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Current status and future needs for grass breeding programs

GenSAP 2018, Billund
Christian Sig Jensen



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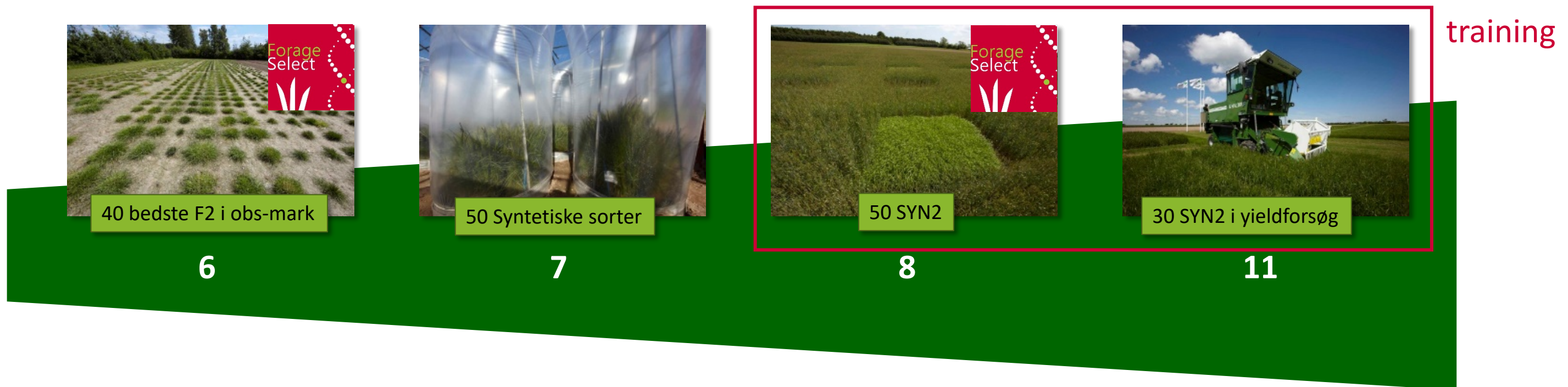
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The Journey



