Status multibreed evaluation
May 2011 - Jan Lassen

Work tasks for 2011

1) Updating the data editing for the multibreed model to be consistent with the data editing for the new yield evaluation model and giving the status of the data pre-processing routines to Faba, MTT and DC. This consists of:
   a) Streamlining the data editing programs.
   b) Report statistics for breed proportions, degree of heterozygosity and recombination within "colour * country group for the new, the old multibreed model and the new routine model.
   c) Compare the Mix99 input data for the multibreed model and insure that allocation to model effects for HF and RDC cows is identical with the allocation in the new HF and RDC models.
2) Run the new multibreed model and validation the model by comparing EBV's with those from the Holstein and the Red Cattle routine evaluation. This consists of:
   a) Run the full setup for the multibreed model incl. heterogen variance correction.
   b) Compute genetic trends and make comparisons with corresponding trends from the new HF and RDC model.
   c) Compute correlations between EBV's from the multibreed model and the new HF and RDC models.

Since last meeting

Since the last meeting I have worked on part 2b and 2c of the work plan. For point 2b and 2c though using a model without HV correction. I have merged the HOL, RDC and RDCxHOL datasets into one and used this dataset for the multibreed evaluation.

At last meeting correlations were relatively low for RDC cows. I have now used RDC standardization factors to generate the trends and correlations for RDC and HOL standardization factors for HOL breed. These factors are coming from the multibreed model and not from the routine/new model. This is done in order to make a more fair comparison between the multibreed model and the New model. All comparisons done in this meeting is between models without HV correction.

The missing HOL cows were lost when deriving the Danish HOL cows from the Solani file. This has now been solved. This though seem to have very little influence on trends and correlations.

Genetic trends

Genetic trends are presented in 4 excel sheets separately for RDC and HOL and for cows and bulls. For HOL the trends look very similar for both cows and bulls when comparing the multibreed model with the new model. There is a slight deviation for the trend for fat both in cows and bulls. Also SD for HOL cows and bulls follow the same pattern, though the SD for the multibreed model tends to be a little bit higher for the multibreed model than for the new model.

For RDC the pattern of the trend is also the same from when comparing the new model with the multibreed model. There is a larger deviation between the models than for the HOL data. This is most pronounced for FIN and SWE. I assume that this could be related to Lier and Viul?

Correlations
Correlations between breeding values from the multibreed model and the new model are much higher for RDC cows than what were presented at last meeting (0,95-0,99 vs 0,90-0,92 at last meeting). The correlation is also higher in general – so for HOL cows (0,98-0,99) and bulls (0,99-1) and for RDC bulls (0,97-1). Correlations are still lowest for RDC. This could be an effect of using the HOL parameters.

Future plans
Incorporate HV correction into the model?