Animal Genetics

Animal Nutrition

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Animal Physiology

stock Farming Systems

Cattle Production

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Pig Production

Horse Production

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SABRE
CUTTING EDGE GENOMICS FOR SUSTAINABLE ANIMAL BREEDING

SABRE Conference @ EAAP

Food Quality and Safety

4th SABRE Conference integrated with 60th EAAP Annual Meeting

SABRE previously organised 3 conferences to disseminate the plans and results of the project: "*Sustainable Animal Breeding*" (September 2006), "*Genomics for Animal Health*" (June 2007 in collaboration with EADGENE - European Animal Disease Genomics Network of Excellence) and "*Welfare and Quality Genomics*" (September, 2008).

We would like to thank the organising committees of EAAP for the opportunity to integrate the 4th SABRE Conference into the 60th EAAP Annual Meeting. We are very pleased that over 30 papers which stated ***"These results are obtained through the EC-funded FP6 project SABRE."*** have been accepted by the EAAP committees to be presented in the poster halls and lecture theatres. These papers will be presented throughout various sessions, in an effort to reach the audiences who are interested in the subjects dealt within the SABRE project.

The following pages will provide you with a first insight into the project. For further details we invite you to attend the SABRE presentations or to visit www.sabre-eu.eu.

Chris Warkup, SABRE Coordinator
Toine Roozen, SABRE Operations Manager

Cutting Edge Genomics for Sustainable Animal Breeding

Animal breeders have made considerable progress in recent decades in improving the economic efficiency of food production (this is one of the reasons the real price of food has fallen), but in recent years animal breeding has become more complex with breeders needing to broaden their breeding objectives. Nowadays breeders want to improve a wide range of traits, such as product quality, welfare related fitness traits and disease resistance. Many of these traits are difficult or expensive to measure and this is where the science of genomics is valuable. Through research such as the SABRE project, scientists are beginning to unravel which genes and which variants of these genes are important to explaining the genetic component of these new selection traits. 'Sustainable Animal BREeding' is the main focus of the SABRE Integrated Research Project.
The European Integrated Research Project "SABRE" (Cutting Edge Genomics for Sustainable Animal BREeding) is an innovative four-year, €23 million pan-European project which utilises the latest techniques in genetic science to develop more economically and environmentally sustainable production systems for cattle, pigs and chickens. The 'headline' objectives of the project are:

- To provide fundamental knowledge on the genomics and epigenetics relating to livestock
- To provide understanding of biological systems central to sustainability
- To identify genes and markers allowing focused breeding for sustainability goals
- To demonstrate the effectiveness of genomics for sustainable breeding
- To disseminate existing knowledge and new results to the user community
- To develop skills and training to best capitalise on new genomics knowledge.

Thirty three leading animal breeding research groups and businesses have joined forces in the project which commenced in April 2006 and has been made possible by a €13.9 million grant under Thematic Priority 5, "Food Quality and Safety", of the 6th Research Framework Programme of the European Union (FP6). The SABRE work programme, involving almost 200 scientists in 14 countries, is divided into 13 Work Packages. These harness key areas of emerging genomic and

Session 15 Poster 19

Polymorphism of the kappa-casein gene in Bosnian autochthones cattle races

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Fifteen purebred Busa cattle and thirteen Gatacko cattle were genotyped for the kappa-casein gene by Polymerase Chain Reaction-Restriction Fragment Length Polymorphism (PCR-RFLP). The allele A,B and C were found and the allelic frequencies were A=0.58 and B=0.42 in the purebred cattle and A=0.46, B=0.46 and C=0.08 in the crossbreed cattle. The genotypes composed of AA, AB, BB and BC was found in this study. The Kappa-casein genotype EE was not found in this study. The differentiation for allelic and genotypic frequencies between the purebred and the crossbred sires was not significant. Various alleles of the kappa-casein gene and their ratio were revealed. The allele B found in this small population will be useful for a sire selection program in the future.

Session 15 Poster 20

Estimation of genetic parameters for calving ease for Simmental cattle in Croatia

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The objective of this study was to estimate the genetic parameters for calving ease of Simmental cattle in Croatia. Data consisted of 135,892 calves, and pedigree included 639,999 animals. Calving ease was scored from 1 to 5 (1 = unassisted, 2 to 5 = various levels of assistance). Calving ease at first calving, and second or later parities where treated as different traits. Variance components were estimated by REML as implemented in VCE-5 package. Statistical model included age at calving, sex, region-year interaction as fixed effects and owner and direct additive genetic effect as random effects. The estimated heritabilities were 0.105±0.005 for calving ease at first calving and 0.078±0.005 for calving ease at second and later parities. These results suggest that model tested can be used for cattle evaluation for calving ease of Simmental cattle in Croatia.

