The Ups and Downs of UAS in Washington Wheat Breeding

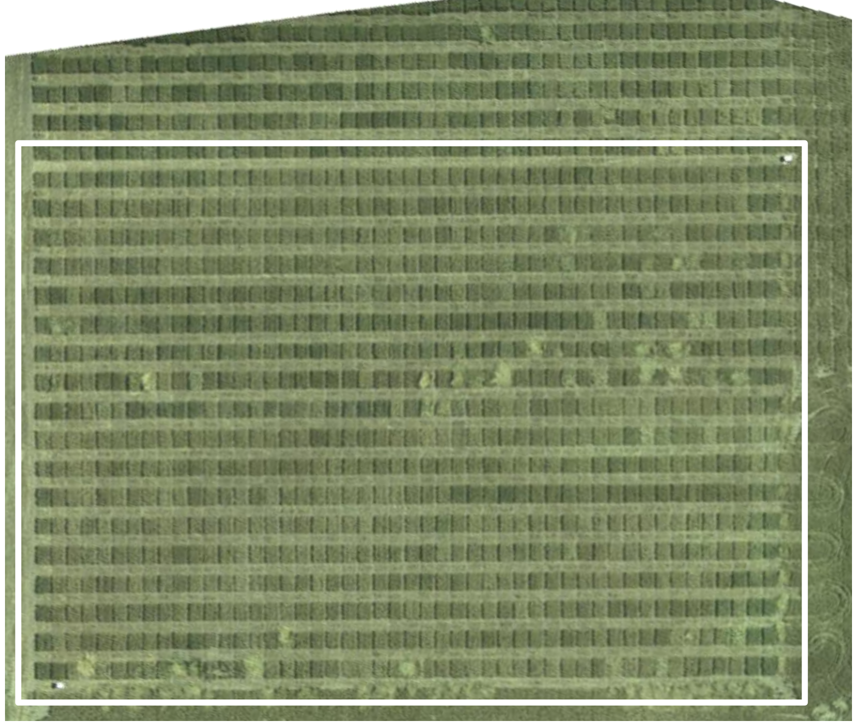
Dr. Arron Carter and Andrew Herr

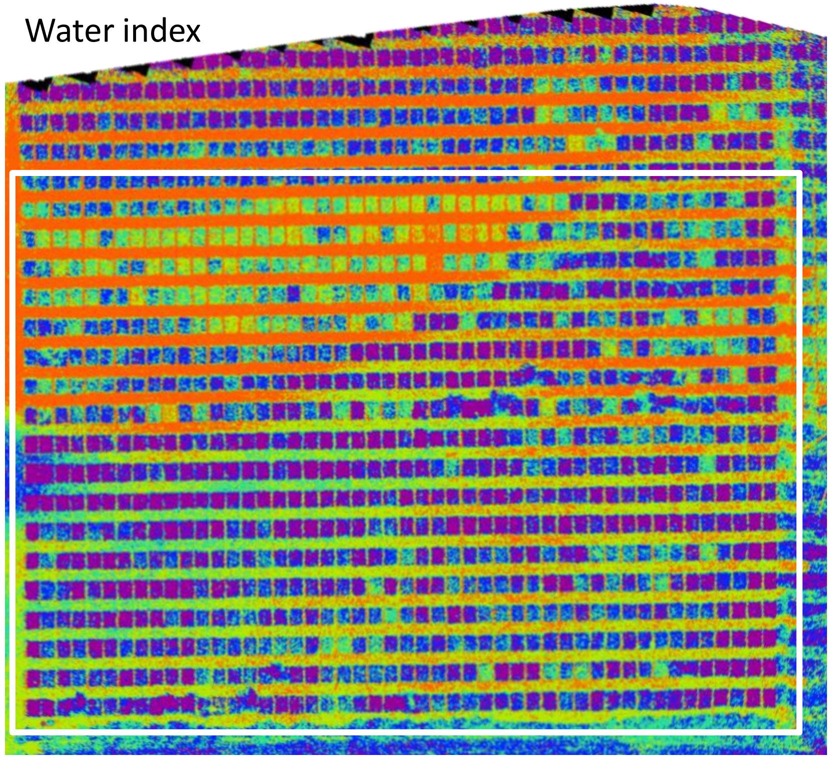
Collaborators: Drs. Mike Pumphrey and Sindhuja Sankaran and Peter Schmuker

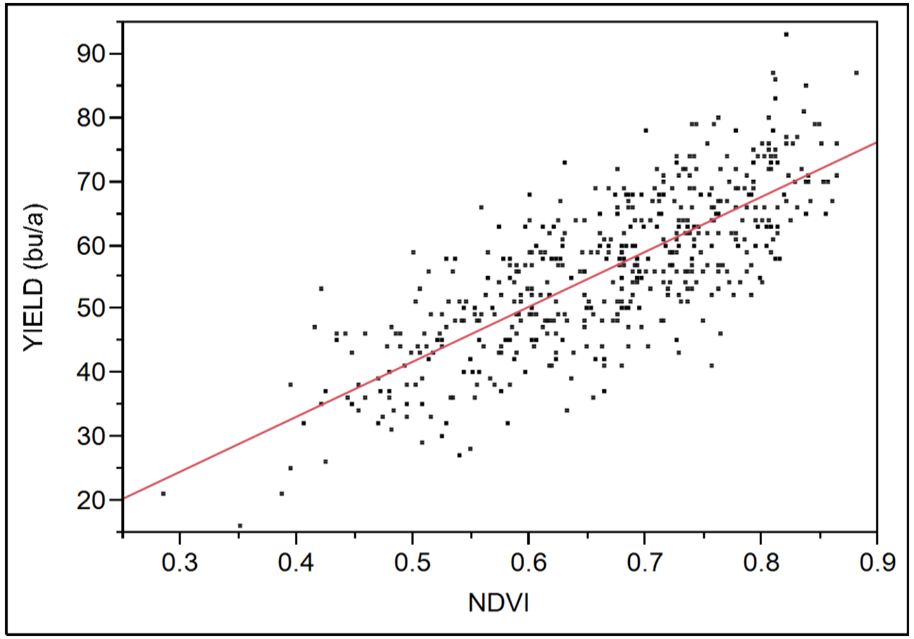
Past students: Karansher Sandhu, Lance Merrick, Dennis Lozada, Jayfred Godoy, and Shiferaw Gizaw

