International Sheep Genomics and the International Goat Genome Consortiums combined virtual meeting



June 8th/9th to June 10th/11th 2021

Chairs: Shannon Clarke (AgResearch, NZ) and Gwenola Tosser-Klopp (INRAE, France)

Session	Title	Presenting	Affiliation	Format	Time allocation
		Author			Presentation +
					Questions
					(min)

Session 1: June 9th 8am NZST/previous day (June 8th 10pm CEST, 3pm CDT etc)

Genome structure and function

1	Functional annotation of the reference Rambouillet sheep genome	Kimberly Davenport	Department of Animal, Veterinary, and Food Science, University of Idaho, USA	Presentation	20
1	A gene expression atlas of the goat brain	María Gracia Luigi-Sierra	CRAG Centre de Recerca Agrigenòmica (CRAG), Spain	Presentation	20
1	High-quality ovine reference genome assemblies	Ben Rosen	USDA, ARS, Animal Genomics and Improvement Laboratory, USA	Presentation	15

1	Underpinning sheep genomics - variant calling from the "1000 Sheep Genome Project" (SheepGenomeDB)	Rudiger Brauning	AgResearch, NZ	Presentation	10
1	An atlas of variant ages in sheep genome	Charlotte Her	Université Grenoble Alpes, France	Presentation	15
1	FarmGTEx and the characterisation of transcriptomic variation in sheep and goat	Pau Navarro	The University of Edinburgh, United Kingdom	Presentation	10
1	Constructing the Ovine Pan-genome	Brenda Murdoch	Department of Animal, Veterinary, and Food Science, University of Idaho, USA	Presentation	15
	Session 2: June 10 th 8am NZS	۲/previous	day (June 9 th 10pm CEST, 3pm	CDT etc)	
2	Expression Profile of Ghrelin gene in goat breeds in Kerala	Charlotte Coretta Rodricks	Department of Animal Genetics and Breeding, College of Veterinary and Animal Sciences, Mannuthy, India	Lightening talk	5
2	Determining developmental transcriptome differences in tissues related to growth traits in sheep using RNA- sequencing	Shernae Woolley	The Roslin Institute and Royal (Dick) School of Veterinary Studies, The University of Edinburgh, United Kingdom	Lightening talk	5
2	Complex Transcriptomic analysis of the early mucosal host	trait studi	es and epigenetics INRAE, URZ, Petit-Bourg (Guadeloupe), France	Presentation	20
	response in goats infected with Haemonchus contortus	Christophe Bambou			
2	Identification of novel loci associated with facial eczema tolerance in New Zealand sheep	Kathryn McRae	AgResearch, NZ	Lightening talk	5
2	Functional genome and microbiome in blood of goats affected by the gastrointestinal pathogen Haemonchus contortus	Yonathan Tilahun	School of Agriculture and Applied Sciences, Langston University, USA	Lightening talk	5
2	A recessive stop-gain mutation in CCDC65 is associated	Maxime BEN	GenPhySE, Université de Toulouse, INRAE,	Presentation	15

2	Genome-wide association studies for meat quality	Andrew Hess	AgResearch, NZ	Presentation	10
	traits in New Zealand sheep imputed to whole-				
	genome sequence				
2	Genome-wide association study of reproductive	Chiraz Ziadi	Departamento de Genética, Universidad de	Lightening	5
	efficiency in Florida dairy goats		Córdoba, Spain.	talk	
2	Genome-wide analysis of copy number variation	Mohsen	Department of Animal Science, Faculty of	Lightening	5
	identifies regions associated with fat deposition in thin	Gholizadeh	Animal and Aquatic Science, Sari Agricultural	talk	
	and fat-tailed sheep breeds		Sciences and Natural Resources University, Iran		
2	Development of epigenetic clocks for New Zealand livestock	Alex Caulton	University of Otago and AgResearch, NZ	Presentation	15
2	Whole genome bisulfite sequencing reveals tissue specific DNA methylation profiles in Sheep.	Suraj Bhattarai	Department of Animal & Veterinary Sciences, University of Vermont, USA	Presentation	15
	Session 3: June 11 th 8am NZST	/previous	day (June 10 th 10pm CEST, 3pn	ו CDT etc)	
	Session 3: June 11 th 8am NZST	/previous		າ CDT etc)	
3	Session 3: June 11 th 8am NZST Industry implementation of genomic improvement in dairy goats using DNA sequencing			Presentation	20
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_	Industry implementation of genomic improvement in dairy goats using DNA sequencing Using sequence variants to better characterize a QTL region and improve the accuracy of genomic	Genomic S	Selection AgResearch, NZ GenPhySE, Université de Toulouse, INRAE,	Presentation	
3	Industry implementation of genomic improvement in dairy goats using DNA sequencing Using sequence variants to better characterize a QTL region and improve the accuracy of genomic evaluation in Saanen goats Accounting for genotype uncertainty of genotyping-by- sequencing data for genomic analyses in New Zealand dairy goats	Genomic s John McEwan Rachel Rupp Andrew Hess	Selection AgResearch, NZ GenPhySE, Université de Toulouse, INRAE, ENVT, France	Presentation Presentation Lightening	15
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3	Y-chromosomal haplotypes in domestic and wild goats reveal ancient paternal bottlenecks and recent introgressions	Hans Lenstra	Utrecht University, Netherlands	Presentation	15
3	Runs of homozygosity to unravel genetic changes associated with domestication and modern selection in goats	Christine Flury	School of Agricultural, Forest and Food Sciences, Bern University of Applied Sciences, Zollikofen, Switzerland.	Lightening talk	5
3	Molecular characterization of the Montecristo feral goats in the Mediterranean context	Elisa Somenzi	Università Cattolica del S. Cuore, Piacenza, Italy	Lightening talk	5
3	Goat genomes from earliest managed herds in the Zagros Mountains, <i>c</i> . 8,000 BC	Kevin Daly	Trinity College, Ireland	Lightening talk	5
3	Genomic analyses reveal the influence of geographic origin and signatures of selection in Boer goats from different countries	Khanyisile Hadebe	Discipline of Genetics, School of Life Sciences, University of KwaZulu-Natal, South Africa	Lightening talk	5
3	Genomic estimation of inbreeding and effective population size in three Czech goat populations	Vostrý Luboš	Czech University of Life Sciences, Czech Republic	Lightening talk	5
3	Whole-genome sequencing reveals selection signals among Chinese, Pakistani and Nepalese goats	Yefang Li	CAAS-ILRI Joint Laboratory on Livestock and Forage Genetic Resources, Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS), China	Lightening talk	5
3	Run of Homozygosis in the main historical lines of Spanish Merino Sheep	Gabriel Anaya	Departamento de Genética, University of Córdoba, Spain	Lightening talk	5