



Avian Genetics and Genomics Workshop

Organised by a Standing Committee: YES NO

Meeting information

Date: 7/27/21

Time: 1:00 AM - 4:00 AM CDT

Number of participants: 86 simultaneous participants; 2019 in-person meeting numbers: 80

Chair

Name: Klaus Wimmers

Affiliation: Research Institute for Farm Animal Biology (FBN Dummerstorf), Germany

Contact email: wimmers@fbn-dummerstorf.de

Co-Chair (optional)

Name: Sue Lamont

Affiliation: Iowa State University, USA

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Agenda

1:00 AM	Introduction.
1:05 AM 85515	<p>Genetic diversity and population structure of Myanmar native chickens using double digest restriction-site associated DNA sequencing (ddRAD-seq). S.L.Y. Mon*¹, M. Lwin², A.A. Maw³, L.L. Htun³, S. Bawm³, K. Kawabe⁴, Y. Nagano^{5,1}, A.J. Nagano⁶, Y. Wada^{5,1}, S. Okamoto¹, and T. Shimogiri¹, ¹<i>The United Graduate School of Agricultural Sciences, Kagoshima University, Kagoshima, JAPAN</i>, ²<i>Livestock Breeding and Veterinary Department, Yangon, MYANMAR</i>, ³<i>University of Veterinary Science, Nay Pyi Taw, MYANMAR</i>, ⁴<i>Education Center, Kagoshima University, Kagoshima, JAPAN</i>, ⁵<i>Faculty of Agriculture, Saga University, Saga, JAPAN</i>, ⁶<i>Faculty of Agriculture, Ryukoku University, Otsu, Shiga, JAPAN</i>.</p>
1:20 AM 85520	<p>Taxonomy Classification of Nigerian Local Turkey Using 12S mitochondrial rRNA gene. Demilade I Ibiwoye*^{1,2}, Foluke E Sola-Ojo¹, David O Aremu¹, Ibraheem A Abubakar¹, Nusrah B Afolabi-Balogun³, Charles A Adeniyi⁴, and Azeezat O Oni³, ¹<i>Univeristy of Ilorin, Ilorin, Kwara, Nigeria</i>, ²<i>Huazhong Agricultural University, Wuhan, China</i>, ³<i>Fountain University, Osogbo, Osun, Nigeria</i>, ⁴<i>Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan, China</i>.</p>
1:35 AM 85517	<p>Transcriptomic analysis of the <i>Musculus complexus</i> in naked neck broiler chickens. A C Mott*, C Blaschka, A Mott, A R Sharifi, and J Tetens, <i>Georg-August University, Göttingen, Lower Saxony, Germany</i>.</p>
1:50 AM 85522	<p>Study on differentially expressed genes in granular layer and theca layer of laying Silky Fowl and White Leghorn. Yurong Tai*¹, Xue Yang¹, Deping Han², and Xuemei Deng¹, ¹<i>China Agricultural University, lab of animal genetic resource and molecular breeding, Beijing, China</i>, ²<i>College of Veterinary Medicine, China Agricultural University, Beijing, China</i>.</p>
2:05 AM	Break.
2:15 AM 85516	<p>Hypothalamic and Ovarian Transcriptome Profiling Reveals Potential Candidate Genes in Low and High Egg Production of White Muscovy Ducks (<i>Cairina Moschata</i>). S. BELLO*, H. Xu, and Q Nie, <i>SOUTH CHINA AGRICULTURAL UNIVERSITY, GUANGZHOU, GUANGDONG, CHINA</i>.</p>