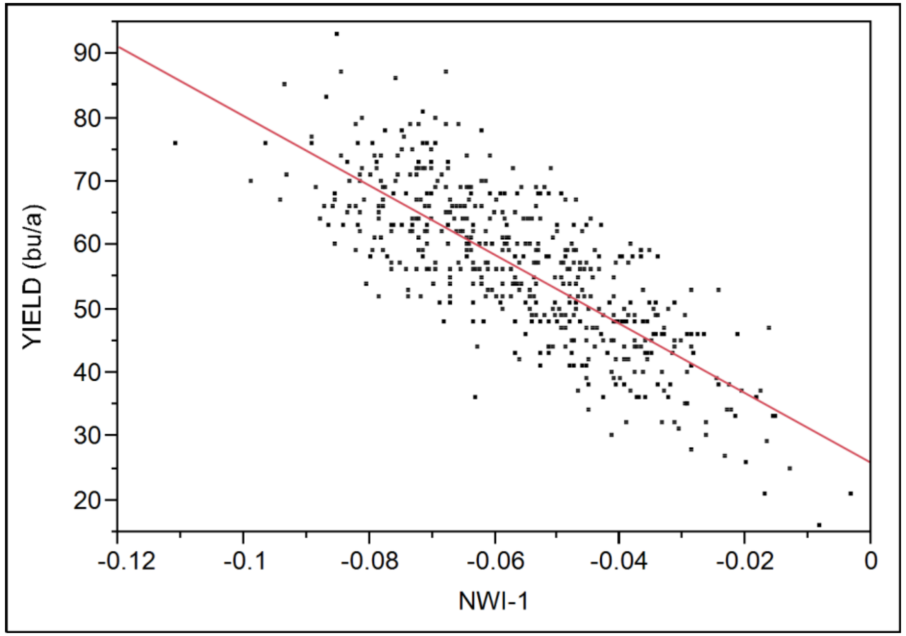
Washington State University
Department of Crop and Soil Sciences
Pullman, WA 99164
ahcarter@wsu.edu

2011-2013 started looking at SRI and correlations to traits, seeing if they could be used for indirect selection

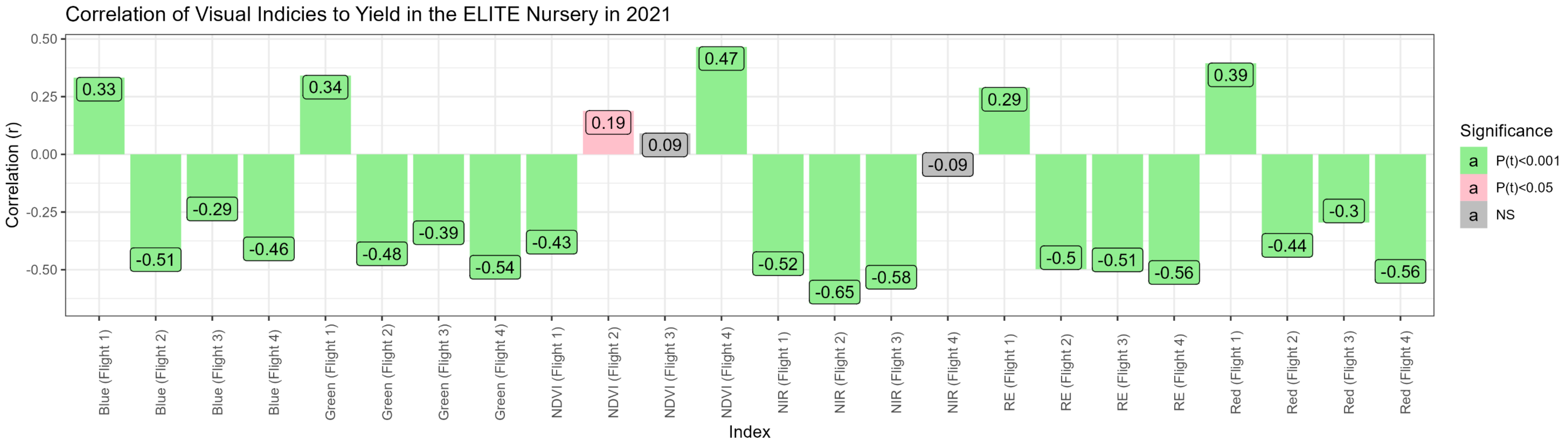








Esten Mason-CSU

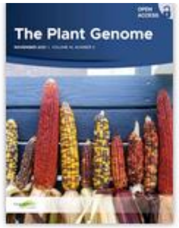


The Plant Genome
OPEN ACCESS

SPECIAL ISSUE: ADVANCES IN GENOMIC SELECTION AND APPLICATION OF MACHINE LEARNING IN GENOMIC PREDICTION
Open Access

Multitrait machine- and deep-learning models for genomic selection using spectral information in a wheat breeding program

Karansher Sandhu, Shruti Sunil Patil, Michael Pumphrey, Arron Carter



Volume 14, Issue 3
November 2021
e20119
This article also appears in:
Advances in Genomic Selection and Application of Machine Learning in Genomic Prediction

