Genome wide association study of methane emissions in Australian Angus

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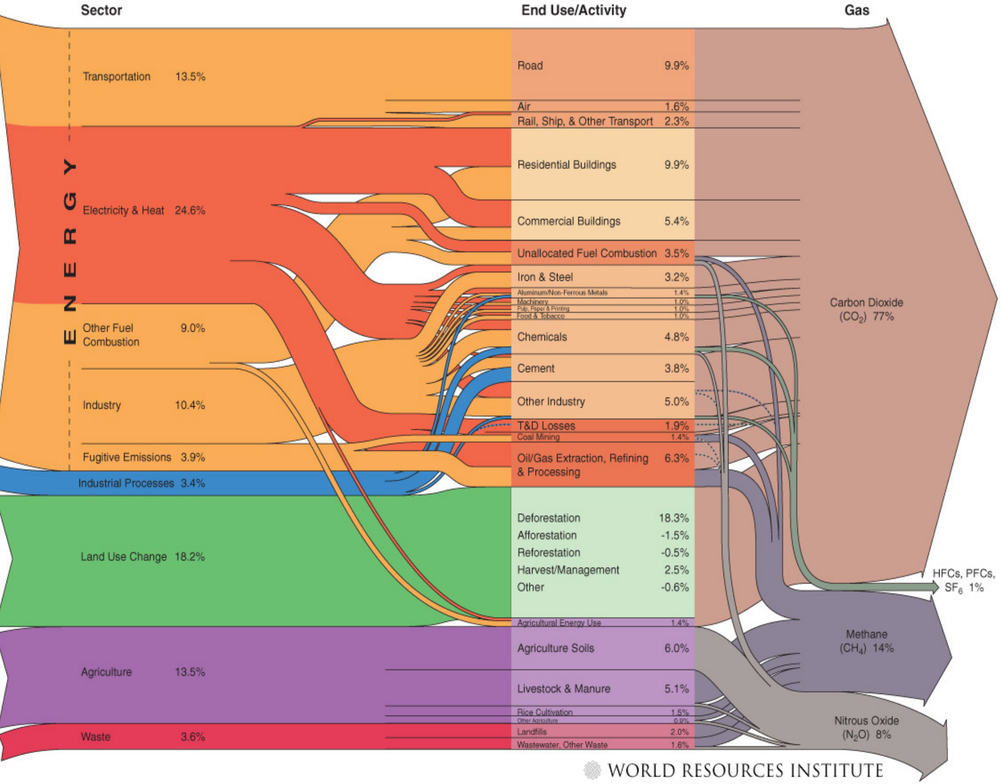
Why is methane (CH_4)important?

World GHG Emissions Flow Chart



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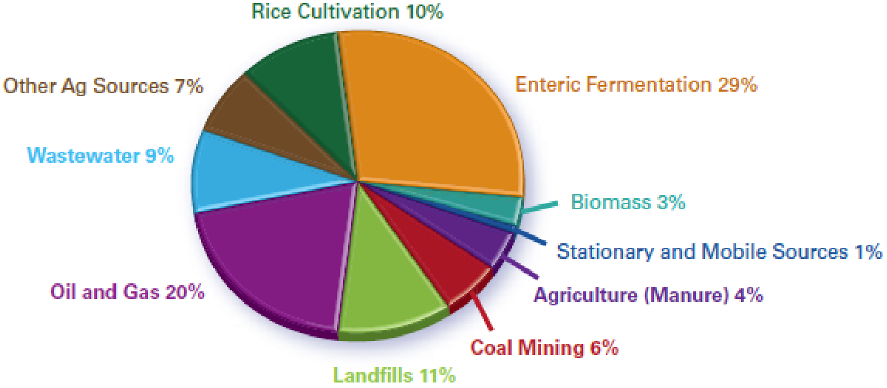
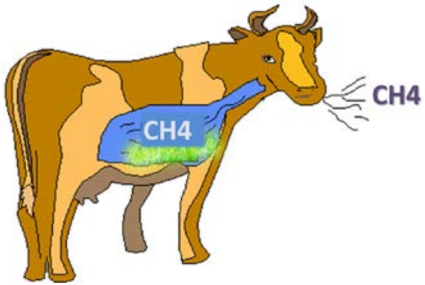
Estimated Global Anthropogenic Methane Emissions by Source, 2010



Unless otherwise noted, all data are from U.S. EPA's *Global Anthropogenic Emissions of Non-CO_2 Greenhouse Gases: 1990–2020* (EPA Report 430-R-06-003), www.epa.gov/climatechange/economics/international.html.