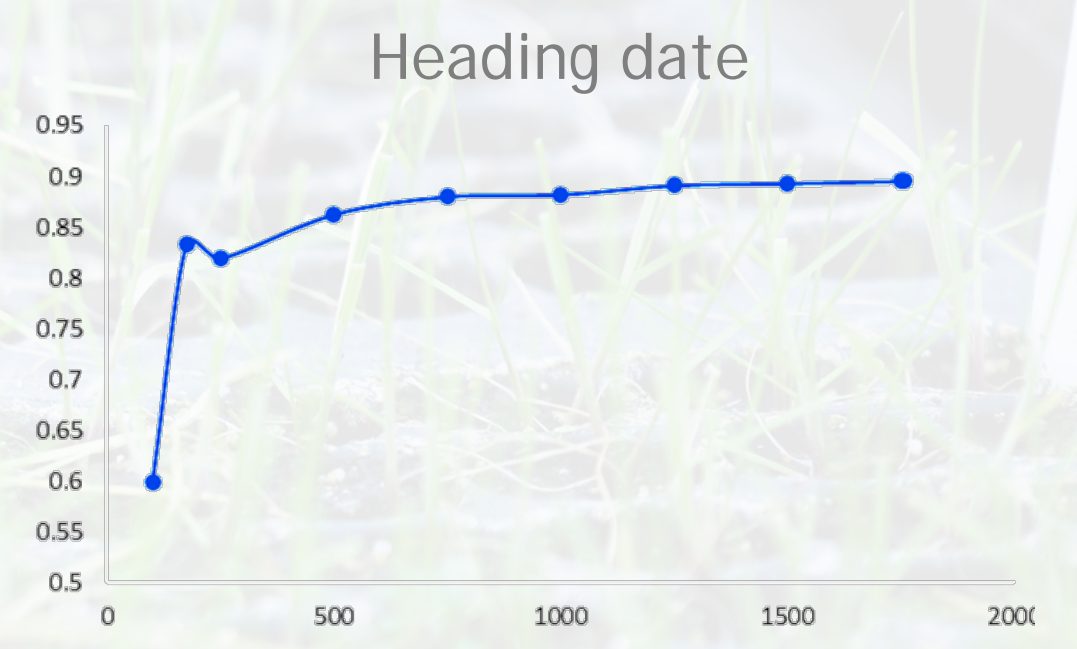
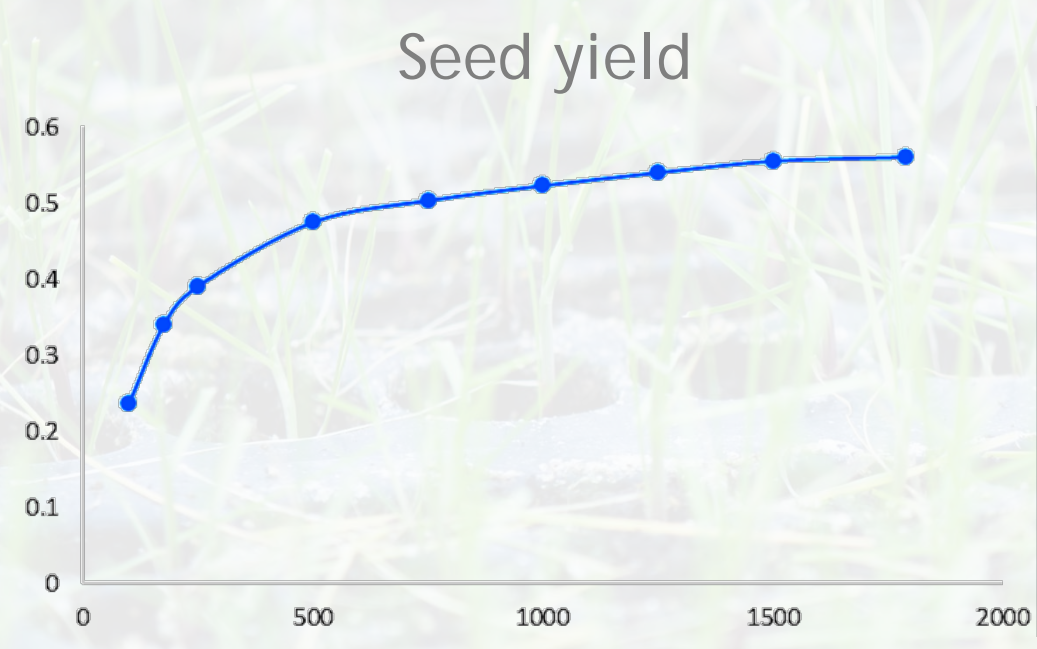
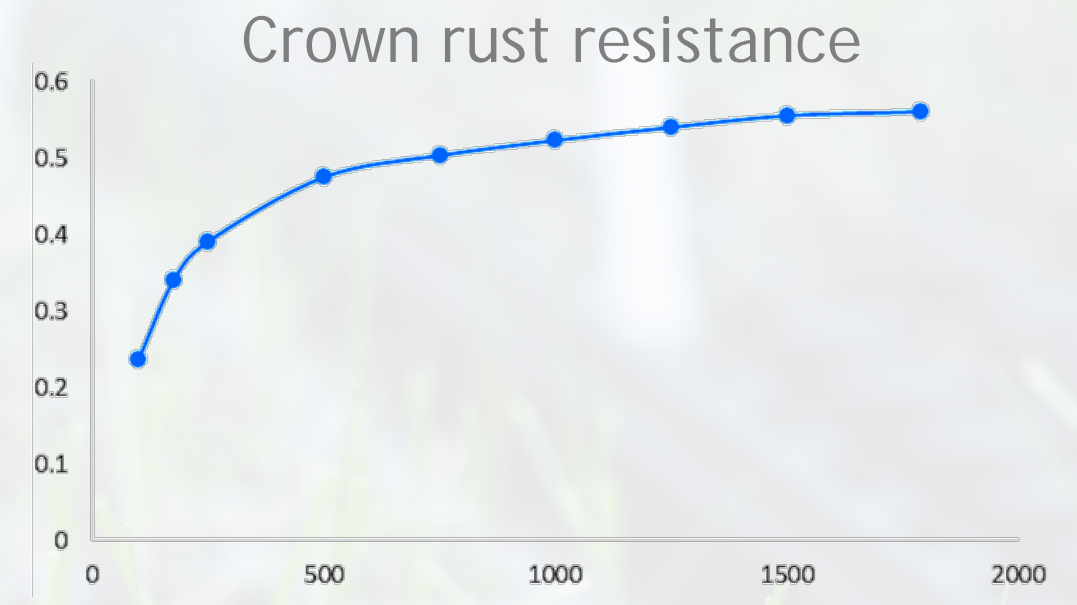
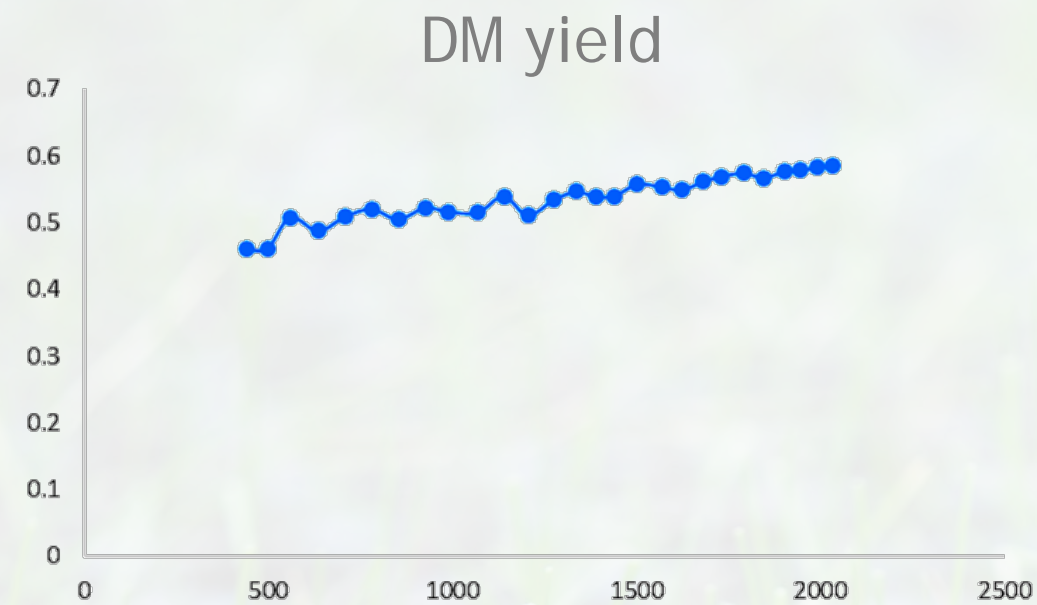