ORIGINAL RESEARCH article
Front. Plant Sci., 12 February 2021 | https://doi.org/10.3389/fpls.2021.613300

Combining Genomic and Phenomic Information for Predicting Grain Protein Content and Grain Yield in Spring Wheat

Karansher S. Sandhu[1], Paul D. Mihalyov[2], Megan J. Lewien[3], Michael O. Pumphrey[1] and Arron H. Carter[1*]

Independent-Validation Accuracies

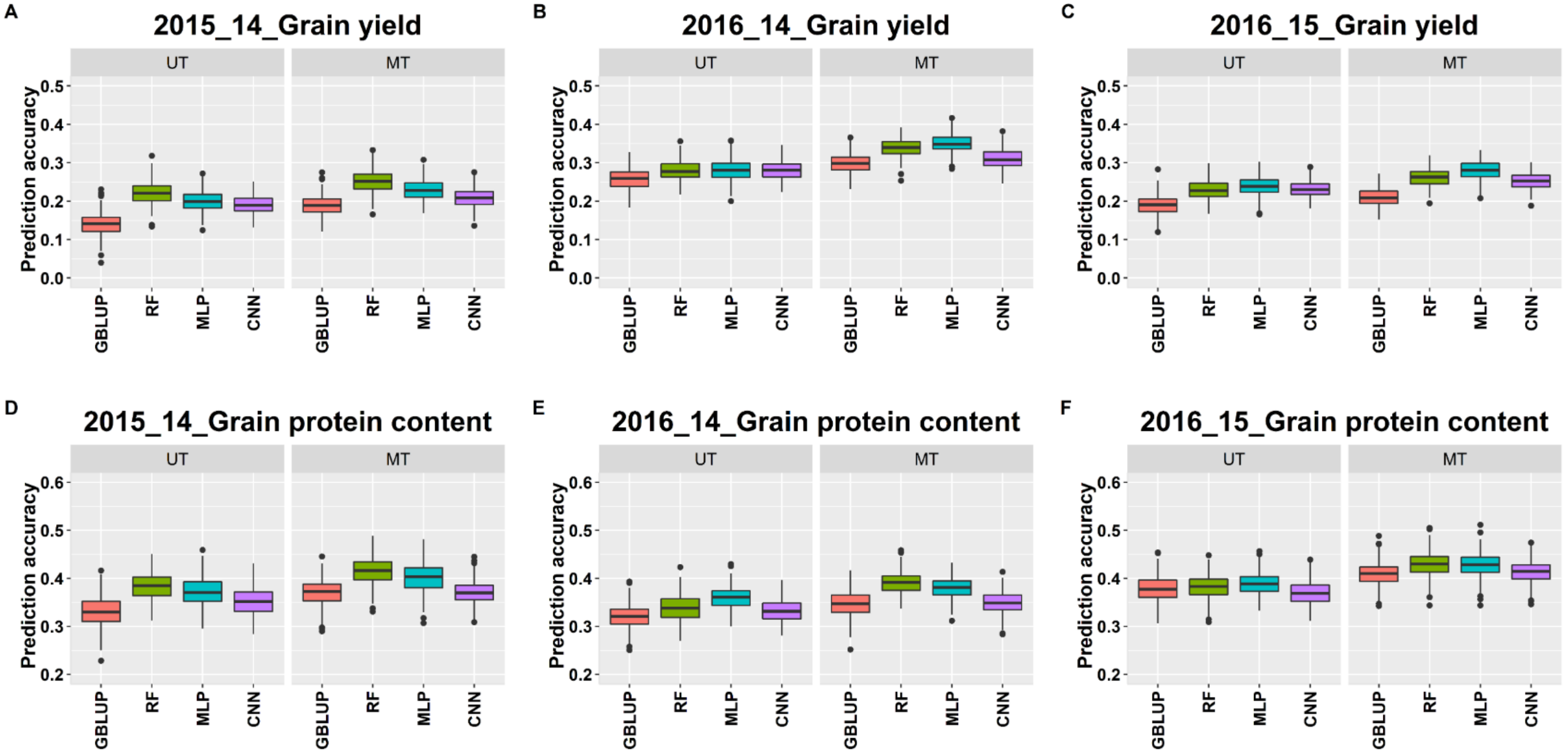
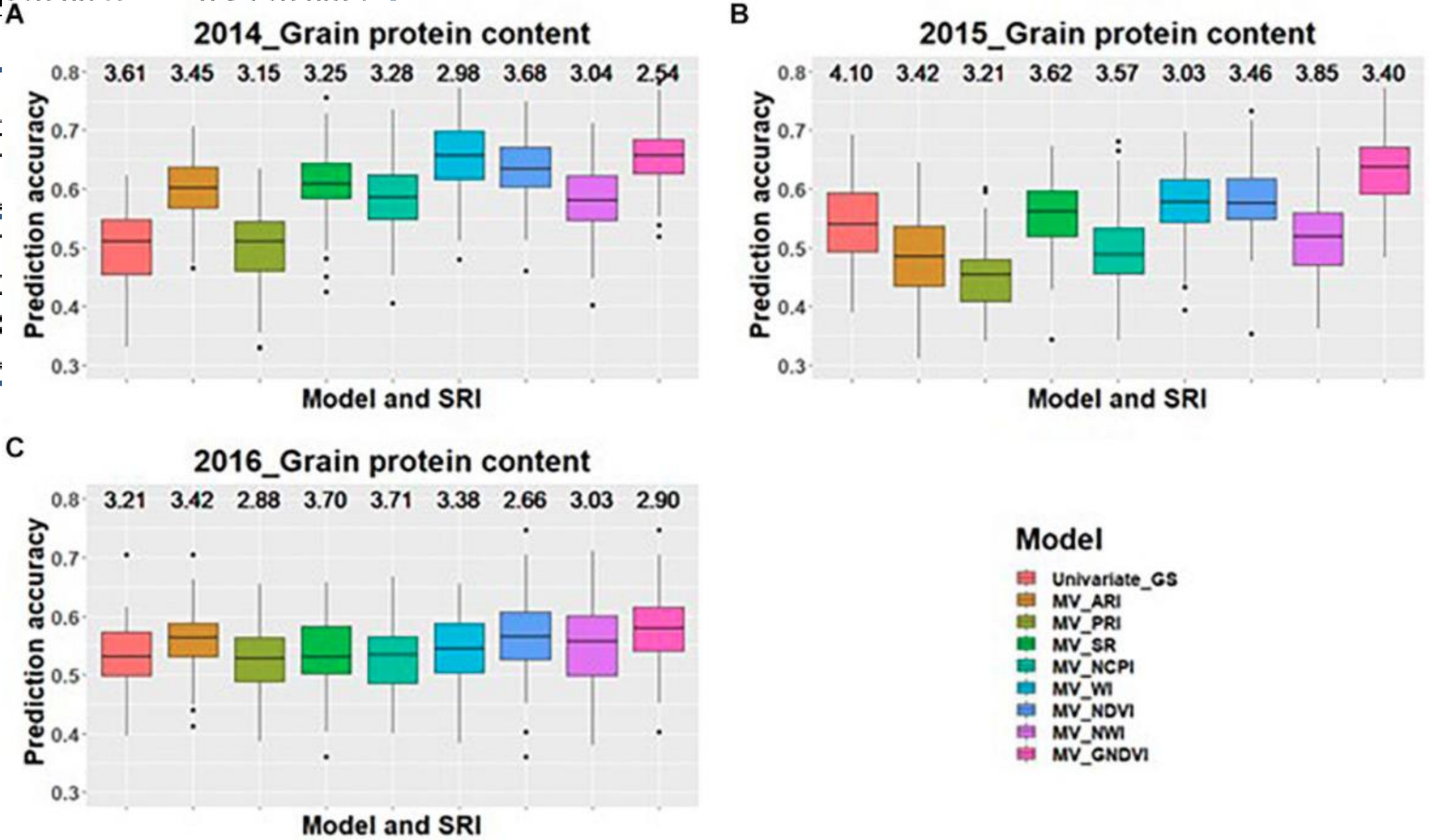


