

First year results from multi-location field testing of genetically diverse oat lines across the NPA region



Morten Lillemo

OatFrontiers workshop Steinkjer 16.10.2025

0

Interreg 

Co-funded by
the European Union

Northern Periphery and Arctic

OatFrontiers

Norwegian University of Life Sciences

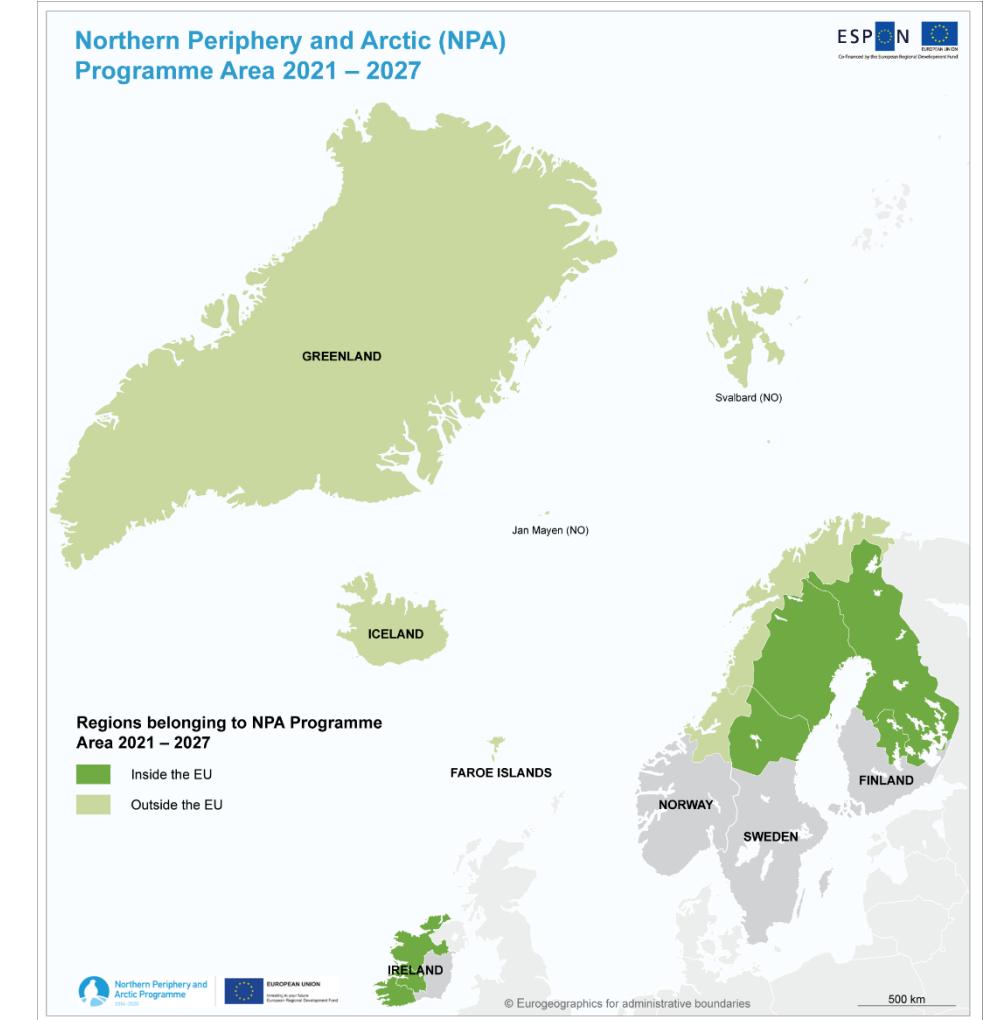
The OatFrontiers project

- Adapting oats to the final Frontiers
- A collaborative project among partners in 5 countries across the NPA region



