GENETIC AND GENOMIC BACKGROUND OF PREDICTED METHANE PRODUCTION BASED ON MILK FATTY ACIDS

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Introduction

- Emission of enteric methane by dairy cattle needs to be mitigated.
- Breeding for lower methane production has a long term and cumulative impact.
- Breeding requires data on many animals, which is labour intensive.
- An indicator to predict methane could be a useful alternative.

Aim

Determine the genetic background of predicted methane production and identify genomic regions associated with this trait.

Material and methods

- 1902 Dutch Holstein Friesian cows with information on milk fat composition and on 50,000 SNP.
- Indicator for methane production is developed by Dijkstra et al. (2011; Anim. Feed Sci. and Technol. 166-167:590-595).

$$\text{Methane (in g/kg DMI)} = 24.60 + 8.74 * \text{C17:0anteiso} - 1.97 * \text{C18:1trans10+11} - 9.09 * \text{C18:1cis11} + 5.07 * \text{C18:1cis13}.$$

Table 1: Descriptive statistics and genetic parameters of predicted methane production.

	Predicted methane production
Mean	23.62 (g / kg DMI)
CV	4 %
Heritability	0.12
Herd effect	0.55

Results

- Predicted methane production has low (genetic) variation, but is heritable (Table 1).
- No SNP were significantly associated (false discovery rate < 0.10) with predicted methane production (Figure 1).

Conclusion

- Predicted methane production is heritable.
- No regions of the bovine genome significantly associated with predicted methane production could be identified.

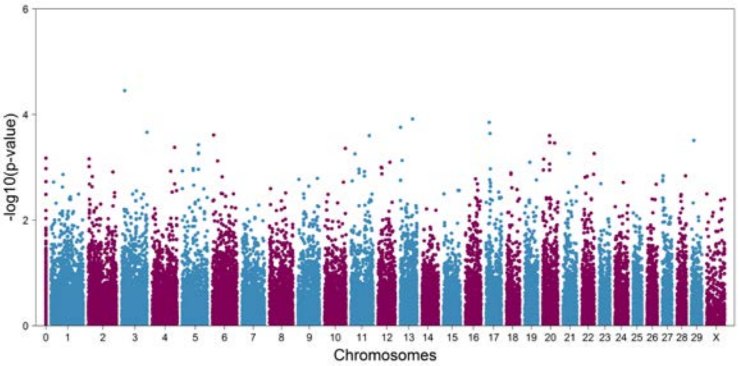

Figure 1: Significance of genome wide association study of predicted methane production.

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