

Session 5: Analysis of large datasets

08.40 *Robust alternatives to best linear unbiased prediction of complex traits.* Professor Daniel Gianola, University of Wisconsin-Madison, USA

09.05 *Efficient multi-trait SNP models for prediction of genomic breeding values.* Senior Scientist Luc Janss, QGG-AU

09.25 **Speed talks:**

- *Accounting for genetic architectures of traits in multi-trait genomic prediction using GBLUP.* PhD Student Emre Karaman, QGG-AU
- *Multi-trait genomic prediction in small-scale recorded traits using correlation at genomic segments with large-scale recorded traits.* PhD Student Grum Gebreyesus, QGG-AU
- *APY in software DMU.* Postdoc Viktor Milkevych, QGG-AU
- *An overview of REML estimation of variance components: flaws and solutions.* Postdoc Beatriz Castro Dias Cuyabano, QGG-AU
- *Integrating metabolomics and genomics.* Adjunkt Pernille Sarup, QGG-AU.