Northern Periphery and Arctic

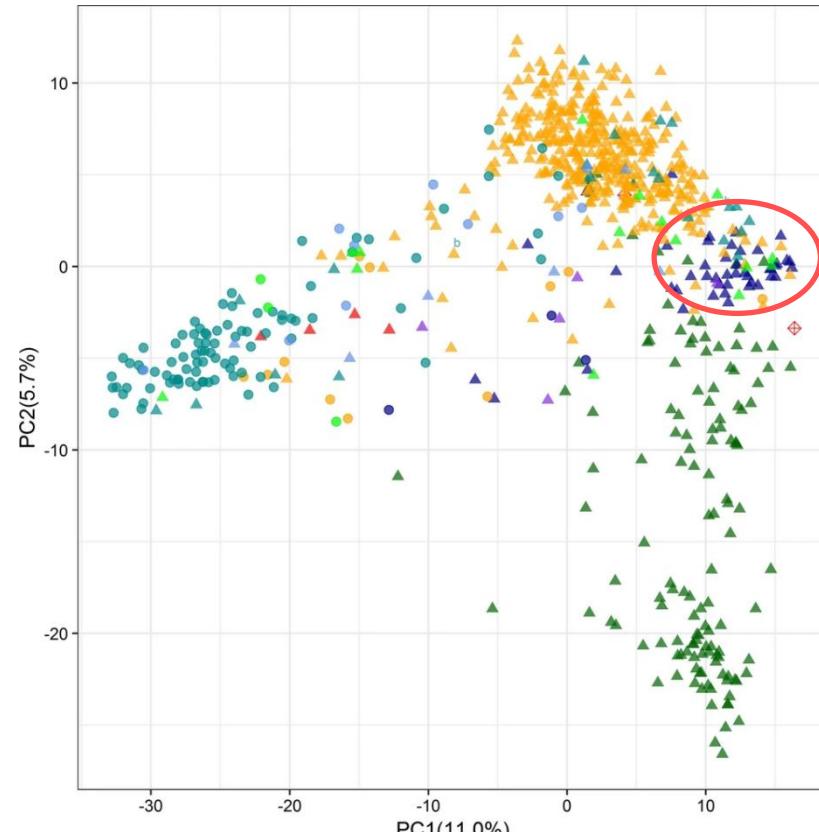
OatFrontiers



Challenges with oat cultivation in the Northern Periphery and Arctic



Why are our oat varieties not good enough?



- Low genetic diversity
- Only a few “founder” landraces contributed to our elite gene pool

Solution:

- Bring in new genetic diversity for desired traits

Oat Recurrent Selection Population

1990's, Kenneth J. Frey (Iowa State University) and
Åsmund Bjørnstad (NMBU)



- Collaborative research efforts to broaden the gene pool of oats
- 20 starting parents (North-American+Nordic),
Avena sterilis introgressions in 7 parental lines

Parents	C0 lines	C2 lines	C4 lines	C6 lines
20	104	101	96	91

+	HPHF
	28

(*A. sterilis* introgressions)

Oat RS population

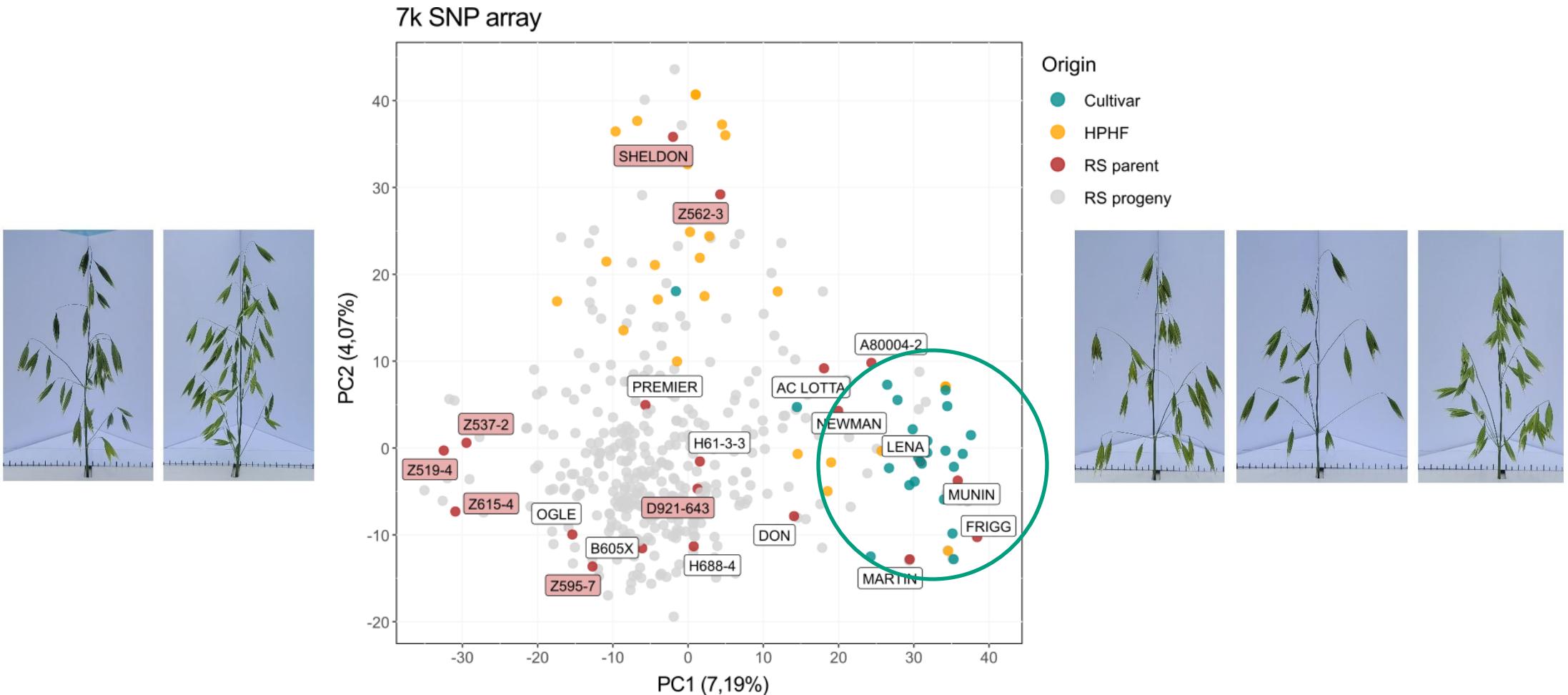
- Agronomically improved progenies
- From crosses with diverse background
- Introgressions from *Avena sterilis*



