

WORK PACKAGE 1 UPDATE

ACTIVITIES AND DELIVERABLES IN 2023

Aktiviteter

- Screening af 180 hestebønnegenotyper i rhizobokse for rodvæksthastighed
- Deep Convolutional Neural Network billedanalyse af rodvæksthastighed
- Genome-wide associationsanalyser og identifikation af SNP-markører koblet til rodvæksthastighed
- Beregning af genomiske forædlingsværdier for rodhastighed og identifikation af de bedste genotyper til udvikling af nye hestebønnesorter

Leverancer

- Notat, som beskriver SNP-markører for rodvæksthastighed, der kan anvendes til markør-assisteret selektion af nyt hestebønne forædlingsmateriale
- Notat om genomiske forædlingsværdier for 180 hestebønnegenotyper
- Udvælgelse af 35 hvidkløvergenotyper til AP2 forsøget i 2024 - liste med genotyper
- Artikel i landbrugsmedierne om arbejdet med rodudvikling i hestebønner

EXPERIMENTAL SETUP

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- 180 faba bean genotypes
- 2 seeds per box
- 3 boxes per genotype (6 replicates)
- 3 batches of 180 boxes



EXPERIMENTAL SETUP



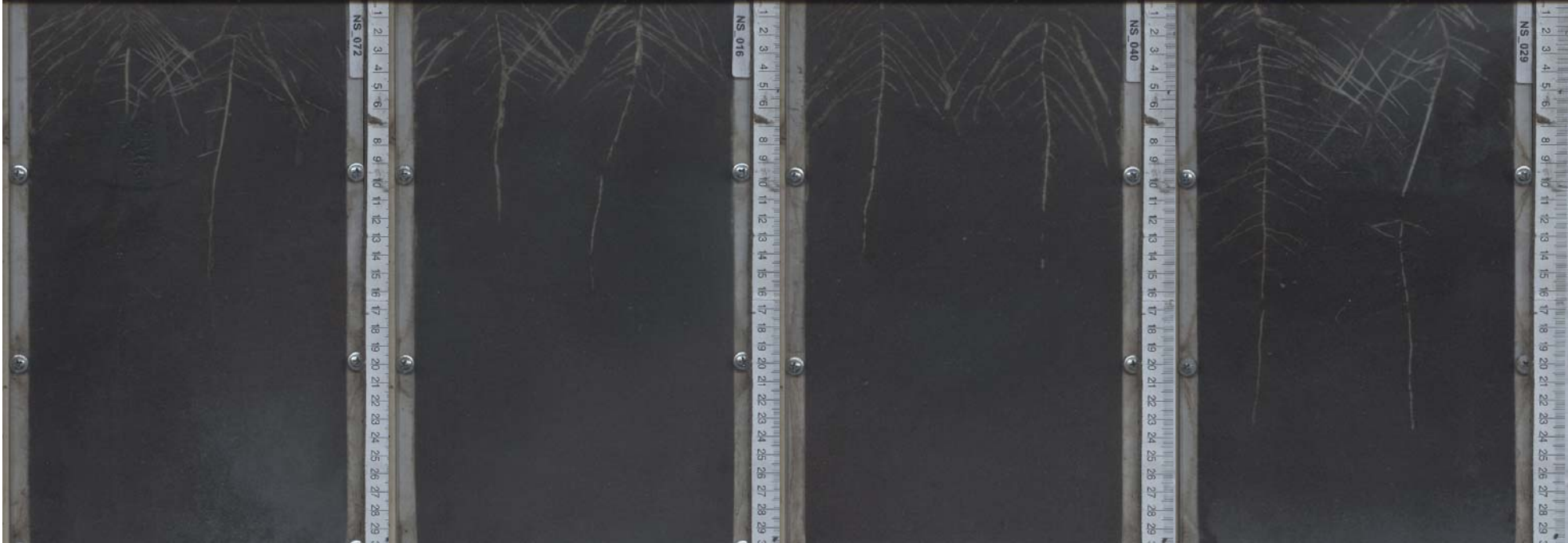
EXPERIMENTAL SETUP



RANDOMLY SELECTED ROOT IMAGES



RANDOMLY SELECTED ROOT IMAGES



TIMELINE

Uneven faba bean germination delays the project quite a lot

- Day 1: Design experiment
- Day 2-3: Prepare and clean greenhouse
- Day 4: Prepare seeds
- Day 5-12: Prepare rhizoboxes (soil etc.)
- Day 13: Irrigate rhizoboxes
- Day 14: Sow faba bean in rhizoboxes (two seeds per box)
- Day 15-60: Grow and maintain plants (pests, diseases, watering etc)
- Day 61-70: Imaging

Status:

- We have completed all three batches (third batch completed last Friday)
- Preliminary analysis suggests that it might be necessary to redo one batch – final decision pending

TRAIT ANALYSIS

Traits

- Total root length
- Median Number of Roots
- Network Area
- Maximum depth/width
- Volume/Surface Area
- Root diameter
- Root Spreading Angle

Discovery

- Genotypic data will be provided by project partners
- Linear-mixed models
- Bayesian variable selection

PLANNED WHITE CLOVER ACTIVITIES NEXT YEAR

Plant material for the 2024 experiment

- 177 white clover genotypes available from the NCHAIN project
- Collected from field trials at DLF in St. Heddinge
- Established in the greenhouse at AU-Flakkebjerg
- Tillers will be used instead of seeds for the experiments

Experimental design plans

- 177 white clover genotypes
- 2 tillers per box
- 3 boxes per genotype (6 replicates)
- 3 batches of 177 boxes
- Experiments and data analysis as outlined for the faba bean experiments in 2023



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