Genomic selection for feed efficiency in dairy cattle: a complex objective

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Feed efficiency and energy balance complex are attractive traits to genetically improve using genomic selection. This is because the feed intake data required to calculate these traits is expensive and difficult to measure, so can only be recorded on a sample of the population, usually in research conditions. Thus animals with phenotypes and genotypes could become a reference population to generate the equations required for genomic prediction. Feed efficiency can be defined in a variety of ways including gross efficiency, which is the ratio of product (such as yield) per unit of feed eaten and metabolic efficiency or residual feed intake (RFI). RFI is the feed an animal consumes adjusted for the predicted energy requirements for maintenance, production and body condition score change. To be able to select for RFI we need to be able to identify cows that are truly efficient, rather than those that appear to cheat by mobilising body reserves. A relevant question is whether it is possible to make this distinction. One approach is to consider RFI in growing heifers, provided this correlates with lactating RFI. Using data on 2,000 heifers from Australia and New Zealand, accuracies of genomic prediction of around 0.4 are achievable. We have also shown that accuracies can be increased by including phenotypes from other countries. Using data from Australia, the Netherlands and the UK an improvement of up to 5.5% in accuracy of genomic prediction was observed. However, the number of high quality phenotypes still limits achieving acceptable accuracies for bull proofs. To address this, a major international collaboration to assemble dry matter intake data on more than 5,000 cows with high quality phenotypes and genotypes has started.