Table 5. Genomic selection accuracies for three different environments (2014-16) using univariate GS model, all spectral reflectance indices in a univariate model at heading and grain filling stage (SRIr), GS + SRI in a covariate model with SRI as covariate, and multivariate GS model for prediction of grain yield and grain protein content in a spring wheat NAM panel.

Trait	Model	Stage	2014	2015	2016
Grain yield	UniGS		0.43 (0.007)	0.40 (0.007)	0.45 (0.007)
	SRI	Heading	0.44 (0.007)	0.07 (0.009)	0.21 (0.007)
		Grain filling	0.50 (0.007)	0.13 (0.009)	0.25 (0.007)
	GS +SRI	Heading	0.52 (0.006)	0.37 (0.007)	0.52 (0.006)
		Grain filling	0.57 (0.007)	0.40 (0.007)	0.55 (0.006)
	Multi-GS	Heading	0.55 (0.006)	0.3[illegible]	[illegible]
		Grain filling	0.58 (0.007)	0.4[illegible]	[illegible]
GPC	UniGS		0.51 (0.002)	0.5[illegible]	[illegible]
	SRI	Heading	0.39 (0.007)	0.3[illegible]	[illegible]
		Grain filling	0.31 (0.007)	0.3[illegible]	[illegible]
	GS +SRI	Heading	0.63 (0.006)	0.5[illegible]	[illegible]
		Grain filling	0.59 (0.005)	0.5[illegible]	[illegible]
	Multi-GS	Heading	0.64 (0.006)	0.5[illegible]	[illegible]
		Grain filling	0.60 (0.005)	0.5[illegible]	[illegible]

