

## Session 55

## Theatre 1

### **Genetic control of environmental variation: Different structures of residual variance in DHGLM model**

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Models of genetic control of environmental variation have been broadly studied with different analysis methods which were applied to different structures of the residual variance. Modeling the environmental variability with fixed, permanent environmental and additive genetic effects has been done firstly for the logarithm of the environmental variance, later for the environmental variance itself and finally for the environmental standard deviation. Up to now the method of Double Hierarchical Generalized Linear Models (DHGLM), had been considered only for the logarithmic scale. We have extended the use of the method of DHGLM to the other structures by the use of new link functions in the DHGLM settings: identity (additive structure of the residual variance), and square root (additive structure of the residual standard deviation). Examples of simulated and empiric data sets have been analyzed with these three link functions. The problem of possible negative residual variances and standard deviations when using identity and square root links has been addressed, as well as the interpretation of the results among structures. It has been found that the use of DHGLM with identity and square root links is feasible, thus the repertoire of easy to use tools for analyzing genetic control of environmental variation has been extended. Comparing differently structured residual variances of quantitative traits might lead to an increased understanding of the connection between genetic control of the mean level and the variation of a trait, as one structure could show up to generally better describe this feature than do the others.

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## Session 55

## Theatre 2

### **Genetics of carcass condemnations and relationships with growth, backfat and uniformity in pigs**

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Carcass condemnations recorded during meat inspection at slaughter plants are indications of reduced health and welfare of pigs and farms differ in incidence. These records offer opportunities for breeding to increase health and welfare of pigs. However, in most cases pedigree data of finisher pigs are lacking. In this study, we used data of 56,319 finisher pigs from three farms with known pedigree and that were scored for 69 carcass condemnations at meat inspection at the slaughter plant. These three-way crossbred pigs were offspring of Pietrain sires. The main aim of this study was to test the hypothesis that uniform animals are more robust and have lower disease incidence. We used a trivariate double hierarchical generalized linear model in ASReml 4. Among the carcass condemnations, incidences were highest for bursitis (14%), pneumonia (14%) and lower for pericarditis (2.5%) and pleuritis (3.4%). The heritabilities for these traits ranged from 0.014 to 0.073 on the observed scale. The genetic variance for residual variance on the log scale was 0.05 for growth rate and 0.20 for backfat thickness showing good opportunities for genetic improvement of uniformity in these traits. The genetic correlations between carcass condemnations and growth rate, backfat thickness and their residual variances were all small and most of them were not significantly deviating from zero. Therefore, the hypothesis that selection for increased uniformity would improve disease resistance and welfare was rejected. However, these results show good opportunities to utilize carcass condemnations at meat inspection in genetic evaluations to improve health and welfare of pigs while improving uniformity in growth rate and backfat at the same time.