

Acknowledgement

- USDA-NIFA FAANG conference grant (H. Zhou et al.)
 - Partial support for the invited speakers, students, postdocs for FAANG and Animal Epigenetics Workshops
- NSF Research Coordination Network grant (Schmidt and McCarthy)
 - Partial support for the students, postdocs for FAANG Workshop
- Genome Canada, Affymetrix and GeneSeek.
 - Support for refreshment



Functional Annotation of Farm Animals Initiative

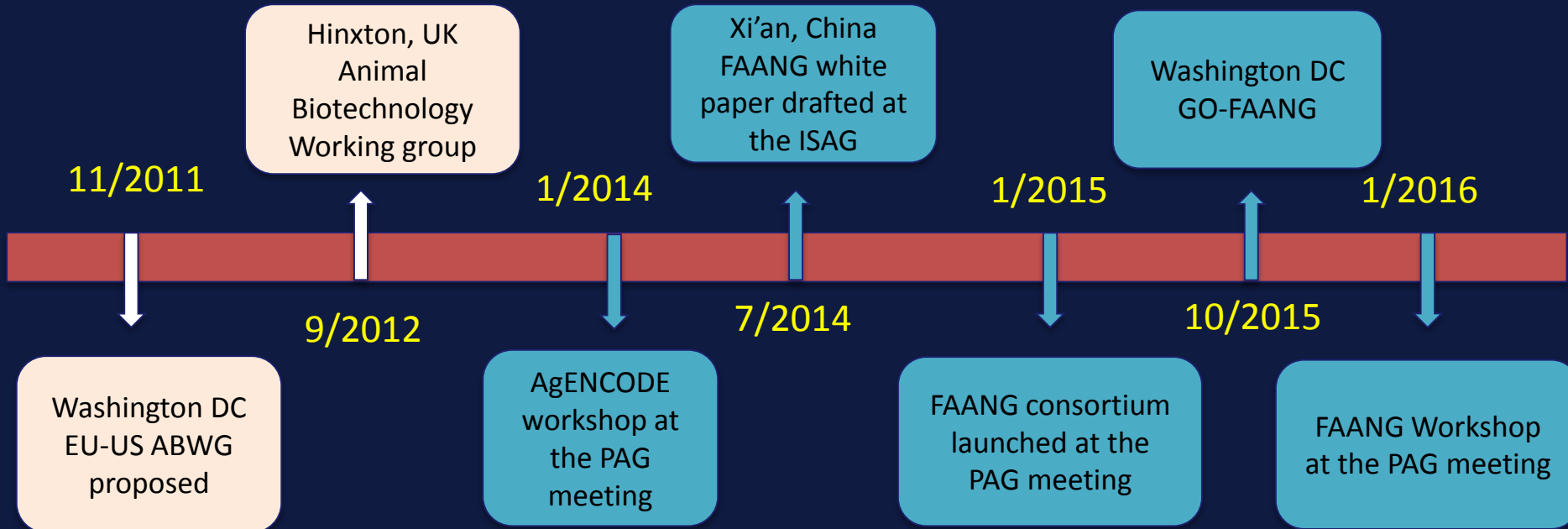
FAANG Workshop

January 12, 2016

**Huaijun Zhou, Pablo Ross, Chris Tuggle, Elisabetta Giuffra, Laura Clarke, Hans Cheng,
Graham Plastow**

**Department of Animal Science, UC Davis
Department of Animal Science, Iowa State University
INRA
EBI
ADOL, USDA ARS
University of Alberta**

FAANG Consortium Roadmap (\$\$\$???)



Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project

Genome Biology 2015, 16:57 doi:10.1186/s13059-015-0622-4

Open Access Paper

> 5,559 views since March 25th

Why is FAANG important?

- Understanding the genotype to phenotype link
- Refining Genomic Selection for genetic improvement
- Improving fundamental understanding of biology

Goal of Workshop

- Promote information exchanges regarding recent FAANG efforts worldwide
- Provide a great forum for the FAANG community to communicate and foster the interactions and collaborations
- Provide support for next generation scientists such as graduate students and postdoctoral fellow to have opportunities to interact and gain novel knowledge and technology from peer scientists from the meeting.

Agenda

- Brief introduction: **Huaijun Zhou** and Chris Tuggle
- Brief Introduction of RCN: **Fiona McCarthy**
- Progress report for each subcommittee
 - Metadata and Data Sharing Committee report: **Laura Clarke**
 - Animals, Samples, and Assay Committee report: **Elisabetta Giuffra** and Huaijun Zhou
 - DNase-seq and ChIP-seq analysis of farm animal tissues: **Pablo Ross**
 - Measuring Chromatin Accessibility using ATAC-seq: preliminary results on porcine tissues/cells: **Kylie Munyard**
 - Functional annotation of livestock genomes using Hi-C: preliminary results on porcine tissues/cells: **Herve Acloque**
 - Bioinformatics and Data Analysis Committee report: **James Reecy** and Mick Watson
 - RNA working group: **Lel Eory**
 - Methylation Working group: **Ole Madsen**
 - Structural working group: **Sylvain Foissac**
 - ChIP-seq working group: **Pablo Ross**
- Progress report on FAANG associated projects
 - WUR-pigENCODE: **Martien Groenen**
 - Canada and FAANG: **Graham Plastow**
 - Strategy to identify regulatory mutations affecting complex traits: **Ben Hayes**
 - Equine FAANG: **Carrie Finno**
- Group discussion: **Graham Plastow, Elisabetta Giuffra, Pablo Ross and Huaijun Zhou**