Genomic selection in the current breeding setup





Training population size and prediction accuracy





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Trait model

$$y = \text{TRIAL} + \text{id} + \text{id} * \text{loc} * \text{yr} * \text{manag} + \text{subblock} + e$$

Across all locations

"Leave one ID out" cross validation (LOO)

"Leave one year out" cross validation (LYO)

Accuracies for predicting phenotypes: $\text{cor}(y_f, \text{GEBV})$

y_f = phenotypes - fixed effects



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Prediction accuracies

	2N			4N		
	h2	LOO	LYO	h2	LOO	LYO
DM yield total	0.60	0.60	0.38	0.40	0.40	0.26
Crown rust resistance	0.56	0.55	0.37	0.71	0.62	0.47
Heading date	0.76	0.88	0.81	0.67	0.79	0.68
Seed yield	0.56	0.66	0.51	0.57	0.65	0.27
Spring growth	0.56	0.66	0.54	0.41	0.53	0.46
Stem regrowth	0.45	0.44	0.18	0.47	0.36	0.36



Selecting F2 families

Dry matter yield



58.38	18.64	-57.48	-24.44
51.23	14.38	-57.89	-10.53
47.75	19.24	-58.36	-27.36
47.48	19.93	-58.47	-42.43
44.94	10.42	-58.57	-16.30
44.53	28.62	-58.76	-7.03
43.47	17.50	-58.81	-40.53
42.16	22.15	-59.03	-47.43
42.04	-4.10	-59.04	-23.50
41.95	10.95	-60.11	-28.03
41.84	-7.70	-60.74	-22.90
41.81	21.31	-61.61	-21.90
39.82	26.87	-61.71	-71.00
39.10	3.07	-63.40	-47.24
39.09	9.28	-64.29	-30.27
38.65	13.16	-65.32	-40.73
38.52	19.25	-65.83	-29.19
38.29	9.43	-66.61	-27.48
37.93	-5.96	-67.62	-18.43
37.51	6.95	-69.05	-36.43

Seed yield



70.41	14.84	-57.48	-24.44
68.42	44.33	-57.89	-10.53
68.09	46.49	-58.36	-27.36
67.17	30.37	-58.47	-42.43
66.70	20.84	-58.57	-16.30
66.60	42.77	-58.76	-7.03
66.44	9.91	-58.81	-40.53
66.35	41.70	-59.03	-47.43
64.72	4.60	-59.04	-23.50
64.63	30.80	-60.11	-28.03
64.20	16.52	-60.74	-22.90
63.98	13.05	-61.61	-21.90
63.29	67.43	-61.71	-71.00
61.73	-17.45	-63.40	-47.24
61.70	18.56	-64.29	-30.27
61.34	16.86	-65.32	-40.73
61.06	16.15	-65.83	-29.19
60.38	12.28	-66.61	-27.48
59.88	43.54	-67.62	-18.43
59.76	20.89	-69.05	-36.43

Rust resistance



3.37	1.45	-2.21	-1.47
3.11	1.05	-2.23	-2.32
2.98	2.02	-2.24	-0.38
2.92	2.11	-2.26	-1.79
2.91	0.63	-2.27	-0.34
2.87	1.80	-2.28	-1.82
2.86	0.75	-2.29	-1.87
2.83	1.43	-2.31	-1.42
2.81	2.30	-2.34	-2.17
2.78	1.08	-2.43	-1.59
2.78	2.05	-2.46	-1.36
2.72	1.38	-2.47	-2.94
2.69	1.82	-2.48	-0.59
2.64	0.43	-2.55	0.15
2.58	0.68	-2.60	-0.99
2.57	1.16	-2.62	-1.53
2.49	0.03	-2.64	-1.61
2.49	1.33	-2.75	0.25
2.46	0.88	-2.82	-1.62
2.41	1.29	-3.26	-1.99

Heading date



11.55	5.97	-13.24	-8.58
11.49	8.54	-13.27	-9.08
11.42	10.65	-13.32	-8.18
11.34	9.91	-13.35	-10.41
11.31	9.13	-13.37	-9.08
10.99	8.75	-13.40	-8.77
10.97	7.79	-13.46	-10.87
10.85	3.06	-13.52	-10.98
10.78	8.89	-13.67	-9.87
10.75	8.38	-13.82	-8.32
10.71	7.58	-14.08	-8.94
10.68	6.98	-14.10	-8.29
10.67	8.19	-14.15	-9.52
10.61	9.08	-14.21	-8.97
10.61	8.68	-14.32	-6.15
10.59	2.20	-14.36	-7.95
10.58	7.33	-14.37	-9.86
10.57	10.41	-14.42	-11.14
10.53	7.45	-14.65	-8.08
10.51	7.66	-15.12	-6.12



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POC1 - Initial results looking good