Strategy

Select for animals that emit less CH_4



What is needed?

- Identify the methane phenotype
- Accurate genetic parameters
  - Large amount of records
- Know the genetic structure of CH_4
  - Genotypes
  - GWAS studies

Objectives

- GWAS to identify SNP associated with CH_4 traits in Angus
- Evaluate two residual CH_4 traits

Description of the population

- 1020 Angus animals (both sexes)
- Growing animals (1-2 years old)
- 2 cohorts (herd and sex)
- Respiration chamber
- 800K Illumina Bovine HD genotypes

Methane traits and related traits

- Methane Production (MP)
- Dry matter intake and weight (DMI and WT)
- Residual methane traits:
  - RGM and RPM

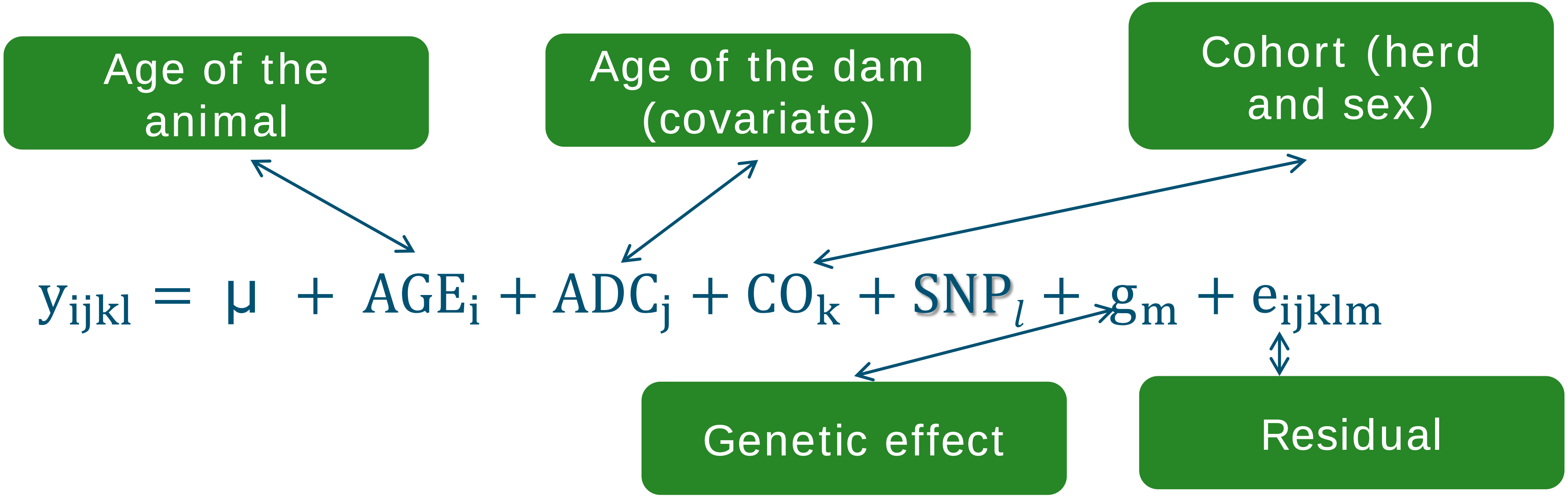
Calculating Residual Methane

- $\mathrm{RPM} = \mathrm{MP} - [(\beta_p \text{ x } \mathrm{DMI}) + (\beta_p \text{ x } \mathrm{WT})$

- $\mathrm{RGM} = \mathrm{MP} - [(\beta_g \text{ x } \mathrm{DMI}) + (\beta_g \text{ x } \mathrm{WT})$

Kennedy et al. 1993. Genetic and Statistical Properties of Residual Feed Intake. *J ANIM SCI* 1993, 71:3239-3250.

