

## Scientific Program - Interbull Open Session, Bled 2024

## Rikli Balance Hotel, ARNOLD I/II

Day	Session	Time	Speaker	Topic
Monday, May 20		08:30	M. Shaffer & SVN	Opening of Interbull Open Meeting
·		08:45	P. van Raden	Breeding programs compared across countries, continents, and breeds using data from proven bulls and genotyped females
	Session I	09:00	T. Lawlor	Heritable variation in gene expression is the key to maximizing genetic gain and preserving genetic diversity with a properly designed breeding program.
Monday, May 20	Genetic Diversity & Production Updates  Chair: Gerben de Jong	09:15	J.T. van Kaam	Next-Level Genomic Selection: Mitigating Inbreeding
		09:30	M. Stephen	Genetic trend in milk fat percent is highly responsive to the relative economic value of milk fat and milk protein in the NZ dairy industry.
		09:45	F.L. Guinan	Genetic parameters for daily milk weights in U.S. Holsteins using pen-based contemporary groups
		10:00	T. Pitkänen	Revision of random regression test-day model has improved genomic prediction for Nordic Red dairy cattle
		10:15	X. WU	Analysis of Factors Affecting Daily Milk Yields: An Initial Case Study in an Automatic Thrice-Milking Farm





Monday, May 20		14:00	J. Jenko	Simulating genetic progress for traits with expensive phenotyping
	Session II	14:15	N. Vargas Jurado	Estimation of variance components for clinical mastitis and somatic cell scores for the Nordic dairy cattle populations
	New Traits	14:30	F. Galluzzo	Genetic evaluation of differential somatic cell count in Italian Holstein
	Chair: Daniele Vicario	14:45	R.B. Stephansen	Genomic Prediction of Genetic Residual Feed Intake Integrating a Novel Energy Sink for Change in Body Reserves.
		15:00	J. Jamrozik	Alternative Residual Feed Intake (RFI) expressions in dairy cattle
		15:15	J. Heise	Breeding for feed efficiency in German Holsteins: the new RZFeedEfficiency
Monday, May 20	Session III	16:00	M. Schrauf	Cross-Validation Assessment of Random Regression Specifications in a Single-Step Genomic Model for Dry Matter Intake
	New Traits	16:15	G. Tarekegn	Using cow carcass weight to select efficient cows
	Chair: Ezequiel Nicolazzi	16:30	R. Kempe	Single-step genomic prediction models for metabolic body weight in Nordic Holstein, Red dairy cattle, and Jersey
		16:45	K.A. Bakke	Genetic correlations between daily dry matter intake, body weight and enteric methane in Norwegian Red dairy cows
		17:00	N. Mejer	Breeding for resilience in the Netherlands and Flanders





		17:15	C. Manzanilla- Pech	Effect of heat stress on methane emissions of Dutch Holstein population
		17:30	N. Gengler	Next steps towards the development of a collaborative genomic evaluation system for residual methane production in Walloon Holstein cows
Tuesday, May 21		08:30	R. Bonifazi	Multi-breed multi-trait single- step genomic predictions for Holstein and Jersey including crossbred animals
		08:45	D. Słomian	Differential handling of missing parents in genetic evaluation of dairy cattle using single step test day SNP-BLUP model
Tuesday, May 21	Session IV: Single Step Methodology Chair: Gert Pedersen Aamand	09:00	A. Legarra	Technical options for all-breed Single Step GBLUP for US dairy cattle
		09:15	H. Alkhoder	A weekly genomic evaluation of newly genotyped selection candidates based on a single-step genomic model
		09:30	R. Rostellato	Genomic-free EBVs computed from Single-Step evaluations as proofs for MACE in France
		09:45	Z. Liu	Guidelines for Approximating Genomic Reliabilities of the Single-Step Genomic Model
		10:00	K. Stachowicz	Single-step evaluation for milking cow survival in Poland
		10:15	A. Chegini	Improving single-step genomic prediction reliabilities for clinical mastitis in Nordic Red dairy cattle and Jersey by applying marker-specific weights





		11:00	H. Eding	Incorporation of external GEBV in the Dutch-Flemish dairy genetic evaluation
Tuesday, May 21	Session V: New Developments in genetic/genomic (inter)-national evaluation	11:15	E.C. Ooi	Designing a Validation Application for Genetic and Genomic Evaluation Systems in the New Zealand Dairy Industry
		11:30	R. Mota	Genomic validation software: USA update including truncated MACE
		11:45	J. Himmelbauer	Modeling unknown parent groups or metafounders in single step genomic BLUP – results of a simulation study
		12:00	B. Cuyabano	Genetic correlations: a parameter or a latent phenotype in genetic evaluations?
Tuesday, May 21	Chair: Urs Schnyder	12:15	J. Vandenplas	Integration of foreign estimates of SNP effects into a single-step genomic evaluation
		12:30	H. Kärkkäinen	SNP MACE for EuroGenomics countries
		12:45	A. Nazari	PREP Database: Extension to Genomic Evaluation
		13:00	M. Shaffer	Closing of Interbull Open Meeting