# ICQG2012

## 4th International Conference on Quantitative Genetics:
## Understanding Variation in Complex Traits

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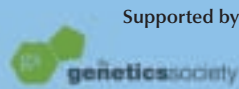
## Edinburgh, 17 – 22 June 2012

# Programme
# &
# Book of Abstracts
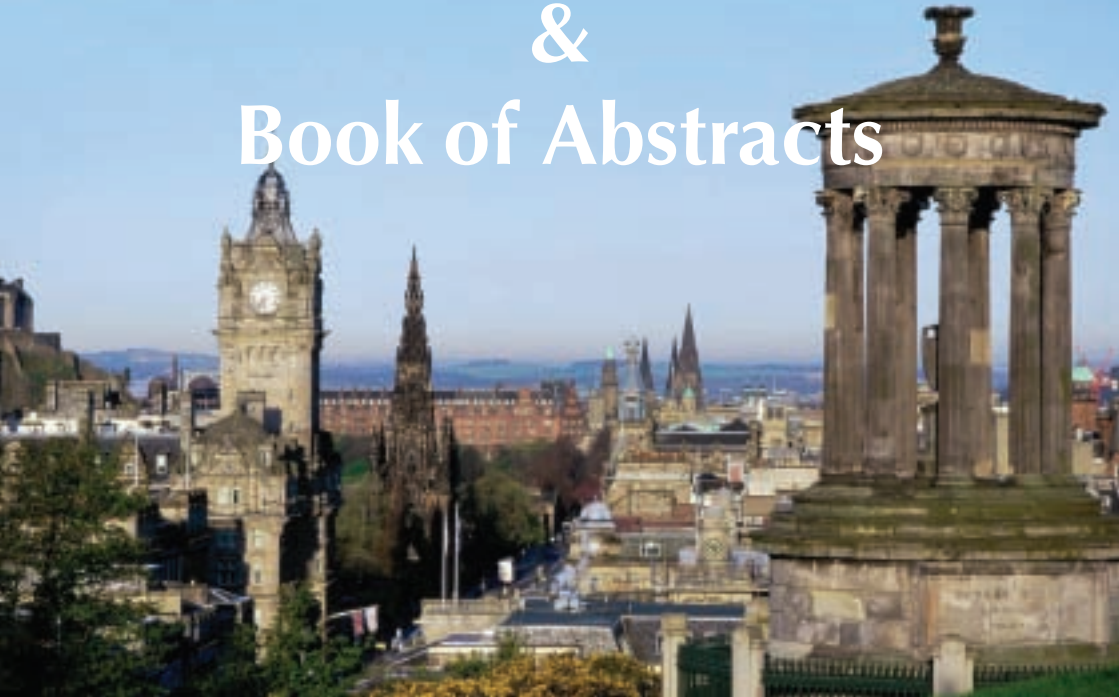
fat indicated negative correlation (<- 0.9).   It suggested that why a highly significant region for both milk and fat have been kept through long selection history.  Hence our approach may help identify some of the missing genetic variation and improve understanding of relationship between complex traits.

**P-180**
**POTENTIAL OF GENOMIC SELECTION IN PERENNIAL CROPS: PRELIMINARY RESULTS IN THE CONTEXT OF EUCALYPTUS AND OIL PALM BREEDING**

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The methodology of selection in plant breeding has markedly evolved with the advent of high throughput molecular technology, the increasingly reasonable cost of genotyping, and the implementation of genomic selection (GS). For perennial crops, the potential of GS is high and gives the opportunity to shorten the breeding cycle by selecting at the juvenile stage using marker information. Here we present preliminary results of GS experiments for two perennials crop, *Eucalyptus* and oil palm, that play an important economical role in tropical regions.
In the case of *Eucalyptus,* a simulation study was developed to test the efficiency of GS in the frame of a recurrent selection scheme for clone production over four breeding cycles. Scenarios crossing broad sense heritabilities (H²=0.6 and 0.1), dominance to additive variance ratios (R=0.1; 0.5 and 1) and training population structure were compared using Bayesian LASSO method. Models including dominance effects are all the more relevant when the R ratio and the training population size are high. The genetic gain per unit time with GS was 1.5 to 3 times higher than with phenotypic selection at mature stage for breeding and clone populations.
For oil palm, we implemented a cross-validation approach with 111 individuals of the last generation of a key breeding population, evaluated through progeny tests including 40,000 individuals and genotyped with 140 microsatellites. The accuracy of GS increased when increasing the training population size and reached 0.6-0.7, according to the trait, with a 3:1 ratio for training and validation populations respectively. The small effective population size detected in this breeding population explains the good GS performance even with a limited panel of markers.
Our studies based on two perennials crops presenting different biological patterns and different breeding contexts suggest very promising results of GS for long rotation plant species.

**P-181**
**PERSISTENCE OF LINKAGE PHASE BETWEEN THE CHINESE AND NORDIC HOLSTEINS AND GENOMIC PREDICTION USING THE COMBINED REFERENCE POPULATION**

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This study investigated the persistence of linkage phase between the Chinese and Nordic Holsteins, and the gain in reliabilities of genomic predictions for Chinese Holsteins by including Nordic bulls in reference population. 80 Chinese Holstein bulls, 2,091 Chinese Holstein cows and 4,398 Nordic Holstein bulls were used in the analysis. Totally, 41,838 SNPs with minor allele frequencies higher than 0.01, were used in the analysis. Genomic estimated breeding values (GEBV) of Chinese Holsteins were predicted using a single-trait GBLUP model based on Chinese Holsteins reference alone, and using a two-trait GBLUP model based on a combined reference population including both the Chinese and Nordic Holsteins. The persistence of linkage disequilibrium (LD) phase between two populations, measured as correlation of *r* (a measure of LD between adjacent markers) was 0.97. Comparing the predictions based