Model



Age of the animal

Age of the dam (covariate)

Cohort (herd and sex)

$$\mathrm{y}_{\mathrm{ijkl}} = \mu + \mathrm{AGE}_{\mathrm{i}} + \mathrm{ADC}_{\mathrm{j}} + \mathrm{CO}_{\mathrm{k}} + \mathrm{SNP}_{l} + \mathrm{g}_{\mathrm{m}} + \mathrm{e}_{\mathrm{ijklm}}$$

Genetic effect

Residual

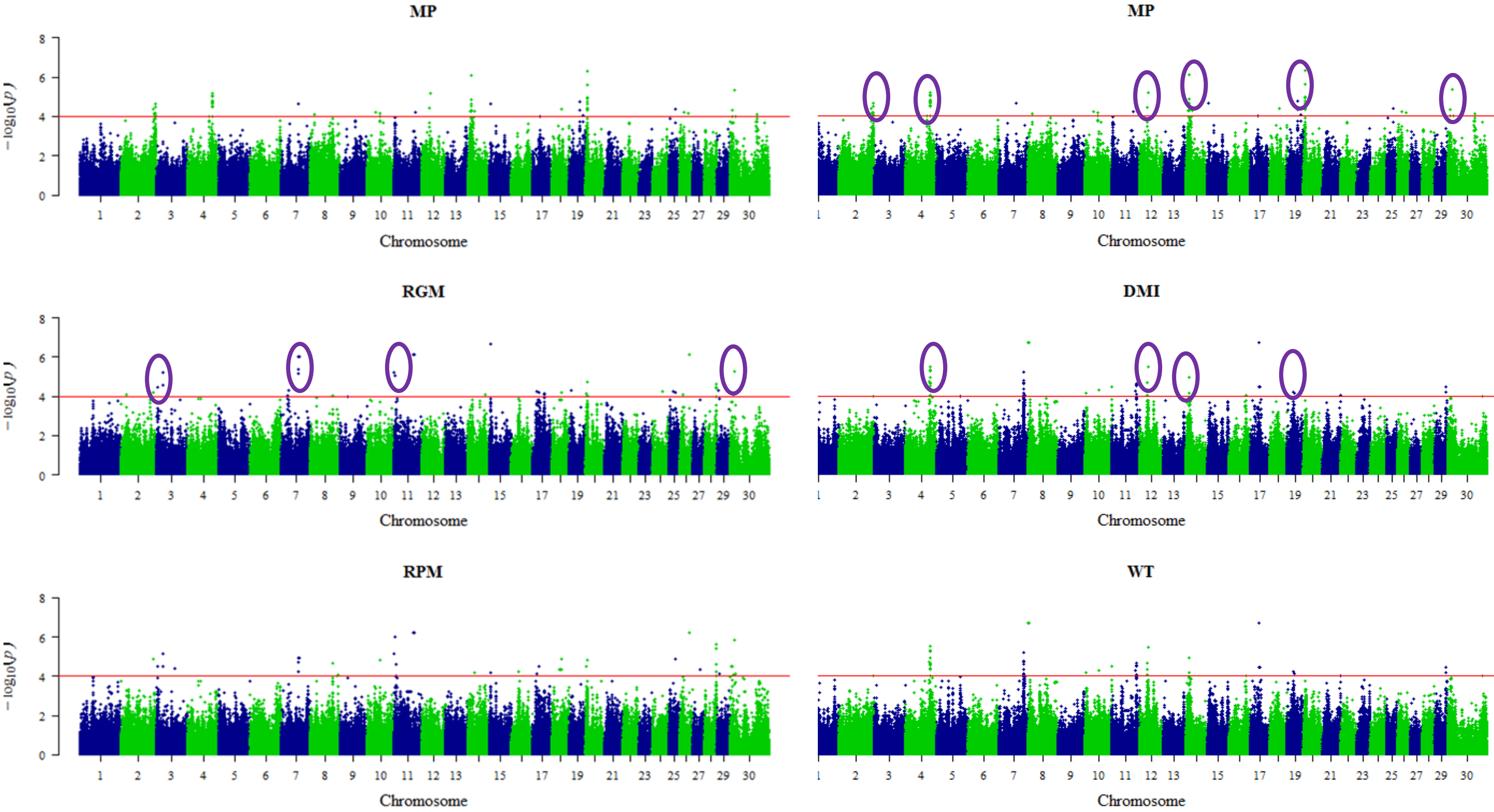
Descriptive statistics

Trait	Unit	Mean	SD	Minimum	Maximum
MP	g/d	132.6	25.5	78.9	250.9
RPM	kg/d	4.9	15.9	-62.4	61.4
RGM	kg/d	-30.3	19.3	-113.3	21.0
DMI	kg/d	6.1	1.3	3.5	9.4
WT	kg	357.7	89.5	156.0	357.7

