

## Scientific Program - 2021 Interbull Virtual Open Sessions

Full videos presentations will be available on www.icar2021.nl starting from April 19th, during the virtual meeting only the 3 minutes' videos pitch for each presentation will be presented.

	Author	Scientific Report Title
Session		
	Opening by Interbull's SC chair (M. Shaffer)	
Monday, April 26 14:00 – 14:45	S. Savoia	"SNPMace" (International SNP Evaluations) - next steps towards the first pilot run.
	H. Kärkkäinen	EuroGenomics full reference SNP MACE: Projecting national full reference
Meta-analytical methods in animal		genotypes to common EuroGenomics
genetic	S. Toghiani	National Index Correlations and Actual vs. Expected Use of Foreign Sires
and genomic evaluation.	12 minutes Interactions with speakers and audience	
	S. Savoia	Interbull genomic evaluation of small Holstein populations (InterGenomics-Holstein).
	K. Mafolo	Establishing genomic predictions for dairy traits in South African
Chair: M. Goddard	K. Walolo	Holstein and Jersey cattle small and predominantly
	8 minutes Int	eractions with speakers and audience & Closing

	JT. van Kaam	Implementation of Ketosis breeding value in Italian Holstein
	K. Schodl	The D4Dairy-Project – How digitalisation and data integration
		pave the way to dairy health improvement
Monday April 26 14:55 – 15:55	J. Jamrozik	Genomic evaluation for resistance to fertility disorders in Canadian dairy breeds
	12 minute	s Interactions with speakers and audience
Implementing new traits in genetic	R. Reis Mota	Use of international clinical mastitis data as independent trait in the USA evaluation system
and genomic evaluation systems: Health & Fertility.	R. Saintilan	Harmonization of maternal traits in Eurogenomics countries
	8 minutes Interactions with speakers and audience	
Chair: B. VanDoormaal	A. Kudinov	Handling of inbreeding and semen sire breed in the Nordic Holstein fertility evaluations as part of EuroGenomics
	S. Biffani	Improving the model for genetic evaluation of calving traits in the US Holstein and Brown Swiss
	8 minutes Interactions with speakers and audience & Closing	

	D. Lourenco	Single-step genomic predictions for yield traits in US Holsteins with unknown parent groups and phenotype-pedigree truncation
<b>Monday April 16 16:05 – 17:10</b>	J. Vandenplas	Interim genomic prediction considering newly acquired genotypes and phenotypes
	A. Kudinov	Single-step genomic predictions of a minor breed concurrently with the large
New developments in Single Step		national genomic evaluations of main breeds
genomic evaluations	12 minut	es Interactions with speakers and audience
and validation methods.	LH. Maugan	An approach to reduce computing time in multitrait single-step evaluations.
	Ø. Nordbø	Including genetic groups as fixed or random effects in large
		scale single-step genomic predictions
Chair: P. Sullivan	Z. Liu	A deregression method for single-step model using all genotype data
	12 minutes Interactions with speakers and audience	
	Y. Masuda	Are ssGBLUP de-regressed proofs unbiased?
	P. VanRaden	Improved genomic validation including extra regressions

## 8 minutes Interactions with speakers and audience & Closing

	E. Pimentel T. Andersen	Effects of use of external information in Single-Step evaluations  for linear type traits in Brown Swiss  Using single-step genetic evaluation for type traits in the Nordic countries
<u>Friday April 30 14:00 – 15:10</u>	H. Alkhoder	Application of a single-step SNP BLUP model to conformation
		traits of German Holsteins
Evneriences with Single Sten	12 minut	es Interactions with speakers and audience
Experiences with Single Step genomic evaluations.	J.	Implementation of single-step evaluations for fitness traits in the
	Himmelbauer	German and Austrian Fleckvieh and Brown Swiss populations
	A. Cesarani	Multi-breed genomic evaluation for dairy cattle in the US using single-step GBLUP
	12 minutes Interactions with speakers and audience	
Chair: Z. Liu	M. Koivula	Meta-model for genomic relationships of metafounders applied on large scale single-step
		random regression test-day model
	S. Biffani	Pitfalls and opportunities of genetic and genomic evaluation in the Buffalo species:
		experiences from Italy
	8 minutes Int	eractions with speakers and audience & Closing

Genetic and Genomic evaluations in beef  direct-maternal genetic correlations between countries  Genomic GxE approaches modelling beterogeneous SNP variances:	and cross bred cattle.	B. Gredler- Grandl	applied to age at slaughter in Irish crossbred beef cattle
direct-maternal genetic correlations between	beef	P. Gradlar	
evaluations due to ignoring		R. Bonifazi	direct-maternal genetic correlations between

	T. Pitkänen	Towards genomics in Finnish beef cattle - genetic multibreed evaluations fitted
Chair: A. Cromie	G. Wiggans	Genomic evaluation of crossbred dairy cattle in the United States
	8 minutes Interactions with speakers and audience & C	

	R. Mrode	Genomic prediction for feed intake in UK dairy cattle
<u>Friday April 30 16:05 – 17:00</u>	R. B. Stephansen	Genomic prediction of residual feed intake in the Nordic breeds using data from research herds and 3D cameras in commercial herds
Implementing new traits in genetic and genomic evaluation systems:	K. Parker Gaddis	Implementation of Feed Saved evaluations in the U.S.
Feed Efficiency & Environmental	G. Kistemaker	Genomic evaluation for feed efficiency in Canadian Holsteins
Impact.	15 minutes Interactions with speakers and audience	
	J.López-Paredes	Dry matter intake, methane emissions and microbiome profiles
Chair: G. Pedersen Aamand		as new traits for feed efficiency
	N. Gengler	First steps to implement genomic evaluations for butter softness
		and spreadability in dual-purpose Belgian Blue cattle
	9 minutes Inte	ractions with speakers and audience & Closing