Parenthesis indicates the standard error

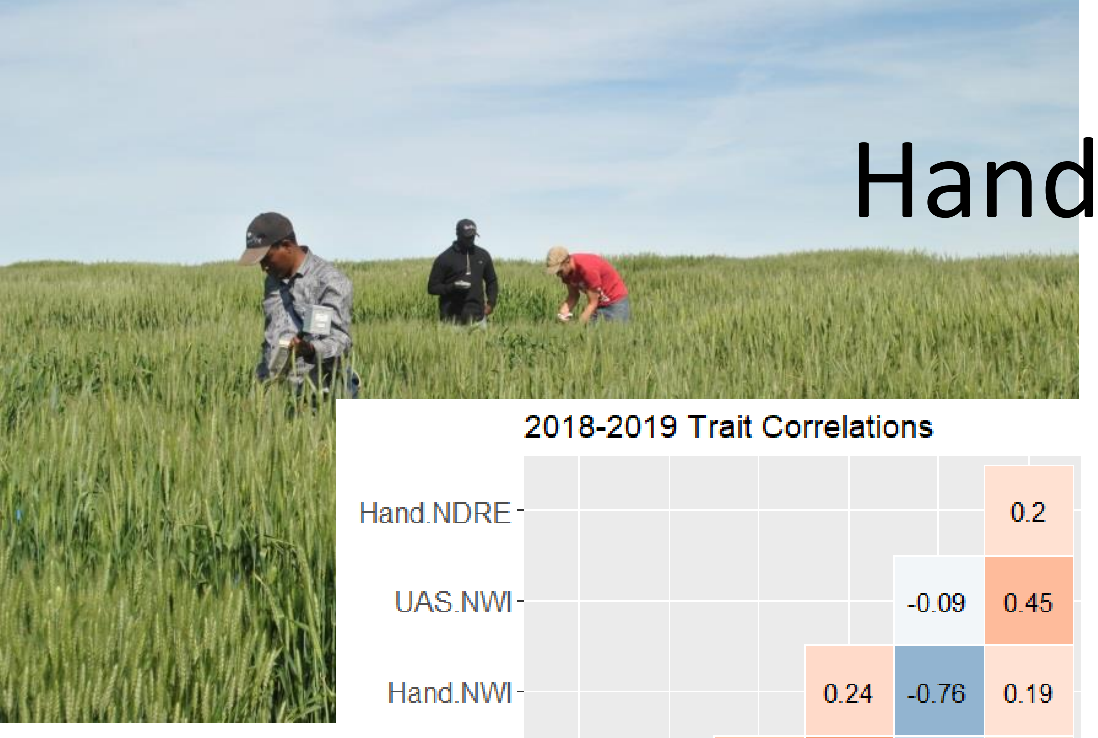


Lozada DN, Godoy JV, Ward BP, Carter AH. Genomic Prediction and Indirect Selection for Grain Yield in US Pacific Northwest Winter Wheat Using Spectral Reflectance Indices from High-Throughput Phenotyping. Int J Mol Sci. 2019 Dec 25;21(1):165. doi: 10.3390/ijms21010165.

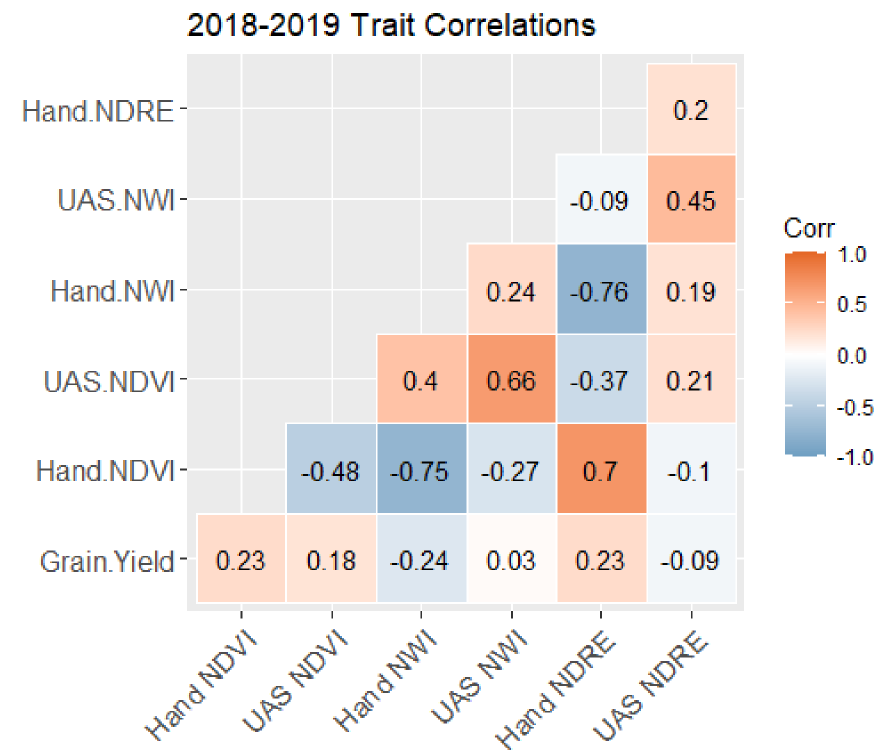
Table 3. Percentage of the top 25% (N= 115) highest yielding lines correctly selected using spectral reflectance indices across four site-years for a Pacific Northwest winter wheat diversity panel.

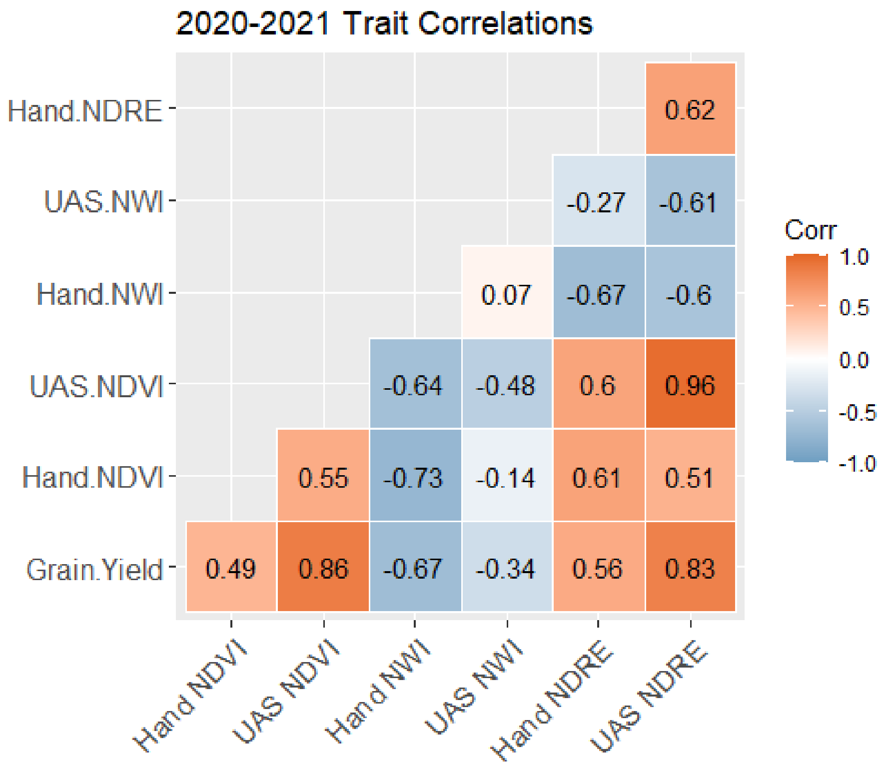
Index [1]	LND17	LND18	PUL17	PUL18
NDRE-1	66.1	47.0	29.6	29.6
NDRE-2	66.1	46.1	26.1	31.3
NDVI	65.2	47.8	31.3	29.6
NWI-1	66.1	50.4	13.9	30.4
SR	65.2	45.2	31.3	27.8

