

## SUPPLEMENTARY MATERIAL

### **Multi-trait multi-environment genomic prediction of agronomic traits in advanced breeding lines of winter wheat**

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The genomic datasets used in this study can be found online repositories at <https://github.com/SunishSehgal/>.

Supplementary Table S1. Information of the experimental sites used in the growing seasons of 2018-19 and 2019-20.

Site	Coordinates	2018-19		2019-20	
		Date	Date	Date	Date
		seeded	harvested	seeded	harvested
Brookings (BRK)	44°18'35.3"N 96°40'14.5"W	9/16/2018	8/6/2019	9/20/2019	7/20/2020
Dakota Lakes (DL)	44°17'34.2"N 99°59'40.6"W	9/28/2018	7/23/2019	9/19/2019	7/17/2020
Hayes (HYS)	44°22'24.8"N 101°02'45.1"W	9/14/2018	7/31/2019	9/17/2019	7/21/2020
Onida (OND)	44°42'57.5"N 100°23'04.2"W	9/25/2018	8/1/2019	9/18/2019	7/28/2020
Winner (WIN)	43°29'57.0"N 99°51'58.4"W	10/2/2018	7/25/2019	9/27/2019	7/15/2020

Supplementary Table S2. Genetic correlation between five agronomic traits evaluated in 2018-19 estimated using the BMTME model. Evaluated traits include grain yield (YLD); grain protein content (PROT); test weight (TW); plant height (HT); and days to heading (HD).

<b>Trait</b>	<b>YLD</b>	<b>PROT</b>	<b>TW</b>	<b>HT</b>	<b>HD</b>
YLD	1	-0.15	0.29	0.00	-0.13
PROT	-0.15	1	0.35	-0.01	0.09
TW	0.29	0.35	1	-0.02	0.07
HT	0.00	-0.01	-0.02	1	-0.01
HD	-0.13	0.09	0.07	-0.01	1

Supplementary Table S3. Genetic correlation between five agronomic traits evaluated in 2019-20 estimated using the BMTME model. Evaluated traits include grain yield (YLD); grain protein content (PROT); test weight (TW); plant height (HT); and days to heading (HD).

<b>Trait</b>	<b>YLD</b>	<b>PROT</b>	<b>TW</b>	<b>HT</b>	<b>HD</b>
YLD	1	-0.44	-0.14	-0.43	-0.18
PROT	-0.44	1	0.25	0.38	-0.14
TW	-0.14	0.25	1	0.39	-0.09
HT	-0.43	0.38	0.39	1	0.18
HD	-0.18	-0.14	-0.09	0.18	1

Supplementary Table S4. Prediction accuracy for five traits recorded at five different environments in 2018-19 using different genomic prediction models (ST-CV1, single-trait model; MT-CV1, multi-trait model with CV1 scheme; MT-CV2, multi-trait model with CV2 scheme; MTME, multi-trait multi-environment model with CV1 scheme). The value in bold indicates the best performing model for given trait at respective location.

