Danang Crysnanto

08.01.1992
Citizen of Indonesia

Hoffeld 24 8057 Zurich
danangcrysnanto@gmail.com

Education

ETH Zurich	Dec 2017 – Present
Doctoral in Animal Genomics	*Zurich, Switzerland*
The University of Edinburgh	Aug 2016 – Aug 2017
*Msc in Quantitative Genetics and Genome Analysis with **Distinction***	*Edinburgh, UK*
Bandung Institute of Technology	Oct 2010 – Oct 2014
*Bsc in Biology (Genetics) with **Cum Laude***	*Bandung, Indonesia*

Publications

First-author publications

1. **Crysnanto D.**, A. S. Leonard, Z. H. Fang, and H. Pausch, 2021. Novel functional sequences uncovered through a bovine multi-assembly graph. Accepted *Proceedings of the National Academy of Sciences USA*

2. **Crysnanto D.**, and H. Pausch, 2020. Bovine breed-specific augmented reference graphs facilitate accurate sequence read mapping and unbiased variant discovery. *Genome Biology*. 21:184

3. **Crysnanto D.**, C. Wurmser, and H. Pausch, 2019. Accurate sequence variant genotyping in cattle using variation-aware genome graphs. *Genetics Selection Evolution* 51:21

4. **Crysnanto D.**, and D. J. Obbard, 2019 Widespread gene duplication and adaptive evolution in the RNA interference pathways of the *Drosophila obscura* group. *BMC Evolutionary Biology* 19:1

Co-author publications

5. Nosková A., M. Bhati, N. K. Kadri, and **D. Crysnanto** et al., 2021 Characterization of a haplotype-reference panel for genotyping by low-pass sequencing in Swiss Large White pigs. *BMC Genomics* 22(290): 1–14

6. Nosková A., C. Wurmser, **D. Crysnanto**, A. Sironen, P. Uimari, et al., 2020 Deletion of porcine BOLL is associated with defective acrosomes and subfertility in Yorkshire boars. *Animal Genetics* 51: 945–949

7. Fang Z. H., A. Nosková, **D. Crysnanto**, S. Neuenschwander, P. Vögeli, et al., 2020 A 63-bp insertion in exon 2 of the porcine KIF21A gene is associated with arthrogryposis multiplex congenita. *Animal Genetics* 51: 820–823

8. Hiltpold M., G. Niu, N. K. Kadri, **D. Crysnanto**, Z. H. Fang, et al., 2020 Activation of cryptic splicing in bovine WDR19 is associated with reduced semen quality and male fertility. *PLoS Genetics*. 16: 1–27

9. Bhati M., N. K. Kadri, **D. Crysnanto**, and H. Pausch, 2020 Assessing genomic diversity and signatures of selection in Original Braunvieh cattle using whole-genome sequencing data. *BMC Genomics* 21(27):1-14

Invited Talks

CIGENE Seminar Series	March 2021
Talk title: Bovine pangenomics	*NMBU Norway*
International Virtual Animal Breeding Journal Club	Sept 2020
Talk title: Bovine pangenomics	*USDA USA*
Plant and Animal Genome Conference (PAG)	Jan 2020
Talk title: Bovine pangenome graph enables unbiased genetic variants discovery	*San Diego USA*
Livestock Genomics session - Genome Informatics	Sept 2018
Talk title: Development of graph-based genotyping pipelines for bovine whole-genome data	*Cambridge UK*
Population Genetics (PopGroup) Conference	Jan 2018
Talk title: Widespread gene duplications in *Drosophila* immune system pathways	*Oxford UK*

Awards

Sir Kenneth Mather Memorial Prize   Jan 2018
Annual award for a MSc or PhD student of any UK University or Research Institutions
which shown an outstanding performance in the area of quantitative and population genetics.   *The Genetics Society*

The Douglas Falcone Prize   Oct 2017
Annual award for the best master's thesis in Quantitative Genetics and Genome Analysis   *The University of Edinburgh*

Bronze Medalist 21st International Biology Olympiad   Aug 2010
Winning a medal on a highly prestigious International bioscience Olympiad   *International Biology Olympiad*

Technical Skills, Language Skills, and Interests

Programming Languages: Python, R, Linux/Unix
Data Science: R Tidyverse, Python Data Science (Numpy, Pandas, Jupyter)
Interactive data visualization: Shiny, Flask
Computational pipelines: Snakemake
Reproducible data analysis: Git, Docker
Others: Affinity Designer, Microsoft Office, LaTeX, vim, vscode
Languages: Indonesian (native), German (A2), English
Interests: Landscape Photography