



第三届世界 绵羊大会 云会议

the Virtual 3rd World
Conference on Sheep

Oct. 16th-18th, 2020. Beijing

会议手册 Conference Manual



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会议日程 Conference Program

Day1 Online Conference

Friday, October 16, 2020

Chairs: Menghua Li

8:00-8:10 (GMT)	Opening welcome	Menghua Li	CAU
15:00-15:10 (BJS)			
8:10-8:20 (GMT)	Congratulatory letter from Chunli Bai (白春礼), the President of ANSO	Jinghua Cao	ANSO
15:10-15:20 (BJS)			
8:20-8:30 (GMT)	Welcome speech from the President of China Agricultural University	Qixin Sun	CAU
15:20-15:30 (BJS)			
8:30-8:40 (GMT)	Welcome speech from FAO, UN (联合国粮食及农业组织)	Paul	FAO
15:30-15:40 (BJS)		Boettcher	
8:40-8:50 (GMT)	Keynote speech: A Snap Shot at Alliance of International Science Organizations	Jinghua Cao	ANSO
15:40-15:50 (BJS)			

Session 1: Germplasm resources

Chairs: Jianlin Han & Hans Lenstra

Plenary talk

8:50-9:30 (GMT)	The state of global gene-banking of animal genetic resources	Paul	FAO,
15:50-16:30 (BJS)		Boettcher	Italy
9:30-10:10 (GMT)	Preliminary analysis of the molecular diversity of British sheep breeds: major types, origin and admixture	Hans Lenstra	UU,
16:30-17:10 (BJS)			Netherlands
10:10-10:20 (GMT)	Coffee time		
17:10-17:20 (BJS)			

Section talk

10:20-10:45 (GMT)	Synthesis of phenotypic and genomic architecture of indigenous African sheep genetic resources	Joram	ICARDA,
17:20-17:45 (BJS)		Mwacharo	Ethiopia
10:45-11:05 (GMT)	A genome-wide multidimensional selection signature analysis identifies novel genomic footprints for Merino-like phenotype in Italian sheep breeds	Elena Ciani	University of Bari, Italy
17:45-18:05 (BJS)			
11:05-11:30 (GMT)	Signatures of positive selection in several populations representing Balkan sheep	Ino Curik	University of Zagreb, Croatia
18:05-18:30 (BJS)			
11:30-12:30 (GMT)	Lunch break		
18:30-19:30 (BJS)			

Session 2: G3: genes, genomics and genetics

Chairs: Rui Su & Ino Curik

Plenary talk

12:30-13:10 (GMT)	Historical introgression from wild relatives enhanced	Menghua Li	CAU,
19:30-20:10 (BJS)	climatic adaptation and resistance to pneumonia in sheep		China

Section talk

13:10-13:35 (GMT)	Deep genome resequencing reveals artificial and natural	Weimin Wang	CAU,
20:10-20:35 (BJS)	selection for visual deterioration, plateau adaptability and high prolificacy in Chinese domestic sheep		China
13:35-14:00 (GMT)	Crossbred mapping populations as promising tool	Tatiana	L.K. Ernst Institute
20:35-21:00 (BJS)	to reveal functional candidate genes: a study case in Russian sheep breeding	Deniskova	of Animal Husbandry, Russia
14:00-14:25 (GMT)	Functional Genomics of early reproduction in domestic	Kisun Pokharel	Natural Resources
21:00-21:25 (BJS)	sheep		Research Center, Finland
14:25-14:50 (GMT)	Deciphering climate-mediated adaptation in European	Mario Barbato	Università Cattolica
21:25-21:50 (BJS)	sheep		del Sacro Cuore, Italy
14:50-15:00 (GMT)	Coffee time		
21:50-22:00 (BJS)			

Session 3: Ancient DNA

Chairs: Matthew Collins & Xingbo Zhao

Plenary talk

15:00-15:40 (GMT)	Reading beneath the lines:parchment as a sheep	Matthew	Cambridge University,
22:00-22:40 (BJS)	genetic resource	Teasdale	UK