Yield
Quality
Disease



Select single plants

2016



50 synthetic crosses

2016



50 multiplication

2017



50 SYN2 in yield tests

2018-19

★ POC 1+2

DUS

Heading date
Architecture
Color

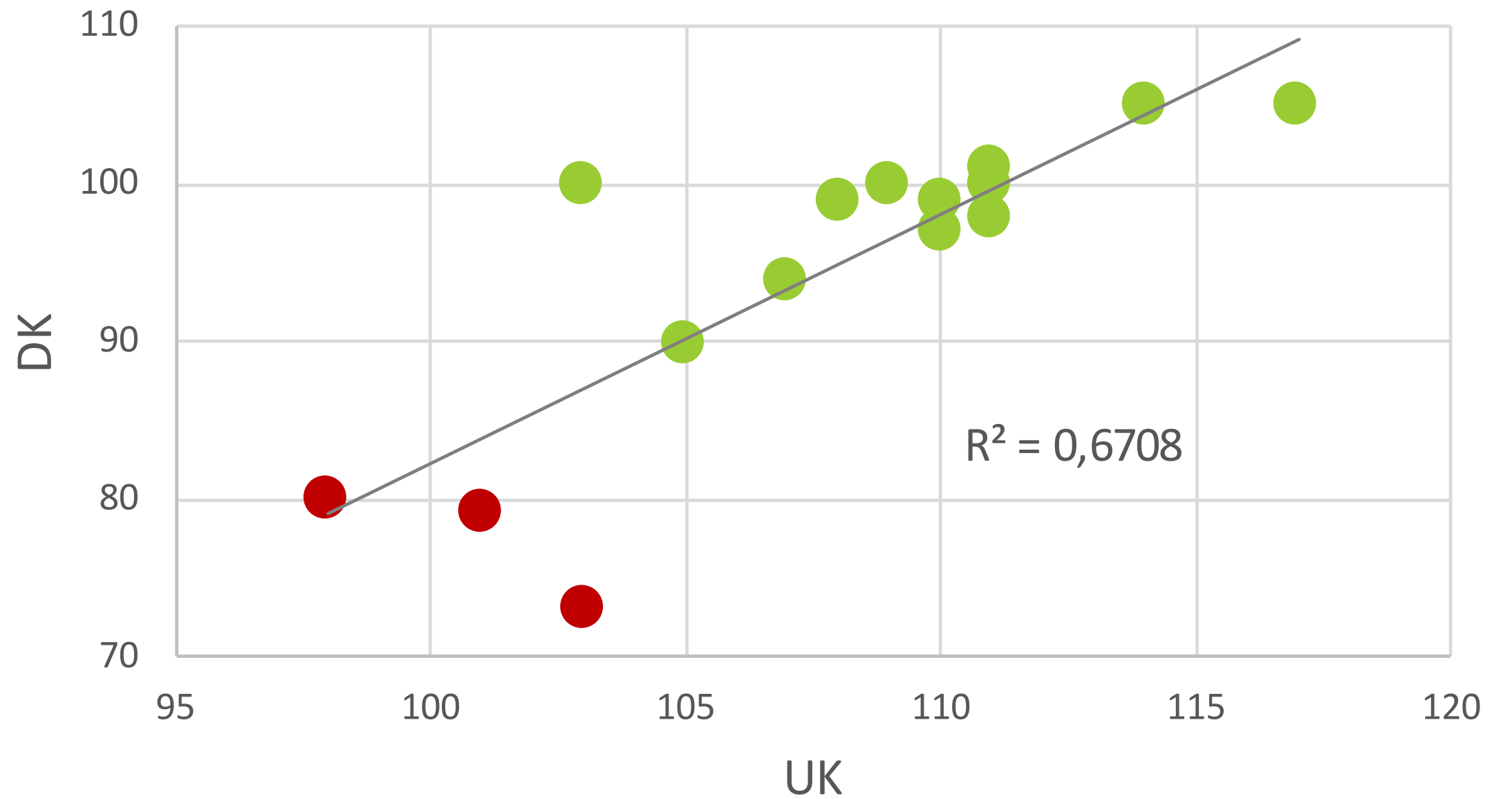


POC 1 - Year 1 results synthetic varieties generated by GS

DM yield cut 1-3 year 1

- 12 lines GS for pos. yield ●
- 3 lines GC for neg. yield ●

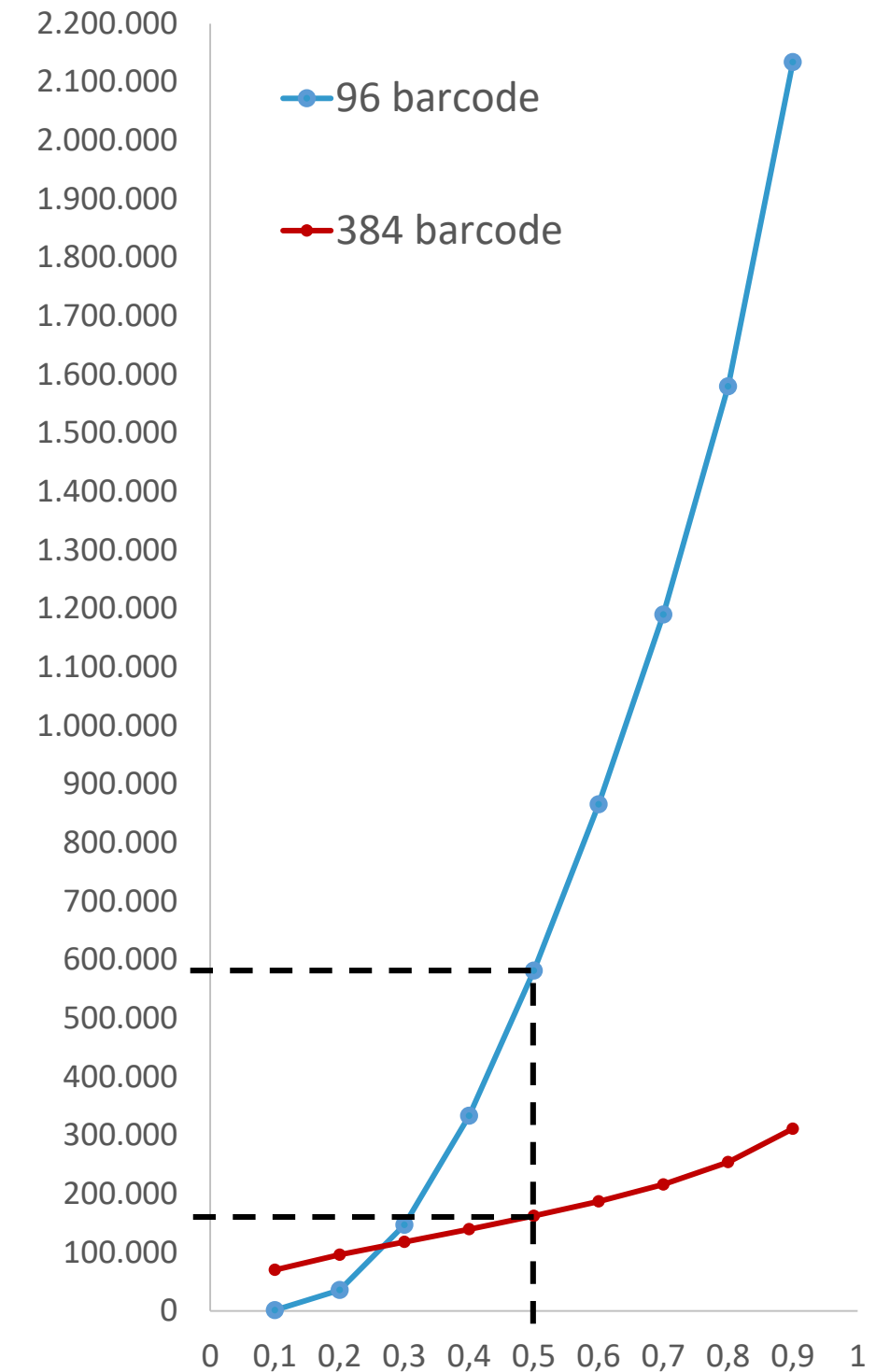
GS-assisted SYNs **1%** better than
Non-assisted SYNs





Challenges along the way: Missing values

DM yield total	96 barcode	384 barcode
h2	0.55	0.55
Cor(y,GEBV)	0.46	0.48
Cor(y,GEBV)/sqrt(h2)	0.61	0.64
bias	1.26	1.15





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Timing



10,000 forældre

0



250 krydsninger

1



250 F2 familier

3



250 F2 i yieldforsøg

