Hi Helen

PH04 and PH05 didn’t like growing in our glasshouse! They are cauliflower genotypes and were extremely late developing their flower buds, but they then failed to open their flower buds which of course means no pods or seed data. There will be image analysis data for the rosette growth available for these plants once Kevin completes that.

Thanks

Fiona

Dr Fiona  M K Corke

Smarthouse Manager

National Plant Phenomics Centre,

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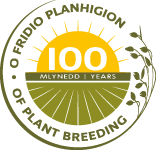
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**From:** [hbehn@uni-bonn.de](mailto:hbehn@uni-bonn.de) <[hbehn@uni-bonn.de](mailto:hbehn@uni-bonn.de)>   
**Sent:** 17 February 2022 15:01  
**To:** Fiona Corke [fic5] (Staff) <[fic5@aber.ac.uk](mailto:fic5@aber.ac.uk)>  
**Subject:** AW: Comparisons for Brassica genotypes EPPN2020 project

[RHYBUDD! E-BOST ALLANOL / CAUTION! EXTERNAL E-MAIL]

Hi Fiona,

what is the reason that PH04 and PH05 are missing in the data table? Maybe I’ve missed that.

All the best

Helen

**Von:** Fiona Corke [fic5] (Staff) <[fic5@aber.ac.uk](mailto:fic5@aber.ac.uk)>   
**Gesendet:** Mittwoch, 16. Februar 2022 15:17  
**An:** [hbehn@uni-bonn.de](mailto:hbehn@uni-bonn.de)  
**Betreff:** RE: Comparisons for Brassica genotypes EPPN2020 project

Hi Helen

You spotted my ‘click and drag’ Excel mistake, the barcode is correct and the genotype code is wrong.

Yes only 3 plants of PH 15 and 7 of PH28

Pod 1 refers to the pod number on branch 1. Pods on individual branches were only counted on the 4 reps that were dismantled for detailed photography at harvest.

Thanks

Fiona

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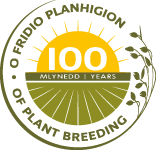
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**From:** [hbehn@uni-bonn.de](mailto:hbehn@uni-bonn.de) <[hbehn@uni-bonn.de](mailto:hbehn@uni-bonn.de)>   
**Sent:** 16 February 2022 11:16  
**To:** Fiona Corke [fic5] (Staff) <[fic5@aber.ac.uk](mailto:fic5@aber.ac.uk)>  
**Subject:** AW: Comparisons for Brassica genotypes EPPN2020 project

[RHYBUDD! E-BOST ALLANOL / CAUTION! EXTERNAL E-MAIL]

Hi Fiona,

I have one more question related to the data sheet `harvest all´: Were there only 7 plants of PH01 and 9 plants of PH02 (see screenshot)? Or were there 8 of both and the genotype code in the table is wrong?

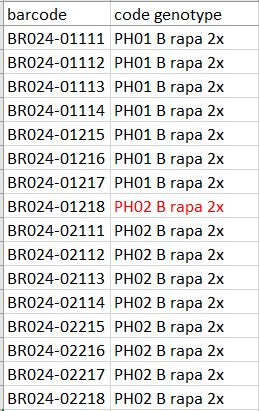
There were only three plants of PH15 (all of them grown in location 1, so no blocking) and seven plants of PH28, right? Ok, I think that’s clear.

Does `pod 1 (2, 3, 4, …)´ mean number of pods on branch 1 (2, 3, 4, …)?

Thanks a lot!

Best wishes

Helen



Hi Helen

A block is one replicate of all genotypes, so 49 plants. It seems to be the best way to handle randomisation when the plants are arranged in long lines rather than on benches.

Yes 49 genotypes in total

BBCH can be applied to all species as it describes a developmental stage which is common to all the plants eg flower buds and flower opening

Thanks

Fiona

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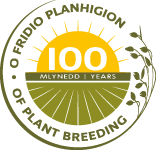
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**From:** [hbehn@uni-bonn.de](mailto:hbehn@uni-bonn.de) <[hbehn@uni-bonn.de](mailto:hbehn@uni-bonn.de)>   
**Sent:** 14 February 2022 16:31  
**To:** Fiona Corke [fic5] (Staff) <[fic5@aber.ac.uk](mailto:fic5@aber.ac.uk)>  
**Subject:** AW: Comparisons for Brassica genotypes EPPN2020 project

[RHYBUDD! E-BOST ALLANOL / CAUTION! EXTERNAL E-MAIL]

Hi Fiona,

thanks for your quick reply! Things are getting much clearer now.

