Infomation on invited speakers:

1. **Fred van Eeuwijk**, Department of Plant Sciences, Wageningen University&Research, Wageningen, Netherlands

   Fred van Eeuwijk is professor in Applied Statistics at Wageningen University. He published more than 120 papers on his major research interests that include statistical genetics, genotype-to-phenotype models, statistical modeling of genotype by environment interactions, quantitative trait locus (QTL) mapping, and association mapping (QTLxE, multiple traits), genomic prediction and data integration (phenotype, genetics, -omics). He is currently president of Netherlands Society for Statistics and Operational Research (VVSOR) and editor of the journal Genetics. He was president Scientific Committee for the 28th International Biometric Conference, Victoria, Canada, July 2016.

2. **Ian Mackay**, IMplant Consultancy, Chelmsford, United Kingdom

   My principal research interest is quantitative genetics and plant breeding. I have published in areas covering experimental design, selection methods, improved approaches to trait mapping, and genomic selection. In December 2017, I established IMplant Consultancy Ltd., consulting in quantitative genetics and breeding. Before this, I worked at the plant science organization NIAB (Cambridge, UK) for 12 years, I ran the Statistical Genetics department of drug discovery company Oxagen Ltd. for six years and I worked as a commercial plant breeder for 19, including nine as cofounder and research director of the company Lion Seeds Ltd.

3. **Marcos Malosetti**, Department of Plant Sciences, Wageningen University&Research, Wageningen, Netherlands

   I am staff member of the Applied Statistics and Mathematics Group of Wageningen University and Research. Agronomist by training (Uruguay), I developed an interest in the application of quantitative methods in biology, particularly in plants. My focus is on statistical modelling of variation of complex traits and its interaction with the environment (genotype by environment interaction). The challenge is to develop sound statistical models that are useful to predict responses, and so, of practical use to intervene in a particular biological system. Methods are good if they can move from the lab to applications, so I dedicate an important part of my effort to disseminate the methods via internal and external courses, and also by being part of a team developing software to deploy the methods. From October 1st 2018, I will start working at Nunhems (www.nunhems.com).