5

- AUG: Harvest and sow seeds
- SEP: Isolate DNA from bulks
- OCT: Prepare GBS libraries
- NOV: Quality checks
- DEC: Sequence libraries
- JAN: Call SNP values
Calculate GEBV
- FEB: Finalize sowing plan



Genotypes different generations

Fisher's exact test for each SNP

	F1		F2		p-value
	ref.	alt.	ref.	alt.	
SNP_1	10	0	15	0	1
SNP_2	0	20	0	30	1
SNP_3	0	10	0	15	1
SNP_4	5	10	6	10	1
SNP_5	3	7	4	6	1
SNP_6	20	5	10	5	0.457
SNP_7	20	5	5	10	0.006



F1 compared with F2 - % SNPs P-value > 0.05

2N	same_set	same_lib	%
F1_F2	1	1	0,966576
F1_F2	1	1	0,974678
F1_F2	1	1	0,970816
F1_F2	1	0	0,963001
F1_F2	1	0	0,960729
F1_F2	0	0	0,959554
F1_F2	0	0	0,945571



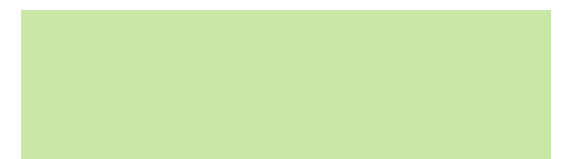
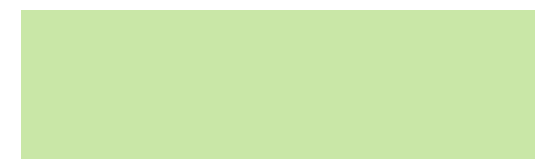
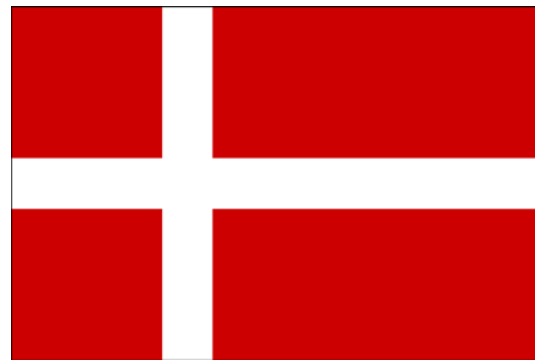
Status and future