Genetic parameters

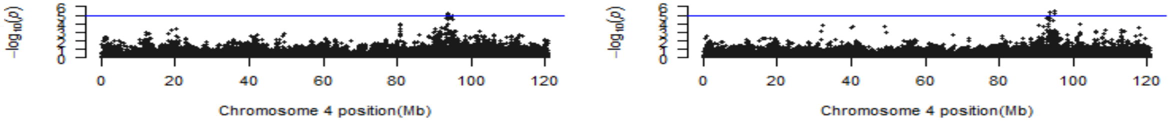
Trait	MP	RPM	RGM	DMI	WT
MP	**0.30 (0.06)**	0.65 (0.11)	0.55 (0.14)	0.83 (0.05)	0.80 (0.06)
RPM	0.71 (0.02)	**0.19 (0.05)**	0.98 (0.02)	0.04 (0.17)	-0.01 (0.17)
RGM	0.62 (0.02)	0.94 (0.00)	**0.15 (0.05)**	0.00 (0.18)	0.00 (0.18)
DMI	0.70 (0.02)	0.00 (0.04)	-0.10 (0.03)	**0.39 (0.06)**	0.98 (0.01)
WT	0.67 (0.02)	0.00 (0.04)	0.03 (0.03)	0.93 (0.01)	**0.41 (0.06)**

- **Heritabilities**, genetic correlations, phenotypic correlations


MP
MP
RGM
DMI
RPM
WT
$-\log_{10}(p)$
0
2
4
6
8
Chromosome
1
2
3
4
5
6
7
8
9
10
11
12
13
15
17
19
21
23
25
27
29
30

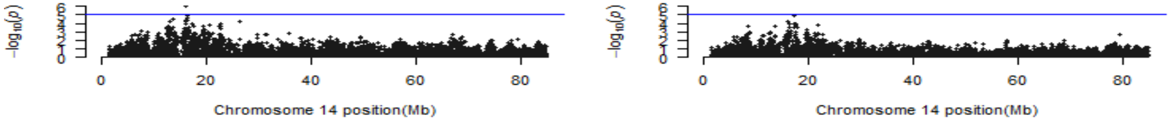
Manhattan plots for MP and DMI

Chromosome 4

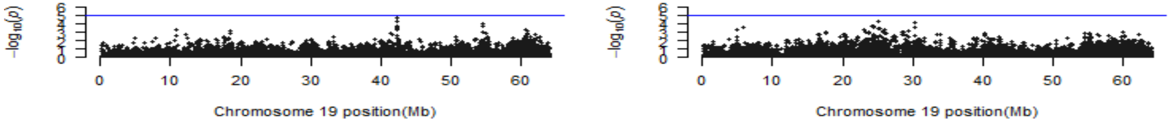


Chromosome 12

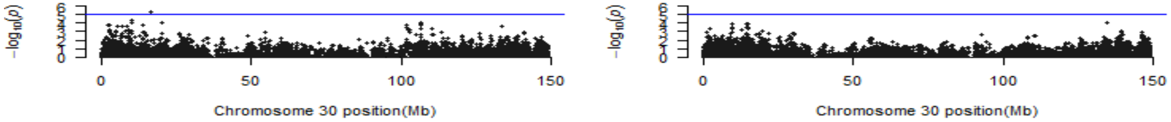
Chromosome 14



Chromosome 19



Chromosome 30



SNPs in common between traits

Trait	MP **(3,304)**	RGM **(3,078)**	RPM **(3,120)**	DMI **(3,364)**	WT **(3,284)**
MP **(803)**		390	591	633	627
RGM **(652)**	93		1,731	104	29
RPM **(647)**	141	369		234	27
DMI **(851)**	101	7	22		3,157
WT **(844)**	104	1	1	830	

* **()** # significant SNP per trait, SNP in common at P<0.005 and SNP in common at P<0.001

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Conclusions

- MP is dependent on DMI and WT
- Chromosomes 2, 4, 12, 14, 20 and 30 had significant SNP for MeP
- RPM and RGM are different traits than MeP

Thank you for your attention

Methane is an **heritable** trait with
significant **SNP** in several **chromosomes**

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Manzanilla-Pech, et al. 2016. Genome wide association study of methane emissions in Angus beef cattle with validation in dairy cattle. doi: 10.2527/jas.2016-0431

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