**Meeting with Annaliese, 22-02-22**

* What is this paper supposed to cover? Research questions from your excel sheets:
  + parent/progeny comparisons,
  + species comparisons and
  + second level analyses for similarity of trends.
* What are the most relevant growth and fertility parameters from this data set (manual measurements)?
  + Fiona will provide seeds/10 pods and total seeds/plant data soon
  + Relevant growth and fertility parameters => check paper (Mason: Agricultural selection and presence–absence variation in spring-type canola germplasm => effects of polyploidy and hybridization on these traits?)
  + To get all the parameters proposed in the proposal, imaging data have to be integrated
  + Henrik will send list of agronomically important traits
  + Best parameters:
    - Height, biomass, growth rate, seeds/pod, seeds/plant, days to flowering
    - Best fertility parameter: seeds/pod. But no heterosis effect on this trait expected.
    - Plant height/biomass: heterosis effect expected
  + Check Danis photos to know differences in phenotypes, particularly of the hexaploids
* Done up to now: Boxplots, descriptive statistics, ANOVAs and ANOVAs for randomized block design for comparisons 1 and 2 (A-Y). How to deal with non-normal distributions?
  + No worries
  + But if we are talking about significance, we need to perform a Kruskal-Wallis-Test
    - Der Kruskal-Wallis-Test (nach William Kruskal und Wilson Allen Wallis; auch H-Test) ist ein parameterfreier statistischer Test, mit dem im Rahmen einer Varianzanalyse getestet wird, ob unabhängige Stichproben (Gruppen oder Messreihen) hinsichtlich einer ordinalskalierten Variable einer gemeinsamen Population entstammen.
  + Some traits are not normally distributed => google
    - Examples
      * Seed set (many sterile plants)
      * Flower colour
    - Quantitative genetic effect
* Next steps: Similar tends between comparison groups for specific traits (second level analysis)?
  + Heat map: Difference parent mean vs. progeny => transgressive segregation? (most interesting phenomenon)
  + Less important: maternal effects = heat map with maternal genotypes as references => differences mother vs progeny
    - Mother = first genotype in table? Check Danis list (email)
  + Check correlation between traits
  + Do PCA for traits
* What are we going to show in the paper: first or second level analyses?
  + Mostly second level analyses
  + First level only examples, eg 5 out of 20 traits show transgressive segregation (write in text, no figure)
* Developmental data: day at which BBCH51 (flower buds visible from above) and BBCH61 (10% of flowers on the main raceme open) have been reached?
* Any joint analysis with imaging data planned or is that going to be a separate paper?
  + Aberystwith prefers to get all the data together first and then decide about den publications
  + We are possibly going to integrate field data from Bonn => discuss with Henrik