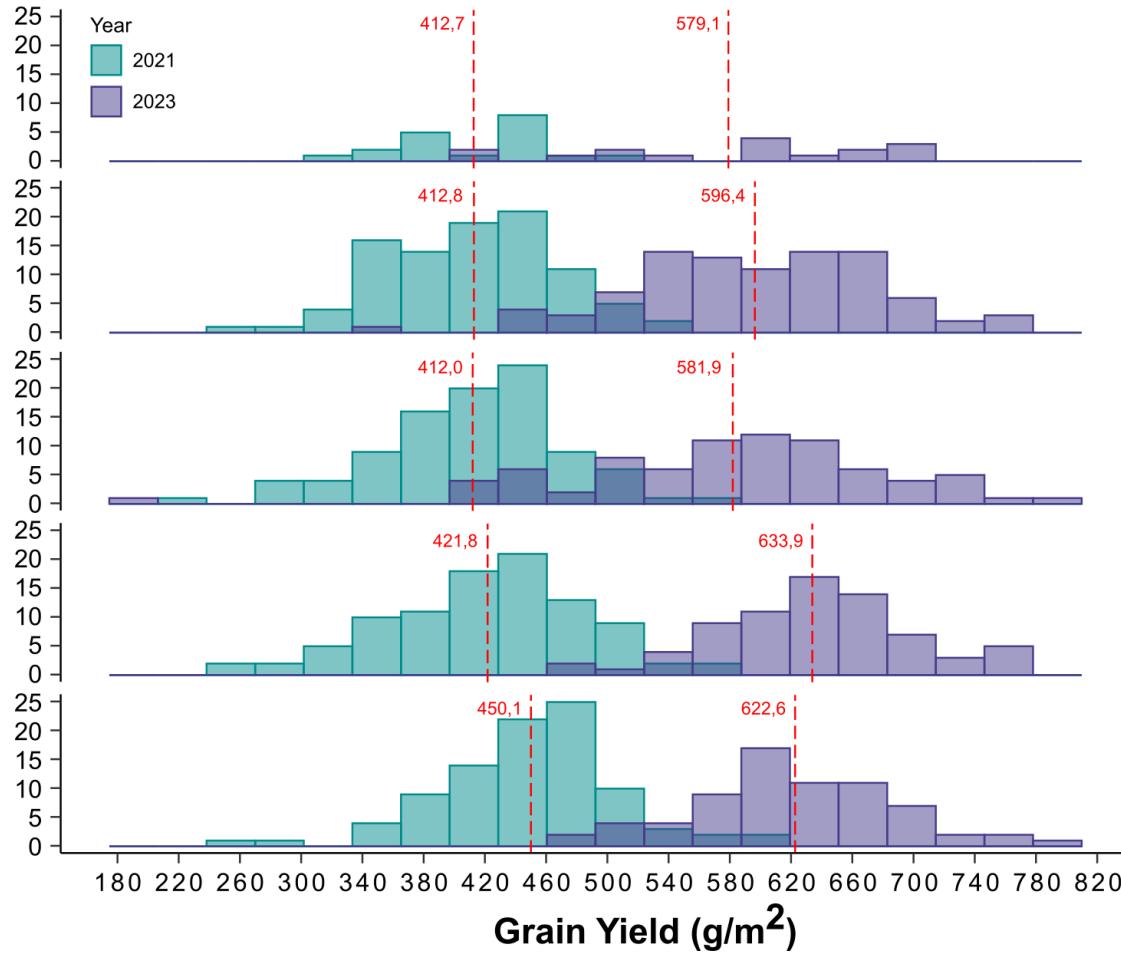
Parents	C0 lines	C2 lines	C4 lines	C6 lines
20	104	101	96	91