[1] NDRE- Normalized Difference Red Edge; NDVI- Normalized Difference Vegetative Index; NWI-1 Normalized Water Index; SR- Simple Ratio



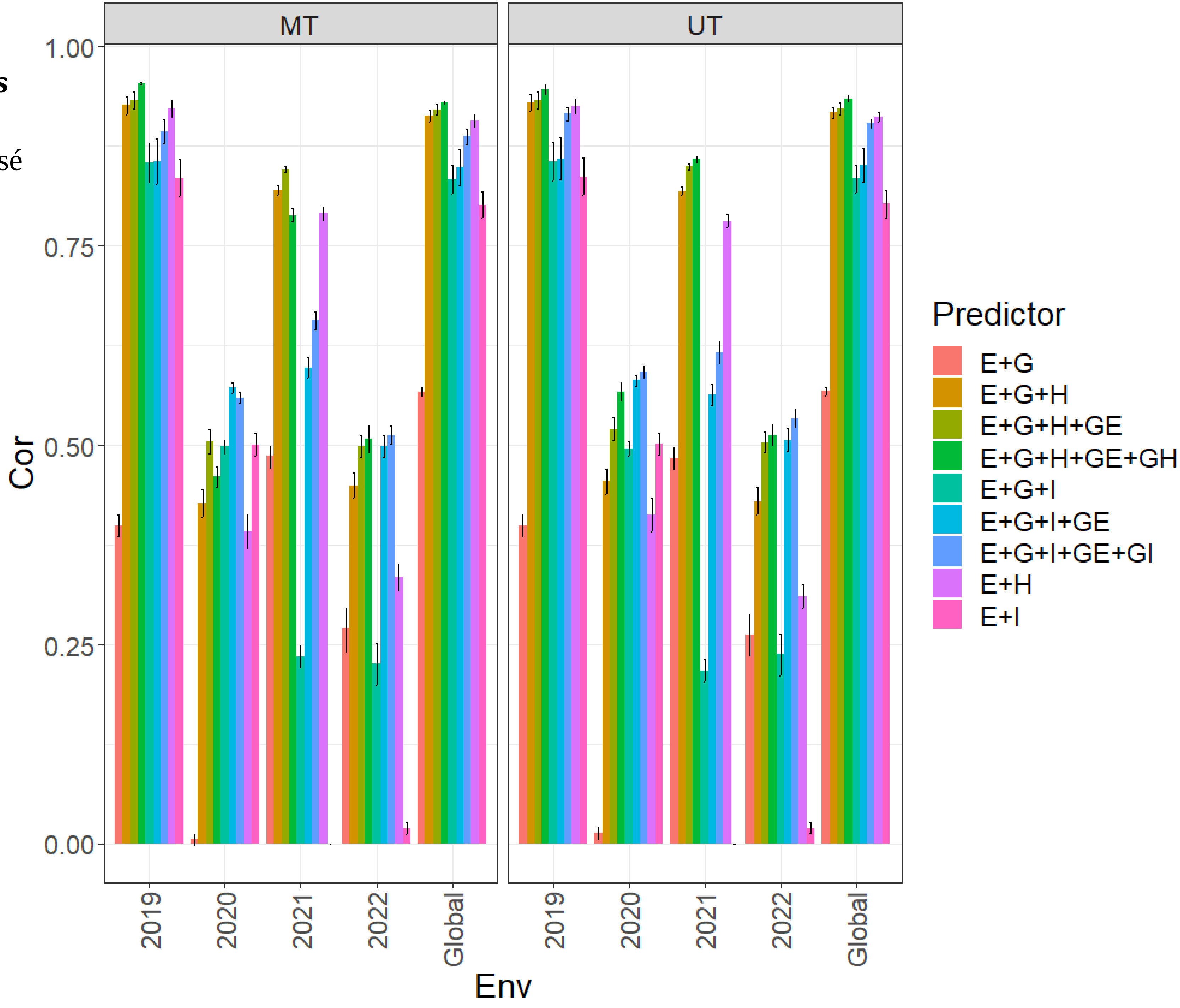
Handheld v Drone



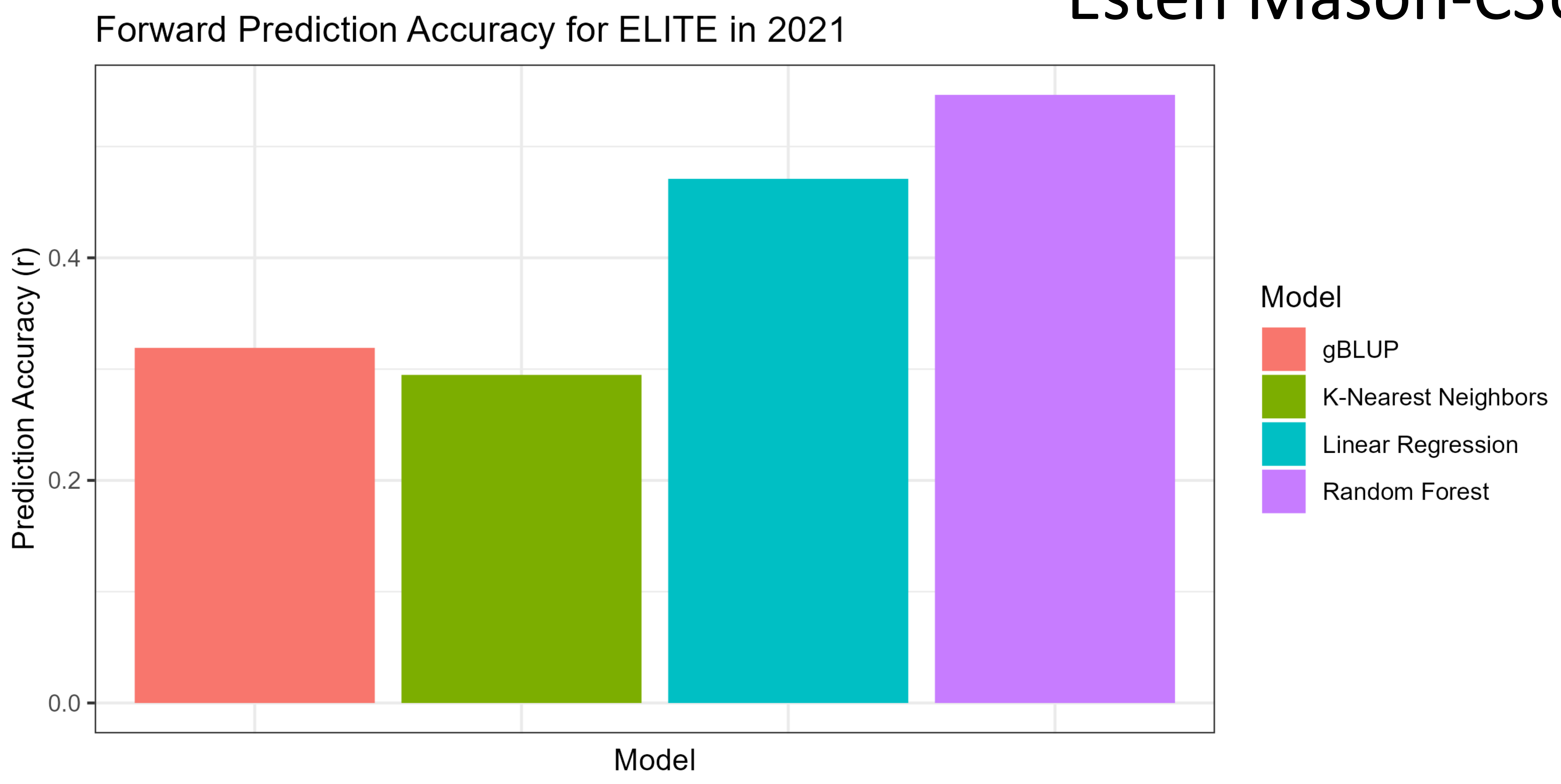