Approaching GxE modelling

Five core sets tested in 3 of 5 locations





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Improving annual breeding gain

$$R_t = \frac{i r \sigma_A}{L}$$

i = Selection intensity

r = Selection accuracy

σ_A = Genetic variace

L = Generation interval





Remote imaging of rust resistance

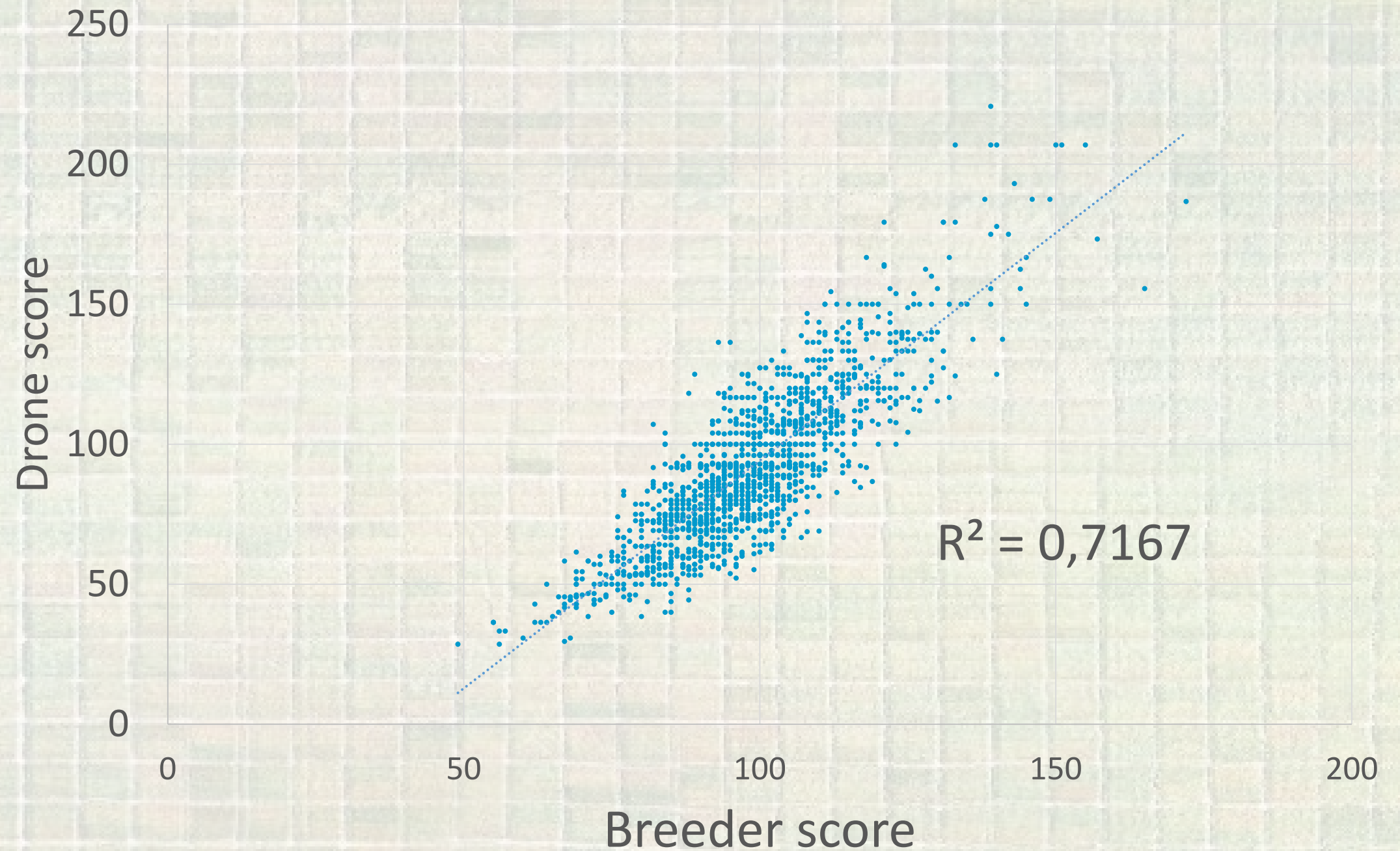
CV

drone 8.0%

VS

breeder 14.1%

2017 RGB





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More phenotypes on single plants