Line/cultivar	Origin	Maternal parent	Paternal parent
H688-4	Iowa	Ogle/Lang	D209-13-3-1/Ogle
Ogle	Illinois	Brave	Unnamed_336
H61-3-3	Iowa	B433/Garland//Holden/3/Clintford	6/B444/4/Ogle
B605X	Iowa	Selection from an irradiated composite cross population	
D921-643	Iowa	A. sterilis, PI317789 (Israel)	*3/Otter
Sheldon	Iowa	A. sterilis, PI317989 (Israel)/Otter	Grundy/3/Noble
Z562-3	Iowa	C19170	A. sterilis, PI324716 (Greece)
Premier	Minnesota	WI X1961-1	Noble
Z537-2	Iowa	Ogle	A. sterilis, PI411976 (Iraq)
Z519-4	Iowa	Ogle	A. sterilis, PI309033 (Israel)
Z595-7	Iowa	A. sterilis, PI1411560 (Eritrea)	Tippecanoe
Z615-4	Iowa	A. sterilis, PI411560 (Eritrea)	Ogle
Frigg	Sweden	Sv0177/Sv56997	Condor
Lena	Norway	Sang	Unisignum
A80004-2	Norway	Mustang/PGR6848	Puhti
Newman	Ottawa, Canada	04352	Donald
AC Lotta	Ottawa, Canada	04186	Tibor
Munin	Norway	Mustang	Pol
Martin	Norway	Gråkall	Tador
Don	Illinois	Pc61/Coker234	Unnamed4050

Genotyping of the material



Yield changes by cycles of selection





Small plot testing at 9 locations in 2024



Interreg  Co-funded by
the European Union

Northern Periphery and Arctic

OatFrontiers

Purpose of the small plot trials

- Evaluate agronomic performance, yield and quality variation of the unique pre-breeding material in the NPA region



