### SELECTION FOR DIVERGENT METHANE YIELD IN NEW ZEALAND SHEEP – A TEN-YEAR PERSPECTIVE

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#### SUMMARY

A flock of 200 breeding ewes (originally selected from extremes of 1,000 genetically diverse animals from national progeny test flocks) have been selected for divergent methane emissions over a ten-year period. Sheep were ranked for breeding using measures from respiration chambers. Over this period, a number of proxies have been investigated and effects of selection on methane emissions, production traits, feed intake, carcass and milk quality have been evaluated. The lines differ on average by 10-12% for methane emissions. Low methane animals appear to be economically favourable, grow more wool, have smaller rumens, are leaner, have different microbiomes and differ in fatty acid profiles in muscle.

#### INTRODUCTION

New Zealand is heavily reliant on pastoral based agriculture. Grazing livestock, however, are responsible for 80% of methane emissions and around 1/3<sup>rd</sup> of the total NZ greenhouse gas emissions (Steinfeld 2006). Maternal sheep production is reliant on feeding and maintaining ~18.5 million breeding ewes through the winter months and successfully rearing at least one lamb. Sheep breeders can obtain breeding values for their stock (Newman 2009), expressed as \$ gross profit per breeding ewe. The sustainability and therefore profitability of this system, however, is facing a new threat as awareness grows of the magnitude and impact of ruminant methane emissions on the environment. Strategies, such as carbon taxes on livestock production, have been put forward to protect the environment and to maintain global food security. Independent breeding strategies exist for increased production and for reduced methane emissions but, to date there has been no data to show whether these breeding objectives might be synergistic, neutral or antagonistic.

Ten years ago, a divergent flock of sheep was created to evaluate the effects of selection for methane on other breeding objectives. Here we describe the main results and describe the flock divergence for methane and other traits over the ten-year period.

#### MATERIALS AND METHODS

This report summarizes the creation of the methane yield selection lines and their subsequent development. Sheep were selected from central progeny test flocks (Maclean *et al.* 2006). Initial extremes of methane yield were selected using born 2007, then 2009, 2010 and 2011 from 4 research progeny test flocks (A, B, C, D). One thousand ewes in total were screened with the top and bottom 100 ewe lambs retained based on methane yield. Ram lambs were screened from 96 born 2009 animals from flock A. The lines were closed in 2012 and currently all sires used since 2012 were born in flock 'GHG' (the methane yield selection lines). Methane measures were performed in respiration chambers with 48-hour measures repeated after 10-14 days. These are described fully in Pinares-Patino *et al.* (2013). At least 96 male and female lambs were measured annually to select the next generation.

#### **RESULTS AND DISCUSSION**

Figure 1 shows changes in breeding value for methane yield over time. The GHG selection lines have diverged every year and do not overlap. Table 1 shows that the average methane yield measured in multiple flocks is 16 g  $CH_4$ /kg dry matter intake (DMI). Currently the average of the GHG selection lines differ by approximately 12%.

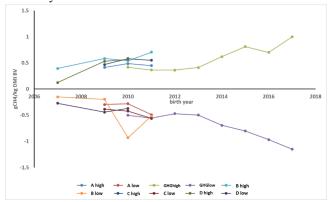


Figure 1. Graph of estimated methane yield research BVs of foundation line ewes by flock (A, B, C, D) and birth year (circles) and GHG selection line progeny

