



## Breeding for improved feed efficiency and reduced enteric methane of dairy cattle

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With the successful incorporation of genomic information into breeding schemes the reliance on very large populations of phenotyped animals is relaxed. This has opened up opportunities to breed for novel traits, like feed efficiency and enteric methane emissions of dairy cattle, even though a reference population of several thousand animals is still required to estimate the contribution of each genomic region to expression of the phenotype under investigation.

In the Netherlands a breeding value for dry matter intake (DMI) is published since April 2016. A breeding value for feed intake in isolation has its limitations. All it says is something about the amount of feed consumed by a cow, irrespective of what that feed is actually used for. Therefore, a breeding value for feed efficiency is published since December 2017. This breeding value for feed efficiency is defined as 'saved feed costs for maintenance' in order to save on feed not used for milk production, but on maintenance and **activity**. These breeding values are estimated with a reference population of 5600 dairy cows, of which 2300 are genotyped. The breeding values are based on a combination of direct feed intake records, predictor traits (e.g., milk yield and live weight) and genomic predictions. Current reliabilities of the breeding values for sires are ~60%. The current aims are:

1. to improve the accuracy of genomic prediction, and
2. to record feed intake on more daughters, so that the predictor traits become less important.

By combining data of multiple countries we demonstrated that using dairy cattle DMI phenotypes and genotypes from multiple populations increased the accuracy of the genomic prediction, but to enlarge this joint dataset further, it is needed to extend it beyond research collaborations. A business model and clear agreements are required for this. The business model is under discussion with the ICAR Feed&Gas Working Group, amongst others, and encompass aspects of amount of data to be shared, and efforts in collecting new feed intake records.

In order to be able to estimate breeding values for enteric methane emissions of dairy cattle in the near future, we are currently recording individual methane emissions on 15 commercial farms in the Netherlands, of which all cows are genotyped. Next steps are:

1. to compare methane emissions of these different farms and identify factors causing these differences, and
2. to estimate genetic parameters for enteric methane; heritability and genetic correlations with production, health, fertility and longevity.

With the experiences in METHAGENE we will then also be able to combine this database with other international databases in order to improve the power of the analyses and increase the accuracy of the genomic predictions. Most likely the first breeding value will also be based on a combination of direct records, predictor traits and genomic predictions.