

R.A.  
Post

Session 22

Poster 14

**Pedigree analysis of the Portuguese Holstein Cattle: inbreeding and genetic diversity trends**

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The objective of this study was to analyze the pedigree information of the Portuguese Holstein cattle to quantify the inbreeding level and the genetic diversity in the population. Pedigree information including 743,107 registered animals born from 1941 to 2009 obtained from ANABLE data base (BOVINFOR), was analyzed using the software Pedig. The current reference population (RP) was defined as the females born from 2004 to 2009 and comprised 123,039 animals with known parents. The equivalent number of known generations was 3.2 and the average number of known ancestors was 42.7 for the RP. Average inbreeding of 110,718 inbred animals was 0.014 and decreased by 0.0011 /yr from 1986 to 2009. The average inbreeding in the all population was 0.0022 and the percentage of inbred animals in the population increased by 2.29%/yr from 1987 to 2009. The average inbreeding in the RP was 0.004. The average generation interval weighted across pathways was 6.05 yr and was higher for sires (8.05) than for dams (4.75) pathway. The number of founders was 75,180 and the effective numbers of founders, ancestors and founder genomes were 359, 199 and 120 respectively. The calculated effective population size was 250. The ten most influential ancestors (all sires) accounted for 17.6% of the RP gene pool. Five out of 24 subpopulations (defined by country of origin of sires) accounted for 87.65% of the RP gene pool. The use of imported germoplasm in Portugal contributed to acceptable levels of inbreeding and genetic diversity in the population. Despite low, increasing rate of inbreeding suggests attention on selection and mating decisions to avoid the known inbreeding depression effects on overall performance of the Holstein dairy herds.

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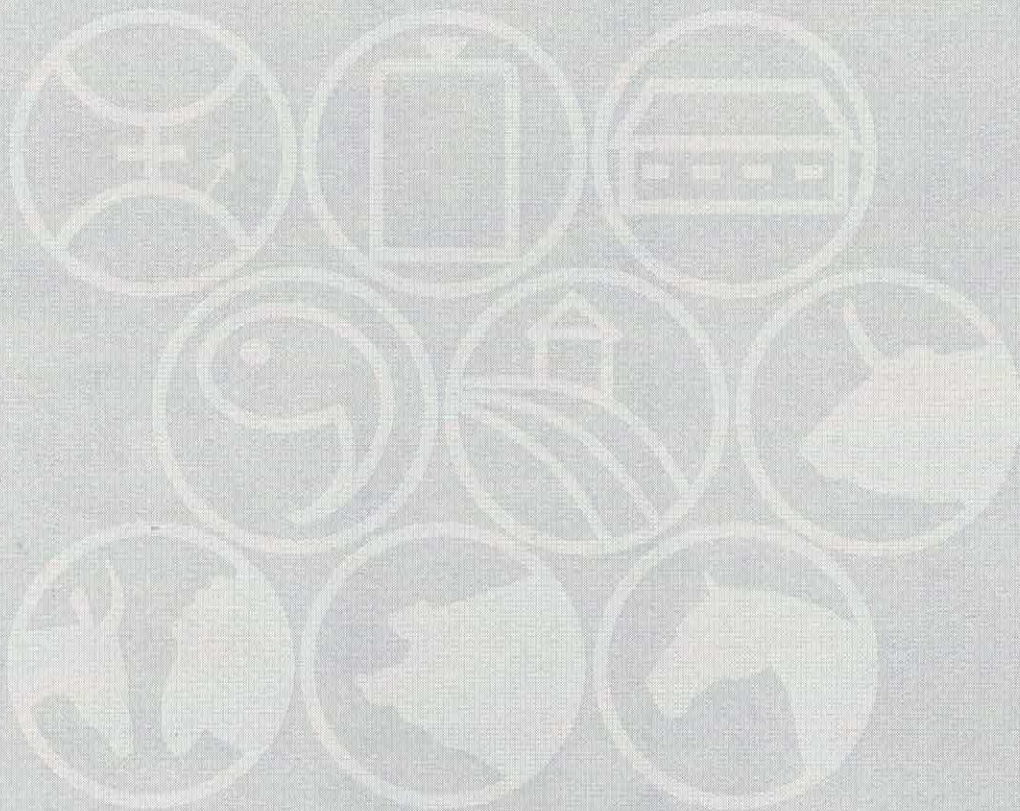
**Comparison of estimation models with data of limited number of animals but intensive recording**

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Variance components were estimated for a data set of body weight of Japanese Black calves having small number of animals but intensive recording; monthly from ages of 0 month (mo) to 16 mo. The data set included 10,295 records of 887 calves measured from 1975 to 2008 at an experimental station of Okayama University. Calves were weaned at 2 or 3 mo of age. Selected heifers were dehorned soon after weaning. Culled heifers and all steers of 8 to 10 mo of age were shipped to a local calf market. Variance components of body weight were estimated by REML using VCE602. Statistical model included fixed effects; contemporary group (year-season-sex), age of calves as a covariate and random effects; animal's direct genetic effect, maternal genetic effect, permanent environmental effect, random residuals. Because of very low permanent environmental effect, it was excluded from the analysis. By multiple trait analysis, low to moderate heritabilities (0.13 to 0.36) were estimated, showing no explicit chronological trend. Heritabilities of maternal genetic effect were in a range of low to high heritability (0.04 to 0.66), however, showing clear downward tendency. Genetic correlations between direct and maternal genetic effect ( $r_{am}$ ) fluctuated around zero. By random regression analysis with 3-order Legendre polynomials for both direct genetic effect and maternal genetic effect, heritability of direct genetic effect showed upward trend (from 0.18 to 0.87) whereas heritability of maternal genetic effect showed downward trend (from 0.65 to 0.097) showing consistent result with the multiple trait model. The  $r_{am}$  consistently showed negative correlations (average: -0.47) throughout the ages.

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