Regarding the block design: What exactly is a block? Does one block consist of several lines? I think we should include the blocks in the ANOVA.

How many genotypes do we have in total? 49 with one genotype from two different years?

Ok, so this BBCH for Canola is applicable to all the other species, as well?

Thanks!

Best wishes

Helen

Hi Helen

Thanks for asking lots of questions, it is always difficult to take over someone else’s project.

       Is `Harvest all´ the complete raw data table? Yes this is all the data I collected

       So, these data have been scored at the time point of harvest of individual plants (different time points within the same genotype)? Is the harvest date the same as the date of the final photo? The harvest data were collected on the fully matured dried out plants. The final photos were taken before this stage, usually as flowering finished, as the older plants tend to get too large to live on the conveyors without getting tangled in each other and damaged.

       All the data in these excel sheets (2021-12-17\_BR024 Polyploid Data) have been assessed manually, right? Yes image based data will come separately from Kevin.

       Do you have a diagram showing the randomized block design? I can't find the compartments C5 and C6 in the complete raw data table. How many plants per genotype (per block and in total)? The randomized block design contained one replicate of each genotype in each block. Plants were randomised in Excel using a random number function. There were 8 reps of each genotype, split between the 2 glasshouse compartment C5 and C6. The attached diagram shows how the plants are arranged and correlates with the  info shown on the right hand side of the barcodes sheet. Reps 1-4 were located in compartment 5 and 5-8 in compartment 6. The temperatures sometimes vary slightly between the 2 compartments as their cooling varies. Rep 1 was in L1 and part of L2 etc.

        Average of pod number = per plant? Total from individual plant

       Growth rate: Has plant height been measured at different time points or only at harvest? I.e., is it possible to calculate a growth rate from plant height data or just from the image analyses? Plant height during plant growth will be available from image analysis. My plant height may be greater than that from images as some of the plants continue to extend upwards after they are removed from conveyor

       Has total (above-ground) biomass in terms of weight been determined? That was difficult, if I remember correctly?! It will be digital biomass as we only measured pod weight

       Could you share the BBCH code(s) you used? <https://www.canolacouncil.org/canola-encyclopedia/growth-stages/>

I am very happy to answer any further questions.

Thanks

Fiona

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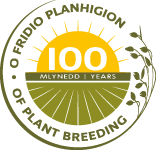
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**Sent:** 14 February 2022 13:08  
**To:** Fiona Corke [fic5] (Staff) <[fic5@aber.ac.uk](mailto:fic5@aber.ac.uk)>  
**Subject:** AW: Comparisons for Brassica genotypes EPPN2020 project

[RHYBUDD! E-BOST ALLANOL / CAUTION! EXTERNAL E-MAIL]

Hi Fiona,

it was nice to meet you last week!

I have only now had the time to look at the data in greater detail and I have a few questions:

       Is `Harvest all´ the complete raw data table?

       So, these data have been scored at the time point of harvest of individual plants (different time points within the same genotype)? Is the harvest date the same as the date of the final photo?

       All the data in these excel sheets (2021-12-17\_BR024 Polyploid Data) have been assessed manually, right?

       Do you have a diagram showing the randomized block design? I can't find the compartments C5 and C6 in the complete raw data table. How many plants per genotype (per block and in total)?

        Average of pod number = per plant?

       Growth rate: Has plant height been measured at different time points or only at harvest? I.e., is it possible to calculate a growth rate from plant height data or just from the image analyses?

       Has total (above-ground) biomass in terms of weight been determined? That was difficult, if I remember correctly?!

       Could you share the BBCH code(s) you used?

Sorry, I have a lot of questions because I wasn't involved in the project previously😉

Thanks a lot for providing this information!

All the best

Helen