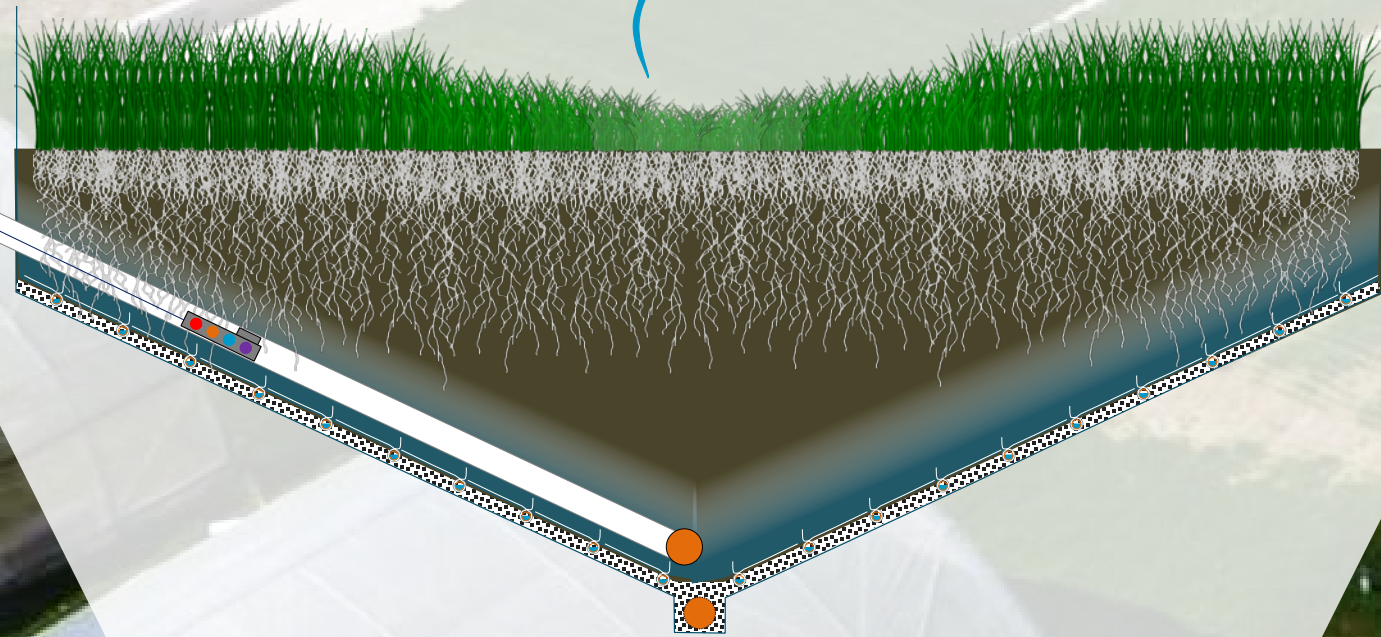
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Predicting future... and future needs