Genomics combined with UAS data enhances prediction of grain yield in winter wheat

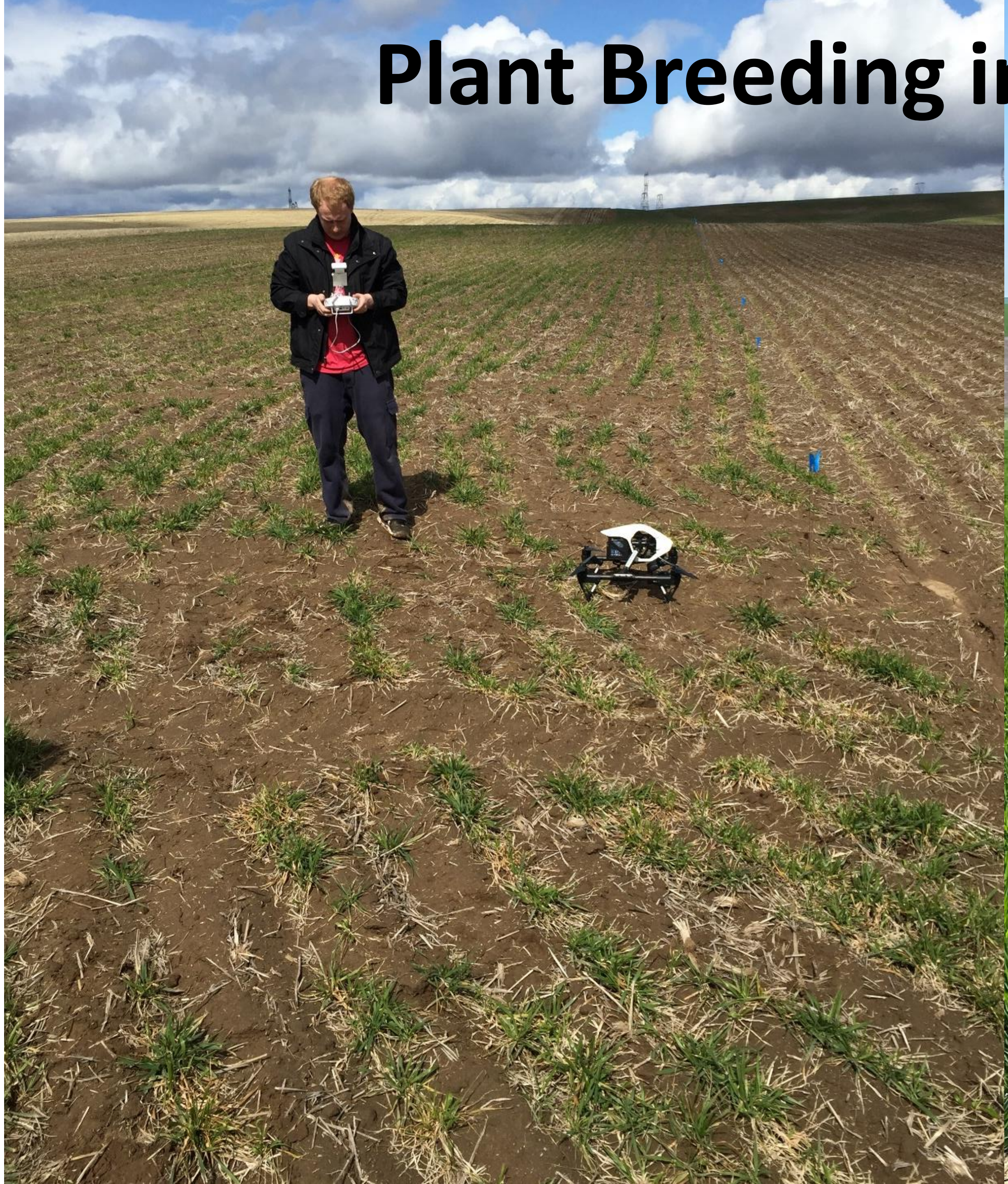
Osval A. Montesinos-López[1], Andrew W. Herr[2], José Crossa[3,4], Arron H. Carter[2*],

