

P-70

**NEW METHOD FOR EFFICIENT PHASING OF SMALL POPULATIONS USING HIDDEN MARKOV MODELS WITH A SCALAR PHASE VARIABLE**

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**Objectives:** Reconstructing phase can help in diverse genetic analysis settings, both in itself, and as a method for imputation of missing genotypes. One popular approach is to use Markov Chain Monte Carlo methodology to iteratively sample the haplotype distribution in each individual as mosaics of all other individuals, treating the phase in each position as a binary parameter. We make such methods deterministic and improve accuracy by analysing local as well as global convergence.

**Methods:** We propose a model where the phasing of individual genotypes is treated as a scalar ordering probability, with no use of pedigree data. This allows traditional, mostly deterministic, algorithms for Hidden Markov Model training to be used. Based on analysing the structure of the likelihood function, we introduce a specific gradient-descent based approach rather than general expectation-maximization, and explicitly included inversion operations, reducing the number of incorrect phase switches.

**Results:** In comparisons against existing state-of-the-art algorithms, including Beagle and MaCH, our implementation performs favourably. Specifically, we look at data from pre-existing simulated datasets for crosses with known phase (our method reduces the number of incorrect haplotype switches, sometimes by more than 90 %), experimental data sampled from natural populations (our method increases average LD block length by more than a factor of 2), as well as simulated data based on human populations (similar results).

**Conclusions:** The use of a scalar variable for representing phase can improve phasing accuracy. In MCMC methods with a binary representation of phase, the presence of multiple highly genetically similar individuals (e.g. full and half siblings, or highly preserved haplotype blocks among more distantly related individuals), can result in optimization being caught in detrimental local minima. The introduction of a scalar variable improves rectifies this. Our proposed method also better lends itself to analysis regarding convergence.

P-71

**ESTIMATION OF GENETIC PARAMETERS FOR METHANE INDICATOR TRAITS BASED ON MILK FATTY ACIDS IN DUAL PURPOSE BELGIAN BLUE CATTLE**

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Dairy production stands out for its large methane emission. Therefore, specific nutritional strategies are being applied to abate methane emission but very little information is available about the genetic variability of methane emission. Methane indicators using traits indirectly related to methane and easily recorded like the mid-infrared (MIR) prediction of fatty acid could be used to conduct genetic studies. MIR methane indicators used in this study were derived from published fatty acid based methane indicators using 597 calibration samples. Genetic parameters of these MIR indicators were estimated by single trait random regression test-day models from 13,389 records collected on 1602 Dual Purpose Belgium Blue cows in their first 3 lactations. For the published indicator showing the highest relationship ( $R^2=0.88$ ) with Sulphur hexafluoride ( $SF_6$ ) methane emission data, the average daily heritability was  $0.25\pm 0.06$ ,  $0.25\pm 0.07$  and  $0.18\pm 0.09$  for the first three lactations, respectively. Similarly, the heritability of lactation yield was  $0.45\pm 0.09$ ,  $0.46\pm 0.11$  and  $0.24\pm 0.14$ . The sire genetic variability was 3.60, 4.08, 1.19 kg<sup>2</sup> of methane for the first three lactations, respectively. The genetic difference between sires having daughters eructing the highest and the lowest methane content was 11.62, 13.01 and 5.98 kg per lactation for

the first three parities. This study suggests that methane indicator traits can be predicted by MIR and the genetic variability of these traits seems to exist. Therefore, it also indicates there is genetic variability of methane content eructed by dairy cows. These first findings might open new opportunities for animal selection programs on methane emission.

**P-72**  
**ANALYSIS OF A LONG-TERM DIVERGENT SELECTION FOR BODY WEIGHT IN CHICKENS WITH AN EXPONENTIAL MODEL**

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The aim of this study is to estimate genetic parameters for body weight in divergently selected lines of chickens with non-linear model. Chickens were divergently selected over 34 generations for high and low body weight (BW) at 8-wk of age. Estimates of body weight for each generation were provided by mixed model. For fitting generation means against generation or cumulative selection differential exponential model was used. Estimates of realized heritability over generations were derived from regression of response to cumulative selection differential. Data were analyzed by SAS, using GLM and NLIN procedures. Fitting the generation means in non-linear model was better for the low line. Coefficient of determination was 90.96% for females and 88.99% for males. In high line,  $R^2$  was 58.10% for females and 63.00% for males. Estimates for selection limit in high line were 2598.4 g and 2144.1 g, for males and females, respectively. Despite good fitting, selection limit have not been accomplished in low line. In high line, half of the selection response was obtained after about 6 to 8 generations, and in low line, about 20 to 28 generations. The estimated realized heritability decreased over generations. Analyses revealed differences between lines. During experiment realized heritability declined from 0.24 to 0.02 in males and from 0.55 to 0.04 in females of the high line. The corresponding decreases in low line were from 0.23 to 0.12 in males and from 0.47 to 0.31 in females. The use of non-linear model is recommended for modeling the response of long-term selection in poultry because of the well fitting and informative parameter estimates.

**P-73 – ABSTRACT WITHDRAWN**

**P-74**  
**RETAINED PLACENTA IN MRIJ CATTLE IS AFFECTED BY HERITABLE AND NON-HERITABLE FACTORS**

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Failure of the timely expulsion of the fetal membranes, called retained placenta (RP), leads to reduced fertility, increased veterinary costs and reduced milk yields. Immune-mediated rejection of the fetal membranes by the maternal immune system plays an important role in the breakdown of the fetal–maternal attachment and RP can be linked to failure of immune-mediated detachment of the fetal membranes. Immune MHC 1 (Major Histocompatibility Complex type I) compatibility between calf and dam depends on whether the paternal MHC I haplotype inherited by the calf is compatible to the MHC I haplotypes of the dam. The objectives of this study were to concurrently look at the heritable and non-heritable genetic aspects of retained placenta and test the hypothesis that a higher coefficient of relationship between dam and calf increases the risk of RP in the dam. The average incidence of RP in 43661 calvings was 4.5%, ranging from 0% to 29.6% among half-sib groups in MRIJ cattle. The average pedigree based relationship between the sire and the maternal grandsire ( $CR_{s^*mgs}$ ) was 0.05 and ranged from 0 to 1.04. Using a sire-maternal grandsire model the  $h^2$  was estimated at  $0.22(\pm 0.07)$  which is