Session 15 Poster 21

SREBP-1 polymorphism in Brown cattle and its effect on milk fatty acid composition

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Sterol regulatory element binding proteins (SREBPs) are transcription factors that play a central role in energy homeostasis by promoting glycolysis, lipogenesis, and adipogenesis. SREBPs belong to the original basic helix loop-helix-leucine zipper family of transcription factors. Differences in expression level and/or mutations of the SREBP gene may affect the expression level of Stearoyl CoADesaturase (SCD), leading to differences in fatty acid composition in the fat tissue of cattle. Two form of SREBP-1 gene were revealed in bovine specie. The L type differ from S type for a 84 bp insertion into the 5th intron. Work conducted on Japanese Black cattle revealed that S type was associated with a higher MUFA percentage than L type in Longissimus dorsi muscle, suggesting an influence of SREBP on desaturase activity. Studies on Holstein cattle report that SREBP gene was monomorphic (only the L allele was revealed). The aim of this work was to investigate the presence of L/S polymorphism in Italian Brown cattle (IBC) and to check an effect on milk fatty acid composition and SCD activity. Results revealed the L/S polymorphism in IBC with prevalence of the L allele. On 351 cows analysed, the genotype frequencies were 71.79%, 24.50%, 3.70% for LL, LS and SS respectively. Milk from SS cows showed higher values of product/substrate ratios for SCD enzyme and higher content of C11 and C15 fatty acids Since the absence of effects on monounsatured fatty acids content could be due to the unbalanced structure of data (very low SS cows), further studies on larger population are needed in order to better arise the role of SREBP on milk fatty acids composition and mammary lipid metabolism.

Session 15 Poster 22

Genetic parameters for growth traits in Braunvieh cattle reared in Brazil

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The object of this research was to estimate direct and maternal heritability coefficients and genetic correlations for growth traits from birth to 550 days of age in Braunvieh cattle reared in Brazil. The weights analyzed were birth weight (BW, kg, N=9,955), weight at 120 days of age (W120, kg, N=5,901), weaning weight at 205 days (WW, kg, N=6,970), yearling weight at 365 days of age (W365, kg, N=4,055), weight at 450 days (W450, kg, N=3,453), and at 550 days (W550, kg, N=1,946). A complete animal model was used for estimate the variance components in single-trait analyses, with the software MTDFREML. Relationship matrix had 35,188 animals, with 18,688 animals with phenotypic measures. Direct and maternal heritability increased from birth to weaning, with estimates of 0.23±0.037, 0.25±0.050, 0.41±0.059 for direct heritability for BW, W120 and WW, 0.08±0.012, 0.15±0.032, 0.22±0.036 for maternal heritability, and 0.18, 0.14 and 0.16 for total heritability estimates.Heritability coefficients estimated for post-weaning weights decreased with age. For W365, W450 and W550 estimations for direct heritability were 0.29±0.061, 0.25±0.057, 0.16±0.060, while maternal heritability were 0.20±0.035, 0.18±0.035, 0.13±0.052, and total heritability were 0.30, 0.35, 0.26. Direct and maternal heritability estimates reached the maximum values at weaning, increasing before and decreasing after that age. However maternal influence is important in this breed until the 550 days of age, maybe due to high milk production of cows. Higher genetic correlations between weights were observed for close ages. Maternal effects should be considerate in genetic evaluation of growth traits until 550 days of age in Braunvieh cattle in the population studied.

Session 49b Theatre 5

Conjugated linoleic acids effects on adipogenesis gene expression in ovine preadipocytes

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Conjugated linoleic acids (CLA) have wide interest regarding their condition of dietary bioactives with potential ability to modify the adipogenesis, although their effects are contradictory and not well understood. In order to explore the effects of these compounds in ovine adipose tissue, we analysed the effect of isomers trans10, cis12 and cis9, trans11 on the differentiation of ovine preadipocytes. Preadipocytes obtained from lamb subcutaneous (SC) and omental (OM) tissues were cultured and induced to differentiate by 1.6 microg/ml insulin, 2nM tri-iodothyronine, 10 nM dexamethasone, 10 microM rosiglitazone and one of the two isomers (50 microM) or a mixture of the two (25 microM each). mRNA expression levels of the transcription factors PRARg, ADD1 and C/EBPa and the lipogenic enzymes lipoprotein lipase (LPL) and acetyl CoA carboxylase (ACC) were analyzed through the differentiation period (7 days) by quantitative real time RT-PCR. The delta delta Ct method was used to calculate the relative gene expression. Data were analysed by Anova. All markers increased their expression during the differentiation process but addition of CLA had little effect on expression levels of the genes analysed as only the levels of expression of ADD1 on the 7th day of differentiation of SC preadipocytes were different from the control treatment ($P>0.05$). These, and previous results showing a tendency to increase the number of cells when CLA were added, suggest that CLA may act through a mechanism that could stimulate lipid filling without involvement of the adipogenesis cascade.