		Total			direct	maternal	Repeatability (s.e.)	
Trait	Mean	s.d.	variance	σ	h <sup>2</sup> (s.e.)	h <sup>2</sup> (s.e.)	2 Day	14 Day
BW, kg	45.9	8.00	23.09	4.80	0.35 (0.05)	0.07 (0.03)		0.89 (0.004)
CH <sub>4</sub> , g/d	24	8.28	7.91	2.81	0.23 (0.04	0.05 (0.02)	0.92 (0.003)	0.65 (0.01)
CO <sub>2</sub> , g/d	1066	99.5	8926.7	94.5	0.34 (0.05)	0.03 (0.02)	0.94 (0.002)	0.76 (0.01)
CH <sub>4</sub> +CO <sub>2</sub> , mol/d	25.64	3.7	5.47	2.34	0.33 (0.05)	0.03 (0.02)	0.94 (0.002)	0.76 (0.01)
CH <sub>4</sub> /(CH <sub>4</sub> +CO <sub>2</sub> )	0.059	0.006	0.00002	0.005	0.17 (0.03)	0.03 (0.02)	0.91 (0.003)	0.43 (0.02)
CH <sub>4</sub> yield, g/kg DMI	16	1.42	1.92	1.39	0.13 (0.02)	0.02 (0.02)	0.85 (0.005)	0.38 (0.02)
DMI, kg	1.573	0.255	0.019	0.140	0.39 (0.05)	0.05 (0.03)	0.97 (0.001)	0.83 (0.01)

Table 1. Genetic and fixed effect estimates from respiration chamber (RC) measurements in sheep <15 mo

Table 2 gives trends for breeding values for standard production traits in the lines over time. Although genetic correlations between methane yield and maternal and production traits have been shown to be generally neutral (Rowe *et al.* 2019 in press), in general, predicted breeding values are favourable in the low methane selection line. The general production index in 2018 was \$13.20 gross margin greater per ewe without including any financial value associated with reduced methane. These differences were driven by greater fleece weights, increased growth, lean yield and greater parasite resistance. Given the narrow genetic base and limited numbers in the population (each year 5 rams are used in each line of 100 ewes), founder effects cannot be disregarded.

## Efficiency and Product Quality

Estimated	2012		2014		2016		2018		2014 - 18	2014 -18
Breeding Value \$	high	Low	high	low	high	low	high	low	$\Delta$ (l-h)	~pval diff.
Weaning weight	1.56	2.21	1.80	2.76	1.84	2.46	2.17	2.72	0.53	0.008
Weaning weight maternal	0.96	1.11	0.78	1.54	0.65	1.62	0.58	1.71	0.91	0.000001
Liveweight 8 months	3.16	3.95	3.44	4.67	3.72	4.70	4.48	5.31	0.60	0.10
Carcass weight	1.09	1.28	1.13	1.62	1.17	1.54	1.43	1.66	0.23	0.04
Adult ewe weight	2.61	1.65	3.34	1.72	3.72	0.90	3.85	1.76	-2.31	0.0001
Lamb fleece weight	0.054	0.057	0.028	0.066	0.036	0.077	0.028	0.082	0.05	0.00002
Fleece weight 12 months	0.36	0.40	0.20	0.47	0.25	0.53	0.20	0.56	0.30	0.00001
Ewe fleece weight	0.30	0.34	0.17	0.41	0.21	0.45	0.16	0.49	0.27	0.000004
Survival	0.023	0.020	0.021	0.030	0.019	0.034	0.019	0.039	0.01	0.003
Survival maternal	0.005	-0.005	-0.001	0.000	-0.008	-0.003	0.003	-0.004	-0.002	0.31
Number lambs born	0.20	0.17	0.20	0.17	0.22	0.23	0.22	0.20	-0.040	0.06
Adult faecal egg count %	-14	-28	-8	-36	-15	-32	-9	-32	-25	0.00003
Summer Faecal egg count %	5	-3	9	-8	4	-1	7	2	-12	0.001
Autumn Faecal egg count %	5	-8	7	-17	0	-11	6	-11	-20	0.00001
Shoulder lean yield	-0.01	0.12	0.02	0.16	0.01	0.18	0.04	0.19	0.14	0.00001
Hindquarter lean yield	-0.04	0.14	0.01	0.18	0.03	0.22	0.05	0.24	0.17	0.00007
Lean leg yield	-0.03	0.05	0.00	0.05	0.01	0.07	0.02	0.08	0.05	0.0005
Fat yield	0.17	-0.19	0.06	-0.16	0.05	-0.16	0.05	-0.18	-0.22	0.000001
Lamb dag score	-0.01	0.14	-0.02	-0.08	-0.09	0.16	-0.14	0.11	0.17	0.02
Adult dag score	-0.04	0.19	-0.19	0.03	-0.27	0.24	-0.23	0.25	0.41	0.0003
*Dual purpose Index **Methane	1413	1960	1239	2615	1221	2804	1491	2811	1239	0.0001
Yield research BV	0.38	-0.45	0.63	-0.78	0.64	-0.75	0.92	-1.09	-1.71	0.000001

