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* 1–30
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(1)

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*