



# ISAG

## CONFERENCE 2017, Dublin, Ireland

### Title of Workshop

STANDING COMMITTEES / WORKSHOPS      Information will be posted online

Organised by a standing committee      yes

Date and meeting time:  
July 18, 2017 from 9:00 till 13:00

Chair, name and contact email:

Richard Crooijmans,  
[richard.crooijmans@wur.nl](mailto:richard.crooijmans@wur.nl)

#### Agenda / programme attached

09:00 Introduction.

Richard Crooijmans, Wageningen University & Research.

09:05 42 The evolving chicken genome reference.

**W. Warren**<sup>\*1</sup>, L. Hillier<sup>1</sup>, C. Tomlinson<sup>1</sup>, P. Minx<sup>1</sup>, M. Kremitski<sup>1</sup>, T. Graves<sup>1</sup>, S. Sullivan<sup>2</sup>, I. Liachko<sup>2</sup>, M. Delaney<sup>3</sup>, J. Fulton<sup>4</sup>, M. Abrahamsen<sup>5</sup>, R. Hawken<sup>5</sup>, M. Miller<sup>6</sup>, and H. Cheng<sup>7</sup>, <sup>1</sup>Washington University School of Medicine, St Louis, MO, USA; <sup>2</sup>Phase Genomics Inc, Seattle, WA, USA; <sup>3</sup>University of California-Davis, Davis, CA, USA; <sup>4</sup>Hy-Line International, Dallas Center, IA, USA; <sup>5</sup>Cobb-Vantress Inc, Siloam Springs, AR, USA; <sup>6</sup>Beckman Research Institute, Duarte, CA, USA; <sup>7</sup>USDA-ARS, East Lansing, MI, USA.

09:25 43 Low number of mitochondrial DNA sequences inserted into the turkey (*Meleagris gallopavo*) nuclear genome:

implications for evolutionary inferences.

G. Schiavo<sup>1</sup>, M. G. Strillacci<sup>2</sup>, S. Bovo<sup>1,3</sup>, A. Ribani<sup>1</sup>, S. I. Roman-Ponce<sup>4</sup>, S. Cerolini<sup>2</sup>, F. Bertolini<sup>1,5</sup>, A. Bagnato<sup>2</sup>, and **L. Fontanesi**<sup>\*1</sup>, <sup>1</sup>Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy; <sup>2</sup>Department of Veterinary Medicine, University of Milan, Milano, Italy; <sup>3</sup>Biocomputing Group, Department of Biological, Geological, and Environmental Sciences, University of Bologna, Bologna, Italy; <sup>4</sup>Centro Nacional de Investigación en Fisiología y Mejoramiento Animal, Instituto Nacional de Investigaciones Forestales, Agrícola y Pecuarias (INIFAP), Col. Centro Veracruz, Mexico; <sup>5</sup>Department of Animal Science, Iowa State University, Ames, IA, USA.

09:40 44 *In situ* and *in silico* improvement of the Japanese quail genome assembly.

**S. Galkina**<sup>\*1</sup>, M. Kulak<sup>1</sup>, A. Saifitdinova<sup>1</sup>, A. Komissarov<sup>1</sup>, A. Dyomin<sup>1</sup>, V. Volodkina<sup>1</sup>, J. Damas<sup>2</sup>, M. Farre<sup>2</sup>, D. Griffin<sup>3</sup>, D. Larkin<sup>2</sup>, and E. Gaginskaya<sup>1</sup>, <sup>1</sup>Saint-Petersburg State University, Saint-Petersburg, Russia; <sup>2</sup>Royal Veterinary College, University of London, London, UK; <sup>3</sup>University of Kent, Kent, UK.

09:55 45 The broiler chicken transcriptome.

**C. Schmidt**<sup>\*1</sup> and S. Lamont<sup>2</sup>, <sup>1</sup>University of Delaware, Newark, DE, USA, <sup>2</sup>Iowa State University, Ames, IA, USA.

10:15 46 The not-so-missing genes in birds.

**T. Hron**<sup>\*</sup>, H. Farkasova, P. Pajer, J. Paces, P. Bartunek, and D. Elleder, Institute of Molecular Genetics of the AV CR, v.v.i., Videnská, Prague, Czech Republic.

**10:30 49 Evaluation of semen characteristic of the high and low sperm motility groups in two different strains of chicken.**

M. Farahi, A. A. Masoudi\*, and A. Ehsani, *Tarbiat Modares University, Tehran, Tehran, Iran.*

**10:45 51 Goose transcriptome provides insights into novel mechanisms of adipogenesis.**

G. Wang<sup>\*2,1</sup>, Y. Liu<sub>1</sub>, L. Jin<sub>1</sub>, D. Shang<sub>1</sub>, C. Gill<sub>2</sub>, M. Li<sub>1</sub>, and J. Wang<sub>1</sub>, <sup>1</sup>Sichuan Agricultural University, Chengdu, Sichuan, China; <sup>2</sup>Texas A&M University, College Station, TX, USA.