Table 2. Mean breeding values by year for GHG flock low and high selection line progeny surviving to at least 4 months of age

\*Dual purpose index is a weighted combination of al traits except methane, \*\*Research methane BV selecting for low methane yield (g  $CH_4$ /kg DMI).

Further investigations into physiological differences between the lines, however, have shown that animals with lowered methane emissions have fundamental physiological differences from their high emitting counterparts. These include 20% smaller rumens (Goopy *et al.* 2013, Bain *et al.* 2014), different microbial fermentation profiles (Kittelmann *et al.*, 2014) and a higher ratio of propionate to butyrate supplied to the animal as an energy source (Jonker *et al.* 2017, Pinares-Patino *et al.* 2011). There is also preliminary evidence that these changes are also associated with a leaner animal (Elmes *et al.* 2014). Furthermore, preliminary analyses on fatty acid profiles in meat suggest differences in intra-muscular fat, feed intake, feeding behaviour and feed efficiency (T. Johnson, personal communication).

#### CONCLUSIONS

Methane yield has been shown to be heritable and therefore under host control. Breeding for lowered methane emissions has been successfully shown to be a permanent and cumulative strategy for the mitigation of methane in sheep. This strategy, however, has resulted in physiological changes affecting the rumen, feeding behaviour, outputs from the rumen and resulting body composition. These changes appear to be economically favourable, however given the limited size of the flock involved these results require validation on a much larger scale. Including methane as part of the national breeding objectives would enable the selection of animals that are low emitters whilst efficient for production. This indicates that breeding is a credible strategy for the mitigation of greenhouse gases from livestock. This is particularly pertinent when considering the targets set by the Paris agreement, one of the first of which, is to reduce global greenhouse gases by 30% by 2030.

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#### REFERENCES

- Bain W.E., Bezuidenhout L., Jopson N.B., Pinares-Patiño C. and McEwan J.C. (2014) Proc. 10th Wld Congr. Genet. Appl. Livest. Prod.
- Elmes S.N., Bain W.E., Greer G.J., Hickey S.M., Young E.A., Pickering N.K., Knowler K.J., Pinares-Patiño C.S. and McEwan J.C. (2014) Proc. NZ Soc. Anim. Prod.

Kittelmann S., Pinares-Patiño C.S., Seedorf H., et al. (2014) PLoS One 9, e103171.

- McEwan J.C., Morris C.A., Fennessy P.F., Greer G.J., Bain W.E. and Hickey.S.M. (2001) Anim. Sci. 73: 241
- McLean N.J., Jopson N.B., Campbell A.W., Knowler K., Behrent M., Cruickshank G., Logan C.M., Muir P.D., Wilson T. and McEwan J.C.(2016) Proc. NZ Soc.Anim. Prod. 66: 368.

Newman S.A.N., McEwan J.C. and Young M.J. (2009) *Assoc, Advmt. Anim, Breed. Genet.* **18**: 624. Pinares-Patiño C.S., Hickey S.M., Young E.A., Dodds K.G., MacLean S., Molano G., Sandoval

E., Kjestrup H., Harland R., Hunt C., Pickering N.K., and McEwan J.C. (2013) Animal. 2: 316.