Purpose of the small plot trials

- Showcase the value of genetic diversity for oat breeding





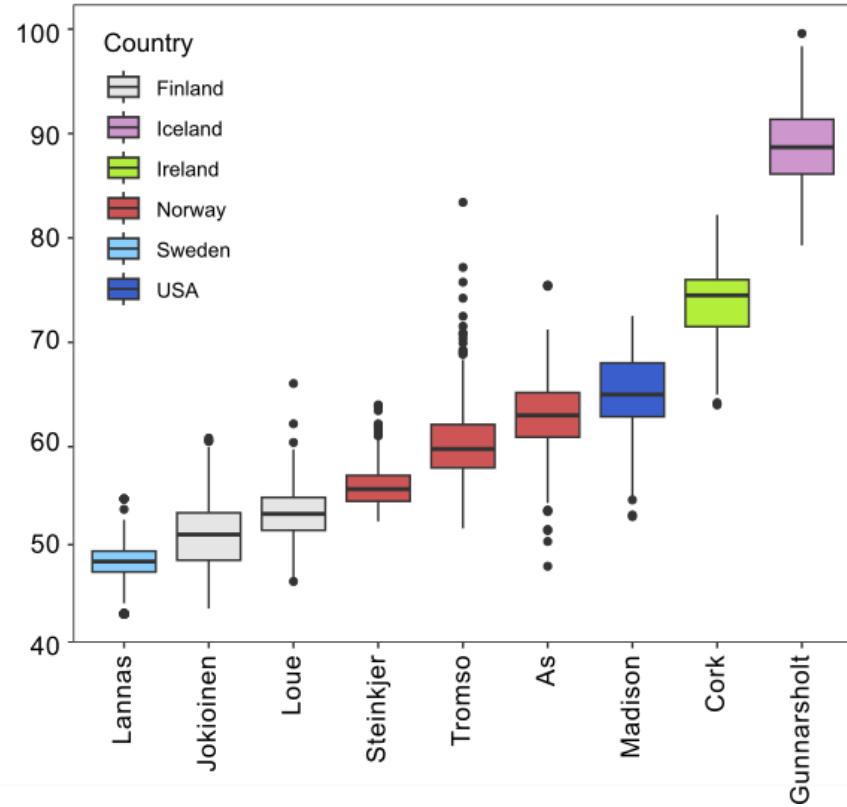
Small yield plots in Ås, 2024

Hillplots in Steinkjer, 2024

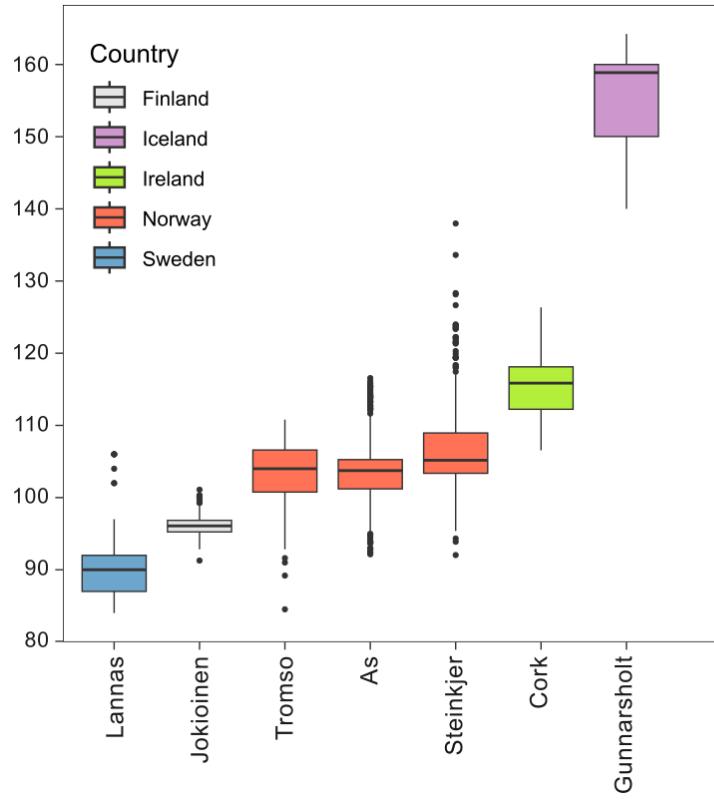


Results of first field season

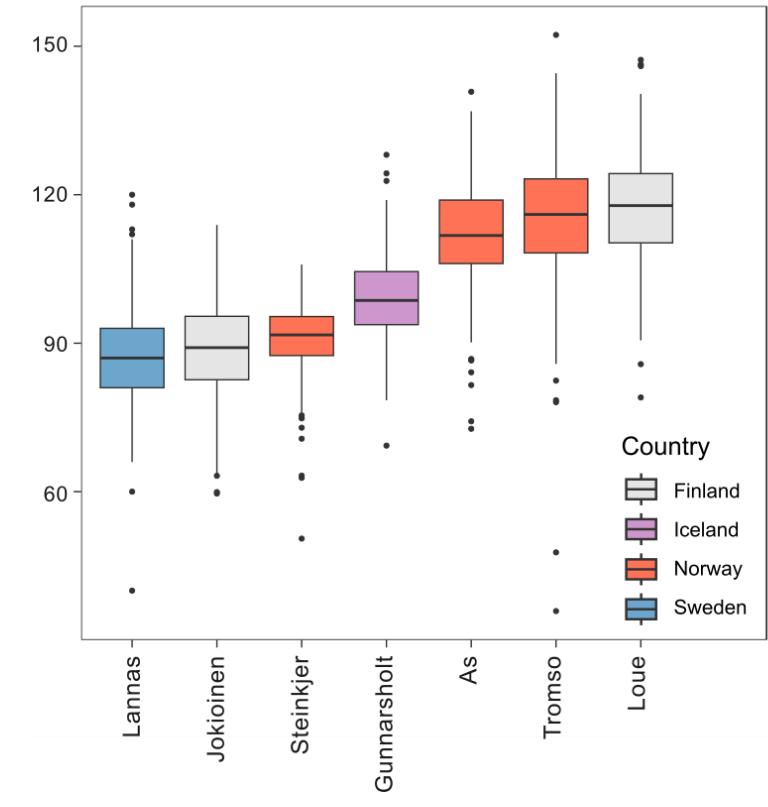
Days to heading



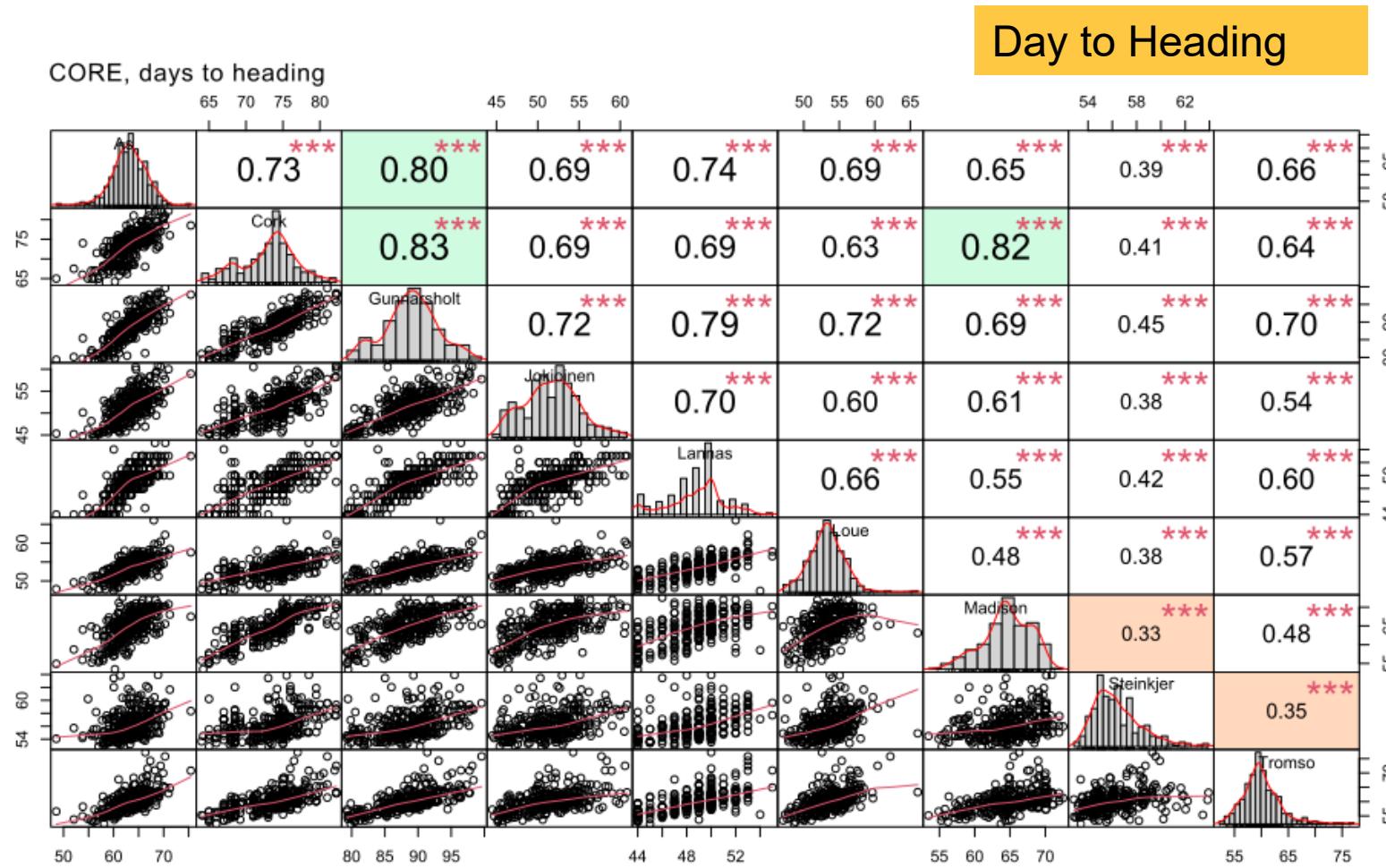
Days to maturity



Plant height

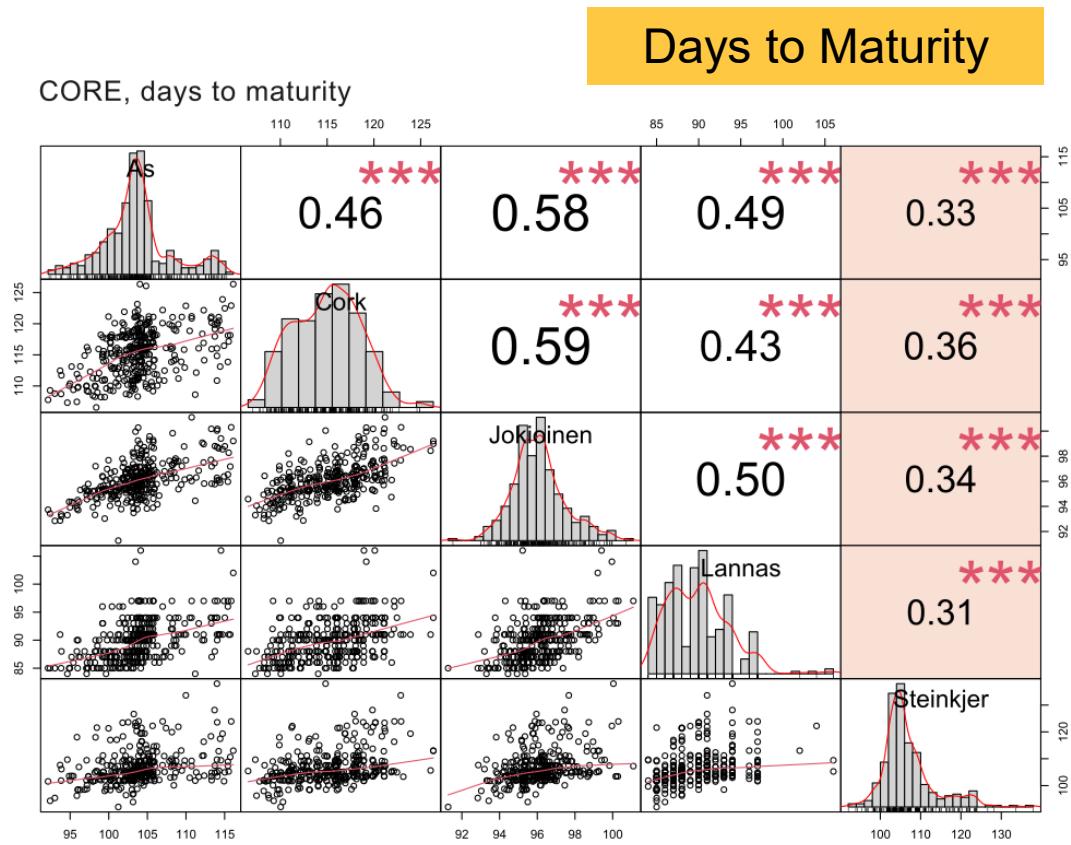


Correlations among locations

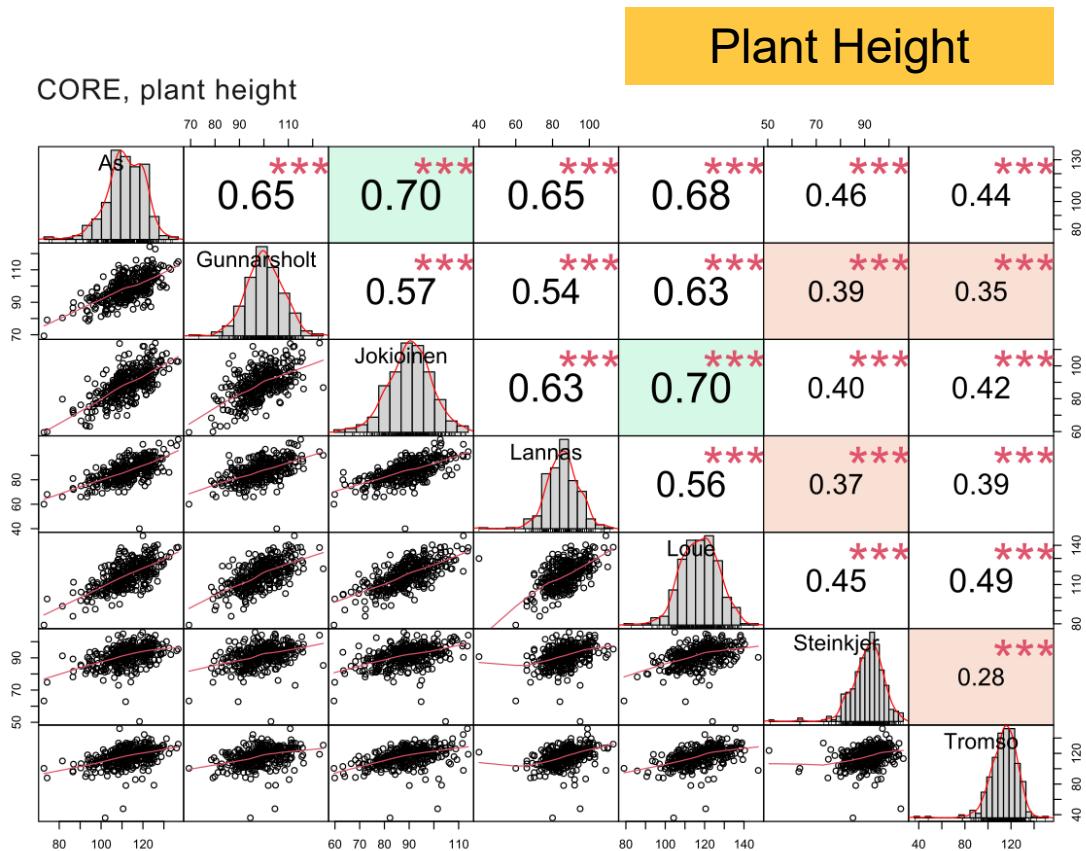


Steinkjer has low correlations with other locations

Correlations among locations



Steinkjer has low correlations with other locations



Some low correlations between locations

Trait variability

Days to heading (9 trials)	
Mean	62.2 days
