

## ORAL

### Technical Session 1

### ICAR / Interbull joint session on “Advances in Genetics and Phenotyping”

## Limits to selection in U.S. dairy cattle after several generations of genomic evaluation

Cole John B.<sup>[1]</sup>, Null Daniel J.<sup>[1]</sup>

[1] Council on Dairy Cattle Breeding

Genomic evaluations were introduced in the United States in 2009, and the generation interval for US Holsteins is now 2.2 y, implying approximately 7 generations of selection have now passed. It is not clear how decreasing generation intervals and increasing selection intensities affect limits to selection.

Lower and upper bounds of selection limits were calculated for 19 traits in US Ayrshire (AY; n = 20,373), Brown Swiss (BS; n = 89,136), Guernsey (GU; n = 11,407), Holstein (HO; n = 9,119,871), and Jersey (JE; n = 928,883) cattle. Traits evaluated were milk, fat, and protein yield; productive life; somatic cell score; daughter pregnancy rate; heifer and cow conception rates; heifer and cow livabilities; early first calving; gestation length; and six health traits (BS, HO, and JE only): hypocalcemia (milk fever), displaced abomasum, ketosis, clinical mastitis, metritis, and retained placenta. Genotypes were imputed to a set of 69,200 SNP used for routine genomic evaluation and haplotypes were phased with Findhap v. 3. Lower bounds (SLL) were predicted by selecting the 29 individual autosomes with the largest direct genomic values (DGV) for each breed-trait combination. Upper bounds (SLU) were calculated by summing the alleles at each locus with the largest allele substitution effects. SLL and SLU were also compared to the largest observed DGV (DGVmax) for each breed-trait combination.

SLL was generally 2 to 4 times larger than DGVmax across breeds and traits, while SLU typically ranged from 5 to 15 times larger than DGVmax. For example, SLL and SLU for HO milk were 2.59 and 9.44 times as large as the maximum observed DGV (5,037.86). In some cases, predicted selection limits were very small (e.g., AY, GU) compared to others (e.g., BS, HO, JE), which may be due to the limited number of genotyped animals in some breeds, but these patterns were not consistent across traits. Selection limits were greater than DGVmax in all breeds studied, although in some cases they were very similar; e.g., in AY early first calving, SLL was 5.90 while DGVmax was 5.88. This situation likely reflects the small size of the genotyped AY population. These results suggest, despite the decrease in generation intervals and increase in selection intensity over several generations, that substantial opportunity for genetic progress remains in the US dairy cattle population.