2:30 AM 85518	<p>nf-iseq pipeline provides a first insight onto chicken transcripts landscape. S GUIZARD*, J SMITH, R KUO, K MIEDZINSKA, J SMITH, M DAVEY, and M WATSON, <i>The Roslin Institute, Edinburg, Scotland.</i></p>
2:45 AM 85523	<p>A new chromosome level turkey genome. C. P. Barros*¹, M. F. L. Derks¹, J. Mohr², B.J. Wood^{2,3}, M.C.A.M. Bink⁴, and M. A. M. Groenen¹, <i>¹Wageningen University and Research, Wageningen, Netherlands, ²Hybrid Turkeys, Kitchener, ON, Canada, ³School of Veterinary Science, University of Queensland, Gatton, QLD, Australia, ⁴Hendrix Genetics Research, Technology & Services, Boxmeer, Netherlands.</i></p>
3:00 AM 85521	<p>Bridge 60k SNP panel for the chicken genome-wide study. Dongwon Seo*^{1,2}, Sunghyun Cho¹, Doohe Lee¹, Minjun Kim¹, Prabuddha Manjula¹, JeongWeon Shin¹, Dajeong Lim³, Hyojun Choo⁴, Jaebeom Cha⁴, Kigon Kim⁴, Ik-Soo Jeon⁴, Kyung-Tai Lee³, ByoungHo Park⁴, Seung Hwan Lee^{1,2}, Jun Heon Lee^{1,2}, <i>¹Division of Animal and Dairy Science, Chungnam National University, Daejeon, South Korea, ²Department of Bio-AI Convergence, Chungnam National University, Daejeon, South Korea, ³Animal Genomics and Bioinformatics Division, National Institute of Animal Science, RDA, Wanju, South Korea, ⁴Poultry Research Institute, National Institute of Animal Science, RDA, Pyeongchang, South Korea.</i></p>
3:15 AM 85519	<p>Genomic signatures of selection for egg production rate using whole genome sequence in Hinaidori chickens. Tatsuhiko Goto*¹, Shiori Fukuda², Kazuhiro Rikimaru², Raman Akinyanju Lawal³, John Pool⁴, and Olivier Hanotte^{5,6}, <i>¹Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Japan, ²Akita Prefectural Livestock Experiment Station, Akita, Japan, ³The Jackson Laboratory, Bar Harbor, USA, ⁴University of Wisconsin-Madison, Madison, USA, ⁵University of Nottingham, Nottingham, UK, ⁶International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia.</i></p>
3:30 AM 85524	<p>Dissecting the polygenic genetic architecture of growth using genotyping by low-coverage sequencing in a deep intercross of the Virginia body weight lines: novel loci revealed by increased power and improved genome-coverage. T Rönneburg*¹, Y Zan^{2,1}, CF Honaker³, PB Siegel³, and Ö Carlborg¹, <i>¹Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden, ²Umeå Plant Science Centre, Department of Forest Genetics and Plant Physiology, Swedish University of Agricultural Science, Umeå, Sweden, ³Department of Animal and Poultry Sciences, Virginia Polytechnic Institute and State University, Blacksburg, VA, USA.</i></p>
3:45 AM	<p>Workshop Business Meeting.</p>

Summary of the meeting

The workshop included ten presentations. The presentations were selected from 29 abstracts submitted for the Avian Genetics and Genomics Section and 10 abstracts that were poultry related but submitted for other sections of the ISAG conference. The selection was based on the rank sum of the individual evaluations by the Standing Committee members and consideration of the different poultry species (chicken, turkey, duck), institutions and geographical locations (all continents). The presentations were organised by topics: Biodiversity/genetic resources; Transcriptomics related to phenotypes; Methods/tools for genome analyses and annotation; Genomics related to QTL. All presentations were pre-recorded and uploaded. They received a lot of interest and were discussed afterwards.

Following the workshop, a business meeting was held. The Standing Committee consisted of six members, two of whom are completing their first term and the other four are in the middle of their second term. Thirteen people participated in the election of Standing Committee members. One member was unanimously re-elected for a second term, the other member did not stand for a second term and stepped down as Chair of the Standing Committee as he/she was running for another position in the Society. Two new representatives to the Standing Committee were nominated and unanimously elected.

The Standing Committee now consists of seven members.

- Susan Lamont (co-chair), Iowa State University, USA
ISAG2014-2023, 2nd term
- Xiaoxiang Hu, China Agricultural University, Beijing, China
ISAG2014-2023, 2nd term
- Svetlana Galkina, Biological Faculty of Saint-Petersburg State University, Russia
ISAG2017-2021, 1st term, re-elected for 2nd term 2021-2025
- Min-Cheng Peng, Chinese Academy of Sciences, Kunming 650223, China
ISAG2019-2023, 1st term
- Adeyinka Abiola Adetula, Chinese Academy of Agricultural Sciences, Shenzhen, China
ISAG2019-2023, 1st term
- Ibiwoye Demilade Israel, Huazhong Agricultural University, China
ISAG2021-2025, 1st term
- Jun Heon Lee, Chungnam National University, Korea
ISAG2021-2025, 1st term
- Klaus Wimmers (chair), Research Institute for Farm Animal Biology (FBN Dummerdorf), Germany
ISAG2017-2021, 1st term, leaving committee

The participants were asked to raise further issues; however, no further discussion was held.

New Committee chair – n.n.



INTERNATIONAL SOCIETY FOR ANIMAL GENETICS

New Committee members – Jun Heon Lee, Ibiwoye Demilade Israel

COMPARISON TEST (2020-2021) ~~YES~~ NO

SIGNATURES

Klaus Winum

Chair K. W