Trait	Env	ST-CV1		MT-CV1		MT-CV2		MTME	
		Mean PA	S.E.	Mean PA	S.E.	Mean PA	S.E.	Mean PA	S.E.
Yield	Brookings	0.28	0.005	0.29	0.02	<b>0.56</b>	0.02	0.26	0.03
	Dakota Lakes	0.32	0.004	0.28	0.03	<b>0.40</b>	0.02	0.36	0.02
	Hayes	0.38	0.004	0.35	0.02	<b>0.41</b>	0.02	0.25	0.03
	Onida	<b>0.43</b>	0.004	0.42	0.01	<b>0.43</b>	0.02	0.35	0.03
	Winner	0.13	0.005	0.03	0.02	0.15	0.03	<b>0.18</b>	0.03
	Average	0.31	-	0.27	-	<b>0.39</b>	-	0.28	-
Protein content	Brookings	0.40	0.004	0.41	0.02	<b>0.45</b>	0.02	0.33	0.03
	Dakota Lakes	0.50	0.004	<b>0.56</b>	0.02	0.51	0.02	0.45	0.03
	Hayes	0.32	0.004	0.34	0.02	<b>0.38</b>	0.02	0.26	0.03
	Onida	0.39	0.004	0.41	0.01	0.39	0.02	<b>0.46</b>	0.03
	Winner	0.15	0.004	0.20	0.02	<b>0.29</b>	0.02	0.13	0.04
	Average	0.35	-	0.38	-	0.40	-	0.32	-
Test weight	Brookings	0.31	0.004	0.31	0.02	<b>0.48</b>	0.02	0.35	0.03
	Dakota Lakes	0.23	0.005	0.23	0.01	<b>0.39</b>	0.02	0.32	0.02
	Hayes	0.50	0.004	0.49	0.02	<b>0.54</b>	0.02	0.52	0.02
	Onida	0.43	0.005	0.41	0.02	0.40	0.02	<b>0.47</b>	0.03
	Winner	0.35	0.005	0.36	0.02	0.32	0.02	<b>0.43</b>	0.02
	Average	0.36	-	0.36	-	0.42	-	0.42	-
Plant height	Brookings	0.26	0.005	0.24	0.02	0.38	0.02	<b>0.44</b>	0.03
	Dakota Lakes	0.16	0.005	0.16	0.02	0.38	0.02	<b>0.41</b>	0.04
	Hayes	0.33	0.004	0.21	0.02	0.31	0.02	<b>0.42</b>	0.03
	Onida	0.16	0.004	0.16	0.02	0.27	0.02	<b>0.45</b>	0.03
	Winner	0.32	0.004	0.30	0.02	0.34	0.02	<b>0.54</b>	0.03
	Average	0.25	-	0.21	-	0.34	-	0.42	-
Heading date	Brookings	0.46	0.004	0.46	0.03	0.44	0.03	<b>0.49</b>	0.02
	Dakota Lakes	0.33	0.005	0.32	0.02	<b>0.47</b>	0.02	0.40	0.04
	Hayes	0.23	0.005	0.24	0.02	<b>0.25</b>	0.02	0.16	0.04
	Onida	0.35	0.005	0.39	0.02	<b>0.40</b>	0.01	0.37	0.03
	Winner	0.35	0.005	0.35	0.02	<b>0.37</b>	0.02	0.37	0.03
	Average	0.34	-	0.35	-	0.38	-	0.36	-

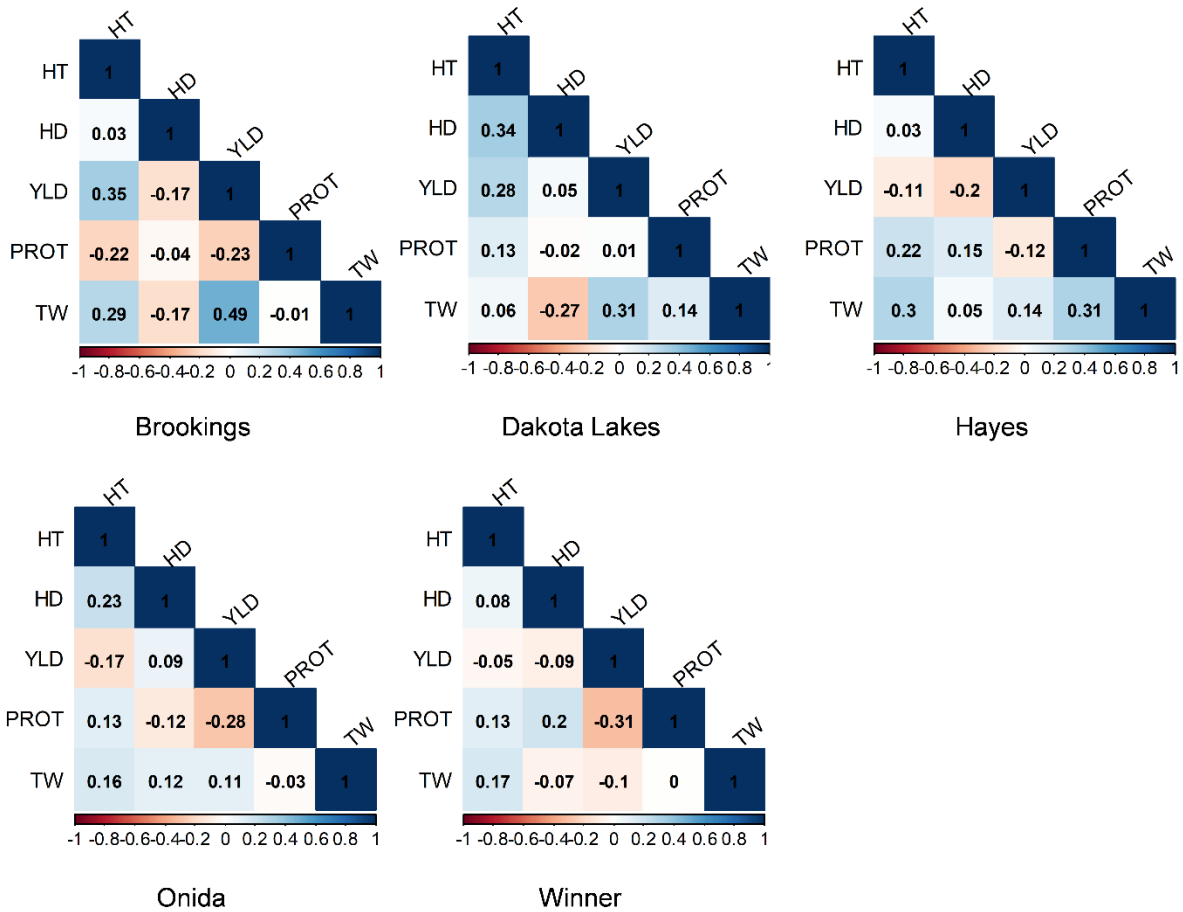
Supplementary Table S5. Prediction accuracy for five traits recorded at five different environments in 2019-20 using different genomic prediction models (ST-CV1, single-trait model; MT-CV1, multi-trait model with CV1 scheme; MT-CV2, multi-trait model with CV2 scheme; MTME, multi-trait multi-environment model with CV1 scheme). The value in bold indicates the best performing model for given trait at respective location.

