

## **International collaborations for breeding for novel traits**

Yvette de Haas

With the successful incorporation of genomic information into breeding schemes the reliance on very large populations of phenotyped animals is relaxed. However, 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. For novel traits, like feed efficiency and enteric methane emissions of dairy cattle, a reference population of this size cannot be easily established within a country, but requires international collaboration. METHAGENE and the Global Dry Matter Initiative (gDMI) are two examples of such intensive and successful collaborations. METHAGENE showed that even when enteric methane emissions of individual animals was recorded with different sensors and with different protocols, there are ways to combine the data for joint analyses, so that partners can take advantage of each other. METHAGENE not only looked at direct records of enteric methane, but also at proxies for methane related to (1) ingestion, (2) rumen, (3) milk composition, (4) hindgut, and (5) the animal itself. No single proxy was found to accurately predict enteric methane emissions, whilst combinations of two or more proxies are likely to be a better solution. Combining proxies can increase the accuracy of predictions, mainly because different proxies describe independent sources of variation in enteric methane emissions and one proxy can correct for shortcomings in the other(s). In gDMI we demonstrated that using dairy cattle dry matter intake (DMI) phenotypes and genotypes from multiple populations increase the accuracy of genomic breeding values (gEBVs) for this important trait, provided a multi-trait approach is used. Data from research herds in Europe, North America and Australasia were combined to estimate the accuracy of genomic prediction for DMI using multi-trait models. The mean accuracy of prediction was 0.44, ranging from 0.37 (Denmark) to 0.54 (the Netherlands). All in all, for novel traits, there is benefit of collaboration, as phenotypic information from other countries can be used to augment the accuracy of genomic evaluations of individual countries.