queenstown Molecular Biology Meeting*, Queenstown. 27-29 August 2018.
- Hess, M.K, Rowe, S.J., Van Stijn, T.C., Brauning, R., Hess, A.S., Kirk, M.R., Attwood, G.T., Janssen, P.H., McEwan, J.C. High-throughput rumen microbial profiling using genotyping-by-sequencing. *Proceedings of the 11th World Congress on Genetics Applied to Livestock Production*, Auckland. 11-16 February 2018.
- Hess, M., Rowe, S., Van Stijn, T., Brauning, R., Hess, A., Kirk, M., Attwood, G., Janssen, P., McEwan, J. Using genotyping-by-sequencing for high-throughput rumen microbial profiling. *MapNet 2017*, Palmerston North. 2-3 November 2017.