Coffee/Tea break Atrium, O'Brien Science Building 11:00 – 11:30

**11:30 52 Integrating genome and transcriptome profiling for dissection of the mechanism of muscle growth and lipid deposition in ducks.**

L. Wang\*, X. Li, J. Ma, Y. Zhang, and H. Zhang, *Lab of Animal Genetic Resource and Molecular Breeding, China Agricultural University, Beijing, China.*

**11:45 53 Liver and whole blood transcriptome response to chronic heat exposure in laying hens.**

F. Jehl<sub>1</sub>, A. Rau<sub>1</sub>, C. Désert<sub>2,3</sub>, M. Boutin<sub>2,3</sub>, K. Muret<sub>2,3</sub>, S. Leroux<sub>4</sub>, D. Esquerré<sub>5</sub>, C. Klopp<sub>6</sub>, D. Gourichon<sub>7</sub>, F. Pitel<sub>4</sub>, A. Collin<sub>8</sub>, S. Lagarrigue<sub>2,3</sub>, and T. Zerjal<sup>\*1</sup>, <sup>1</sup>GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France; <sup>2</sup>INRA, UMR1348 Physiologie, Environnement et Génétique pour l'Animal et les Systèmes d'élevage, Saint-Gilles, France; <sup>3</sup>Agrocampus-Ouest, UMR1348, Rennes, France; <sup>4</sup>UMR INRA/INPT ENSAT/INPT ENVIT-GenPhySE, Castanet Tolosan, France; <sup>5</sup>INRA, Plateforme GENOTOUL, Castanet-Tolosan, France; <sup>6</sup>INRA, SIGENAE, Castanet-Tolosan, France; <sup>7</sup>INRA-PEAT, Nouzilly, France; <sup>8</sup>URA, INRA, Nouzilly, France.

**12:00 54 Mapping QTLs affecting Marek's disease by selective DNA pooling in eight lines across 15 generations.**

E. Lipkin<sup>\*1</sup>, J. Smith<sub>2</sub>, D. Burt<sub>2</sub>, M. Soller<sub>1</sub>, and J. Fulton<sub>3</sub>, <sup>1</sup>Dept. of Genetics, Silberman Life Sciences Institute, The Hebrew University of Jerusalem, Jerusalem, Israel; <sup>2</sup>The Roslin Institute and Royal (Dick) School of Veterinary Studies, The University of Edinburgh, Easter Bush, Midlothian, UK; <sup>3</sup>Hy-Line International, Dallas Center, IA, USA.

**12:15 55 Genome-wide association study of complex traits in response to Newcastle disease virus in chickens.**

K. Rowland<sup>\*1</sup>, H. Zhou<sub>2</sub>, R. Gallardo<sub>3</sub>, T. Kelly<sub>2,3</sub>, A. Wolc<sub>1,4</sub>, and S. J. Lamont<sub>1</sub>, <sup>1</sup>Iowa State University, Department of Animal Science, Ames, IA, USA; <sup>2</sup>University of California-Davis, Department of Animal Science, Davis, CA, USA; <sup>3</sup>University of California-Davis, School of Veterinary Medicine, Davis, CA, USA; <sup>4</sup>Hy-Line International, Dallas Center, IA, USA.

**12:30 Concluding Remarks.**

Richard Crooijmans, Wageningen University & Research.

**12:35 Workshop Business Meeting.**

**13:00 Meeting ends.**

**Number of participants at meeting:**

**60**

## **Summary of the meeting** including votes, decisions taken and plans for future conferences

In total 11 abstracts have been selected for an oral presentation where only one author was not able to present and no invited speaker was invited for this workshop. There were two larger presentations one on improving the chicken genome and one on chicken transcriptome. The program was based on the following topics:

1. Improving genotypes (chicken, Quail Turkey)
2. Avian transcriptome
3. Use of transcriptome to study traits (adipogenesis, muscle growth and fat deposition and heat stress)
4. QTL and Whole Genome Association of disease traits (Marek and new Castle disease)

The standing committee Avian genetics and Genomics for the next meeting was discussed. Dr. Swetlana Galkina and dr. Klaus Wimmers were included in the standing committee for the ISAG 2019 meeting. Prof dr. Martien Groenen , dr. Alain Vignal, prof dr. Ning Li and Richard Crooijmans will redraw as members where Susan Lamont and Xiaoxiang Hu can be re-elected for another four years at the ISAG 2019. Richard Crooijmans will be chair at the ISAG2019 meeting.

### **Committee members** (the new committee)

Chair	term of service	E mail address:
Richard Crooijmans	ISAG 2014-2019	richard.crooijmans@wur.nl
Other members	term of service	E mail address:
Alain Vignal	ISAG2014-2019	alain.vignal@toulouse.inra.fr
Martien Groenen	ISAG2014-2019	martien.groenen@wur.nl
Susan Lamont	ISAG2014-2019	sjlamont@iastate.edu
Ning Li	ISAG2014-2019	ninglcau@cau.edu.cn
Xiaoxiang Hu	ISAG2014-2019	<a href="mailto:huxx@cau.edu.cn">huxx@cau.edu.cn</a>
Swetlana Galina	ISAG2017-2021	svetlana.galkina@mail.ru
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