Range	55.1 – 69.4

Days to maturity (7 trials)	
Mean	110.5 days
Range	102.6 – 120.1

Plant height (7 trials)	
Mean	101.5 cm
Range	72.1 – 124.8

Early lodging (5 trials)	
Mean	25.4 %
Range	3.9 – 73.8

Late lodging (7 trials)	
Mean	48.0 %
Range	22.7 – 88.8



Grain yield (4 trials)	
Mean	2.89 t/ha
Range	1.7 – 3.9

Protein (2 trials)	
Mean	12.4 %
Range	10.6 – 16.4

Fat (2 trials)	
Mean	6.4 %
Range	5.1 – 9.8

Some promising lines

- Lines with early maturity, lodging resistance and decent yield:

Accession	Name	Cycle	Days to heading	Days to maturity	Plant height	Loding (%)	Yield (t/ha)	Protein (%)	Fat (%)
NMBU_3291	FRIGG	P	60.5	106.4	93.1	11.4	3.6	12.5	5.7
NMBU_3002	IA91126	C0	61.3	106.0	99.9	20.8	3.4	12.5	6.0
NMBU_3011	IA91177	C0	58.2	104.8	89.0	3.9	3.1	13.1	6.5
NMBU_3115	IA91255	C0	59.7	106.9	90.7	14.8	3.1	11.9	6.5
NMBU_3343	IA93275	C2	63.2	105.3	102.7	16.9	3.0	12.9	6.1
NMBU_3054	IA96206	C4	57.4	106.1	99.4	23.1	3.0	12.3	6.3
NMBU_3040	IA93300	C2	61.1	104.8	98.3	19.8	3.0	12.9	6.2

- Earliness combined with high protein (and high fat):

NMBU_3411	J-762-1	HPHF	59.0	104.1	94.8	16.0	2.2	14.3	6.7
NMBU_3207	IA91252	C0	57.6	107.1	100.8	14.3	2.5	13.9	6.3
NMBU_3412	Y33-2-8	HPHF	59.0	106.5	92.0	25.8	2.6	13.7	5.8
NMBU_3431	N364-2	HPHF	60.7	110.6	85.6	17.0	2.4	13.2	9.1

Significant genetic markers for agronomic traits and yield

Marker	Trait	Chromosome	Position (Mbp)
GMI_ESCC4504_192, GBS_8200, GBS_8201, GBS_8202	Days to heading; days to maturity; Yield	7D	468.7-469.2
GBS_2735	Lodging	6A	354.4
GMI_GBS_34860	Plant height	5C	596.7
GMI_DS_LB_3922	Plant height	7A	66.6
GBS_5247, GBS_5301	Yield	5D	410.3-418.8

Significant genetic markers for fat and protein content

Marker	Trait	Chromosome	Position (Mbp)	Phenotypic variance explained (%)
GBS_5724	Fat	1A	301.5	14.7
ZOT004108	Fat	4C	13.3	8.8
LOT009207	Fat	4C	16.7	27.9
GBS_9035	Fat	4C	30.5	9.0
GBS_5439	Fat	6A	410.6	7.6
LOT060730	Fat	6A	413.7	15.0
GBS_5659	Protein	7D	445.1	18.0
GBS_3199	Protein	2C	73.4	15.0
GBS_8202	Protein	7D	469.2	7.8

Summary and way forward

- Useful trait variation identified in the data from 2024
- Promising results from the genetic analyses
- New field trials in 2025 yet to be analyzed
- Prospective outcomes:
 - suitable crossing parents for further breeding
 - genetic markers for traits of interest