Section talk

15:40-16:05 (GMT)	Retroviral insertions confirm the ancient origin of	Eve	Tartu University,
22:40-23:05 (BJS)	native sheep in Estonia and provide guidance for the conservation program	Rannamäe	Estonia
16:05-16:30 (GMT)	Insights into sheep demographic history by	Fusun Ozer	Hacettepe University
23:05-23:30 (BJS)	archaeogenetic analysis of Anatolian ancient sheep		Ankara, Turkey

Day2 Online Conference

Saturday, October 17, 2020

Session 4: Molecular breeding

Chairs: Lawrence Alderson & Caihong Wei

Plenary talk

8:00-8:40 (GMT)	The conservation of native and locally-adapted breeds:	Lawrence	Chairman of
15:00-15:40 (BJS)	their potential to contribute to genetic diversity and future systems of livestock production	Alderson	Countrywide Livestock, UK
8:40-9:20 (GMT)	Using genomic information in dairy sheep breeding in	Juan Jose	Universidad de Leon,
15:40-16:20 (BJS)	Spain	Arranz	Spain

Section talk

9:20-9:40 (GMT)	Sheep breeding in Gansu sheep breeder company Ltd,	David William	Australia
16:20-16:40 (BJS)	China	Osborn	
9:40-10:00 (GMT)	Feasibility of a genomic selection approach based on	Antonello Carta	GRIS Sardinia,
16:40-17:00 (BJS)	a female informative population in Sarda dairy sheep breed		Bonassai, Italy
10:00-10:10 (GMT)	Coffee time		
17:00-17:10 (BJS)			

Session 5: Nutrition and meat

Chairs: David Pethick & Hailing Luo

Plenary talk

10:10-10:50 (GMT)	The role of nutrition for meat quality of lamb	David Pethick	Murdock
17:10-17:50 (BJS)			University, Australia



Tatiana Deniskova

PhD in Biological Sciences (Genetics), senior Researcher, head of the group for molecular genetics and genomics of small ruminant, Department of Biotechnology and Molecular Diagnostics, L.K. Ernst Federal Science Center for Animal Husbandry, Moscow region, RUSSIA. Her research topics are diversity and phylogenetic of the domestic and wild small ruminants based on various methods (STR and SNP-markers, mtDNA). Currently I focus on functional genomics of sheep, including mapping of QTLs and candidate genes associated with fat deposition in the sheep tails as well as with body sizes and growth -relation traits, as well as on goat maternal origins.

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Crossbred mapping populations as promising tool to reveal functional candidate genes: a study case in Russian sheep breeding

Deniskova T., Petrov S., Sermiyagin A., Dotsev A., Bagirov V., Brem G. and Zinovieva N.
L.K. Ernst Federal Science Center for Animal Husbandry, Russia

Abstract

Successful implementation of genome editing technologies creates possibilities for target improving the economically important traits in livestock. Creating crossbred mapping populations by crossing farm animals with contrast variants of desired traits provides high significant data on revealing of candidate genes of interest to be rapidly introduced in animal populations by genome editing. Although Russia has rich resources of domestic sheep, there are no specialized locally adapted meat breeds were developed. To overcome this weakness of national sheep breeding, we established two crossbred mapping populations in our experimental farm. The first one is set up to address growth, carcass and meat quality traits and includes the progeny of fast-growing Katahdin meat breed and slow growing Romanov ewes. The second one comprises the offspring of fat-tailed Karachaev and thin-tailed Romanov breeds to identify candidate genes associated with fat deposition in the tails of local sheep. High-density SNP data were generated using Ovine Infinium HD SNP BeadChip. Phenotypic data including body weight, nine body measurements, and tail measurements, were recorded in the age of 6, 42, 90, 180, and 270 days. The first genome-wide association studies have resulted in identification of the genes, associated with skeletal muscle growth and meat quality related traits, and involved in carbohydrate and lipid metabolism. The detected genes can be introduced into the populations of well-adapted local sheep breeds to improve their growth, carcass and meat quality traits. Genotyping of backcrosses from Katahdin × Romanov population was financed by RFBR No. 17-29-08015. The Karachaev × Romanov progeny was studied within RSF No. 19-16-00070. The samples of Romanov ewes were genotyped within theme No. 0445-2019-0026.