**ALA4.1 Development of simulated QTL mapping populations**

**Prerequisites**

Basic understanding of simulation modeling and simulation in plant breeding; It would be desirable, if students have attended the Quantitative Methods (experimental design, field data analysis) and the Quantitative Genetics course, in particular the eModule on Quantitative Genetic Models.

**Purpose**

Reinforce the ability to use simulation to ask genetic questions.

**Background**

Simulation in plant genetics and plant breeding is useful to determine limitations of methods to be used and to help design experiments. Here, we will prepare mapping populations, which can be used to practice QTL mapping in eModule 5. This will be useful to determine the impact of type of population, trait architecture, marker density, population size, heritability, among others, on the power / ability of QTL detection.

**Tasks**

The main purpose is, to get familiar with data simulation. An important task of this exercise is, to establish the data needed for a QTL mapping analysis of grain yield by simulation. Two different types of populations will be used, a F2 and a DH population (N=200 each). For field testing of the F2 population, F2 individuals will be represented by F2:3 individuals. Both populations are tracing back to the same original cross. In other words, the trait architecture is identical in both mapping populations. Both populations will be evaluated in three environments. There are significant G x E interactions. The species studied here has 5 chromosomes of 100 cM length each. Dominant marker costs are low, the mapping individuals will be mapped with markers in 1 cM spacing. Six QTL control this trait. Two QTL are linked in coupling, two in repulsion. The remaining two QTL are unlinked and located on different chromosomes than the two linked QTL pairs.

1. Describe input parameters of genetic architecture that you chose based on the constraints above, such as QTL location, effect.
2. Create a simulated DH population evaluated in 3 environments, using the above mentioned conditions.
3. Create a simulated F2:3 population evaluated in 3 environments, using the above mentioned conditions.
4. Do a proper field data analysis, as learned in Quantitative Methods, and present key phenotypic data for both populations, including means across and for individual environments, variance components (G, E, GxE), heritability estimates.

**Tentative answers** (can differ, based on context / assumptions made)