Session 49b Theatre 6

The use of ultrasounds to predict lean meat proportion of lamb carcasses

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The objective of this work was to study the use of ultrasounds to predict lean meat proportion of lamb carcasses. One hundred and twenty lambs (80 males and 40 females) of Churra Bragançana Portuguese local breed with a mean live weight of 23.0±6.9 kg were used. Lambs were scanned using an ALOKA SSD-500V ultrasound machine, equipped with one probe of 7.5 MHz, at lumbar and sternal regions. The images were analysed in order to measure the longissimus muscle depth (LD), subcutaneous fat thickness (SF), between the 12th and 13th vertebrae, and breast bone tissue thickness at 3rd (BT3) sternebrae. Lambs were slaughtered after 24 h fasting and carcasses were cooled at 4 °C for 24 hours. Carcass left side was dissected into muscle, subcutaneous fat, intermuscular fat and bone and remainder (major blood vessels, ligaments, tendons, and thick connective tissue sheets associated with some muscles). The LD, SF, BT3 and hot carcass weight were fitted as independent variables to predict lean meat proportion. of carcasses. Hot carcass weight explained 18,9% of lean meat proportion with a mean square error of 3.5%. Model including tissues measurements explained 57.2% of lean meat proportion with a root mean square error of 2.6%. These results indicate that carcass tissues measured by ultrasounds can be used to predict the lean meat proportion of Churra Bragançana lambs.

Session 49b Theatre 7

Statistic-genetical analysis of auction price of Texel, Suffolk and German white-headed mutton rams

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The impact of performance traits recorded at licensing as well as various factors that affect auction price were determined for Texel, Suffolk and German white-headed mutton rams in Schleswig-Holstein. Furthermore, genetic parameters for the performance traits and for the auction price were estimated. Data used in this study were collected from 1988 to 2007 by the Sheep Breeding Organisation in Schleswig-Holstein, Germany. The auction prices in the range from 150 to 1,000 € of rams of mentioned breeds between 170 and 270 days of age were included in the analysis. General Linear Models and Multiple Regression Analysis were used to identify the impact of traits and effects on the auction price. Estimation of (co)variance components was carried out using multivariate animal model. From the traits recorded at licensing, live weight, followed by type traits of conformation and muscle mass, had the highest impact on the auction price. The results indicated that ultrasound measurements of muscle and fat depth had a minimum impact on the final auction price. The effect of breed, Prion Protein genotype and owner of the ram attached the importance of customers and affected significantly the auction price of the rams. The estimates of genetic parameters showed favourable genetic correlations between auction price and other performance traits.

Session 49b Theatre 8

Influence of breed, farm, age at first lambing and number of lambing on length of productive life in sheep

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The life performance of female sheep is one of the most important economic traits in sheep husbandry. The objective of this study was to perform a survival analysis to estimate the effects on length of productive life in sheep. Therefore, a dataset with 16,972 female sheep from a breeding association of northern Germany was analysed. The data included information about the breed, lambing dates, number of lambs each lambing, date of birth, date of death or culling, farm and breeder, total number of lambings in lifetime associated with the total number of born lambs alive or dead in lifetime. About 25% of the records were right-censored. A proportional hazard model assuming a Weibull distribution for the baseline hazards function was applied (Survival Kit V3.12). The final model included the effects of the breed (n=7) and the age at first lambing in classes (n=4) as fixed effects, the farm (n=319) as random effect and the lambing number (n=10) as a time-dependent effect. All effects showed a significant effect on length of productive life ($P<0.001$). The German Blackheaded Mutton breed showed the lowest risk ratios being culled (RR=0.55) compared to the Texel breed (RR=1.00). The highest culling risk within the effect of the breed was found for the Suffolk breed (RR=1.19). By increasing number of lambings the hazard slightly decreased from first (RR=1.00) until seventh lambing (RR=0.09). Thereafter, the risk ratio increased until the tenth lambing and higher. The hazard rate of the effect age at first lambing showed an unexpected trend. If ewes were older than two years at first lambing the risk ratio decreased (RR=0.74) compared to the age at first lambing from 395 till 455 days (RR=1.00).