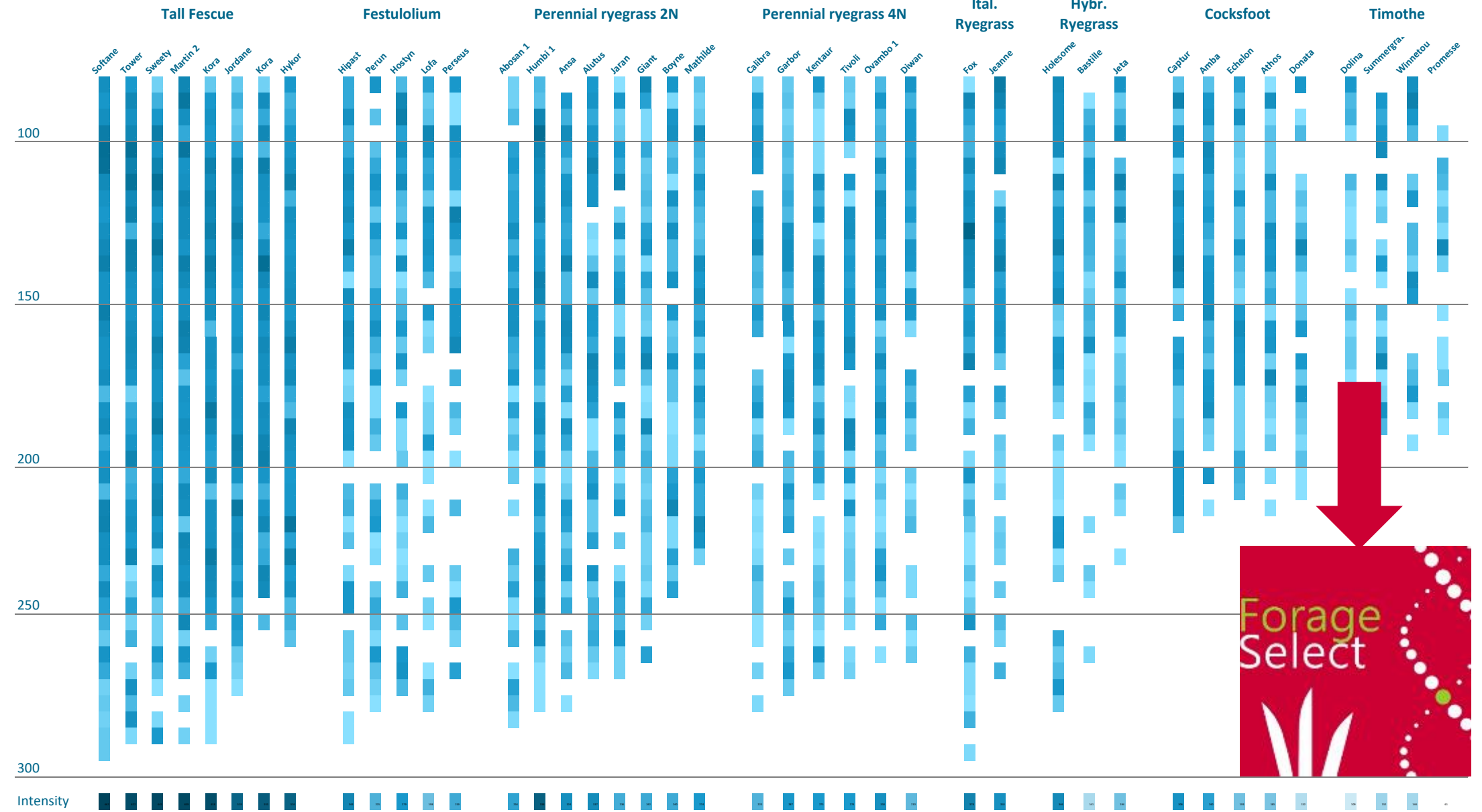
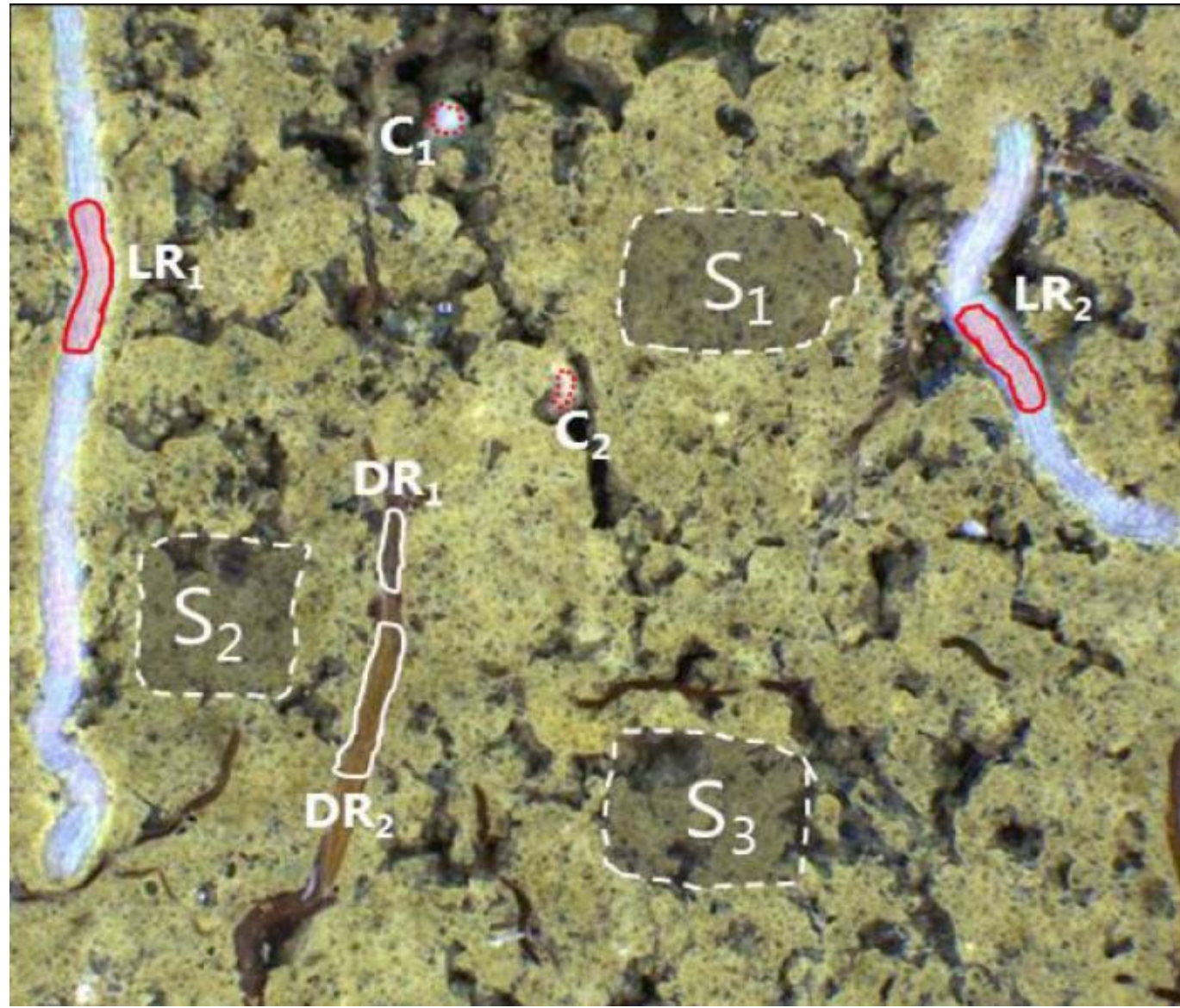
Rad Max

root deeper produce more





LDA, NND, and GBLUP





GS for protein refinery



Industrial scale
Biorefinery

Partners

- Aarhus University
- Copenhagen University
- DLG
- DLF
- Danish Crown
- Agro Business Park

Operational
2019



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Conclusion

Future needs:

1. Address deflation issues
2. Adapt GS models to half sib systems
3. Develop robust simulation software for outbreeding plants
4. Approach GxE at different angles (core sets, epi-GBS?)
5. Improve phenotyping accuracy by remote imaging
6. Measures to adapt breeding fast to new situations