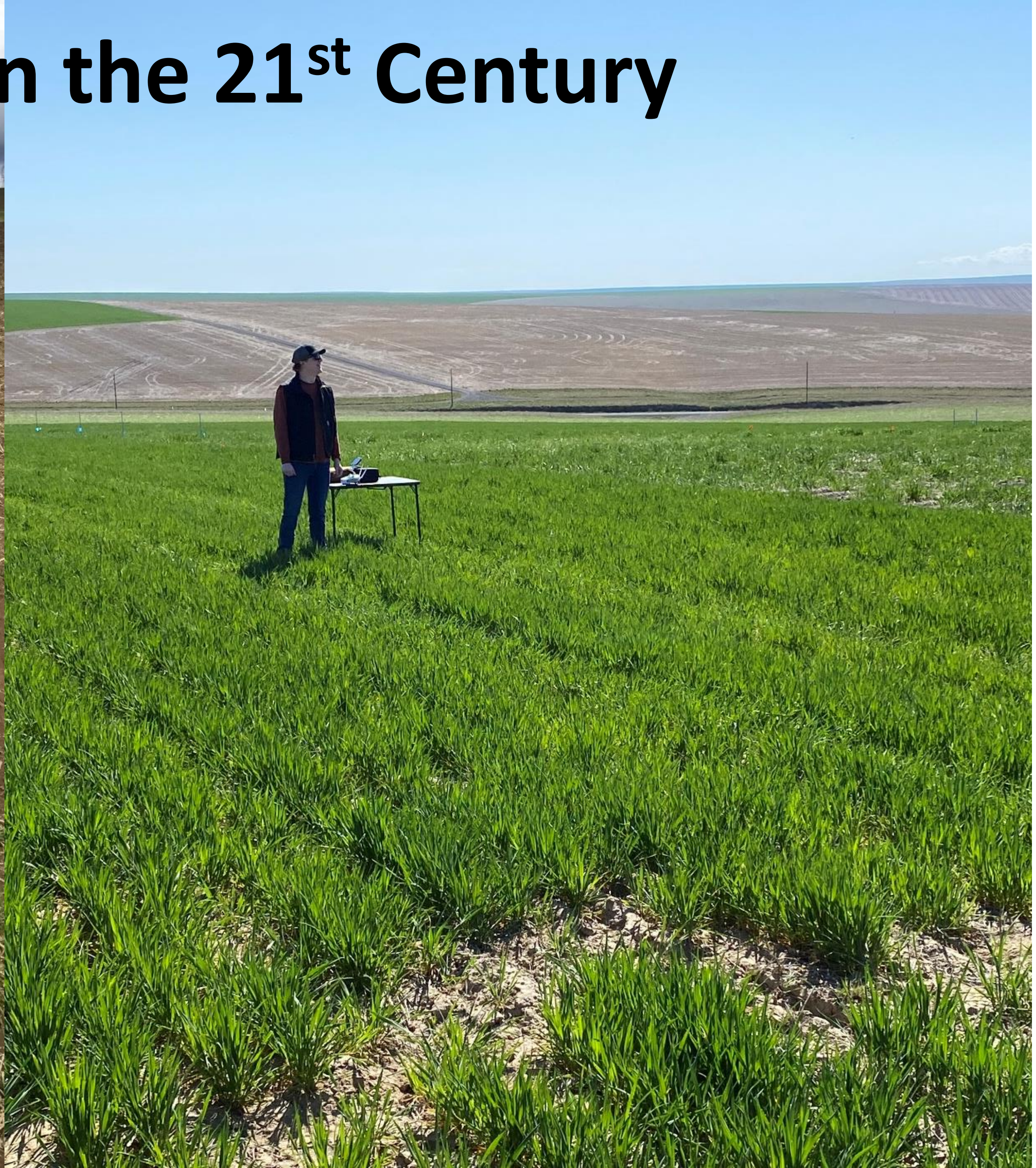


Esten Mason-CSU



Plant Breeding in the 21st Century





Plant Breeding in the 21st Century

- Ensure data is calibrated well and collect as much data as possible every year
- SRI and Model performance will vary across traits and programs
- SRI traits very useful in predicting in-season performance, but not in predicting the next year (negative selection)
- Multi-year SRI data useful in developing prediction models or combining with genomic selection
- Use selection models as another trait along with current year data

Thank you!