

## Session 50

## Theatre 9

### Dissecting purebred-crossbred interaction for feed intake in pigs: feed ingredients

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In pig breeding traditionally selection takes place in purebreds (PB) on nucleus level while on the commercial level crossbred animals (CB) are used. It has been shown that the realized genetic trend in PB on nucleus level is not fully expressed in CB, especially for feed efficiency traits like daily feed intake (DFI) and average daily gain (ADG). Both a genetic correlation lower than one and a reduced additive variance in CB are responsible. One of the possible causes might be a genotype by environment interaction or more specific a genotype by feed interaction. To test this hypothesis a trial was set up where littermates were split and fed either a corn/soy diet (CS) as is typically fed to grower-finishers in the Americas or a wheat/barley/by-product diet (WB) as is common in Western Europe. Animals fed a WB-diet started off a little slower but consumed around 300 g feed more per day during the finishing phase than animals fed a CS-diet. Because of different energy densities of the diets, the energy intake over the entire grower-finisher phase didn't differ between diets. The results suggest that DFI during the starter phase is limited by volume and DFI during the finishing phase is determined by energy demand and perhaps to a lesser extent by the nutritional history of an animal. Preliminary results show that the genetic correlation ( $r_g$ ) for ADG is 1.0 between both diets. For DFI the  $r_g$  is lower (0.89), although not significantly different from one. Regardless of the diets used, weekly averages of feed intake show genetic correlations differing from 1.0 among each other. Especially DFI during the first month after penning seems a somewhat different trait compared to DFI during the remainder of the growing-finishing period. The different distribution of feed intake over the growing-finishing phase might have caused the somewhat lower  $r_g$  for DFI. However, the additive variance for ADG and DFI for animals fed a WB-diet was decreased by around 30% compared to CS-fed animals. Giving rise to different expected genetic trends depending on the selection and production environment.

## Session 50

## Theatre 10

### Partitioning genetic variance of metabolizable energy efficiency in dairy cows

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Residual energy intake (REI) in dairy cows describes the overall efficiency of an animal in using metabolizable energy. Better understanding of the relationship between the overall efficiency and the different energy pathways is desirable for developing genetic evaluations. In this study our aim was to assess the partitioning of genetic variance of adjusted metabolizable energy (ME) intake, we call it metabolizable energy efficiency (MEE), by four energy pathways: ME use for maintenance, milk production, growth, and ME utilization from tissue. A random regression model was applied, which described the pathways by fixed partial regression coefficients on metabolizable body weight, energy corrected milk, body weight gain and body weight loss, and by two likewise sets of random partial regression coefficients, one set for each, permanent environment and additive genetic effect (pMEE model). Obtained results were compared with estimates from repeatability models for MEE and REI. The conceptual difference between latter two models is that for MEE the cows' energy requirements were fitted directly by the model. All models were tested on data collected from 1998 to 2014 at Luke's experimental farms in Jokioinen. The data included 12 350 weekly MEI and REI records from 495 primiparous Nordic Red dairy cows from lactation week 2 to 40. We found that pMEE fitted the data best and resulted in lowest residual variance, but heritability estimates were higher for MEE (0.26) and REI (0.33). In contrast, overall heritability for MEE, derived from the pMEE model estimates for a cow with average energy requirements, was 0.19. Derived heritability for partial MEE was 0.05, 0.06, and zero for maintenance, milk production, and for the intercept and remaining energy pathways. Genetic correlations between the five regression coefficients varied between -0.02 and 0.03 except for a fairly high negative correlation (-0.61) between the maintenance and milk production pathways.