Trait	Env	ST-CV1		MT-CV1		MT-CV2		MTME	
		Mean PA	S.E.	Mean PA	S.E.	Mean PA	S.E.	Mean PA	S.E.
Yield	Brookings	0.29	0.006	0.27	0.03	<b>0.52</b>	0.02	0.39	0.03
	Dakota Lakes	0.33	0.005	0.33	0.02	<b>0.57</b>	0.02	0.46	0.03
	Hayes	0.50	0.004	0.52	0.02	<b>0.71</b>	0.01	0.44	0.02
	Onida	0.44	0.003	0.41	0.02	<b>0.50</b>	0.02	0.46	0.03
	Winner	0.27	0.005	0.23	0.02	<b>0.67</b>	0.01	0.43	0.02
	Average	0.36	-	0.35	-	<b>0.59</b>	-	0.43	-
Protein content	Brookings	0.41	0.005	0.41	0.02	0.58	0.02	<b>0.62</b>	0.02
	Dakota Lakes	0.34	0.004	0.36	0.02	0.59	0.01	<b>0.67</b>	0.02
	Hayes	0.40	0.004	0.40	0.02	0.56	0.02	<b>0.59</b>	0.02
	Onida	0.26	0.005	0.22	0.02	0.31	0.02	<b>0.52</b>	0.03
	Winner	0.34	0.004	0.35	0.02	<b>0.66</b>	0.01	0.58	0.02
	Average	0.35	-	0.35	-	0.54	-	0.60	-
Test weight	Brookings	0.56	0.003	0.57	0.01	0.59	0.01	<b>0.64</b>	0.02
	Dakota Lakes	0.58	0.004	0.58	0.02	0.61	0.01	<b>0.63</b>	0.02
	Hayes	0.58	0.004	0.57	0.02	0.64	0.01	<b>0.67</b>	0.02
	Onida	0.60	0.003	0.60	0.02	0.59	0.02	<b>0.66</b>	0.02
	Winner	0.37	0.005	0.33	0.02	0.50	0.02	<b>0.53</b>	0.02
	Average	0.54	-	0.53	-	0.59	-	0.63	-
Plant height	Brookings	0.35	0.004	0.35	0.02	0.40	0.02	<b>0.51</b>	0.02
	Dakota Lakes	0.31	0.005	0.26	0.02	0.43	0.02	<b>0.44</b>	0.02
	Hayes	0.43	0.004	0.41	0.02	0.53	0.02	<b>0.59</b>	0.02
	Onida	0.28	0.005	0.24	0.03	0.43	0.02	<b>0.48</b>	0.02
	Winner	0.28	0.005	0.27	0.02	0.36	0.02	<b>0.41</b>	0.03
	Average	0.33	-	0.31	-	0.43	-	0.49	-
Heading date	Brookings	0.37	0.004	0.41	0.02	0.42	0.02	<b>0.58</b>	0.02
	Dakota Lakes	0.29	0.004	0.27	0.02	0.30	0.02	<b>0.54</b>	0.02
	Hayes	0.29	0.005	0.36	0.02	0.32	0.03	<b>0.48</b>	0.04
	Onida	0.44	0.004	0.46	0.02	0.45	0.02	<b>0.56</b>	0.02
	Winner	0.35	0.004	0.31	0.02	0.39	0.02	<b>0.48</b>	0.02
	Average	0.35	-	0.36	-	0.38	-	0.53	-

Supplementary Figure S1. Illustration of different cross-validation schemes used to evaluate different genomic prediction models.

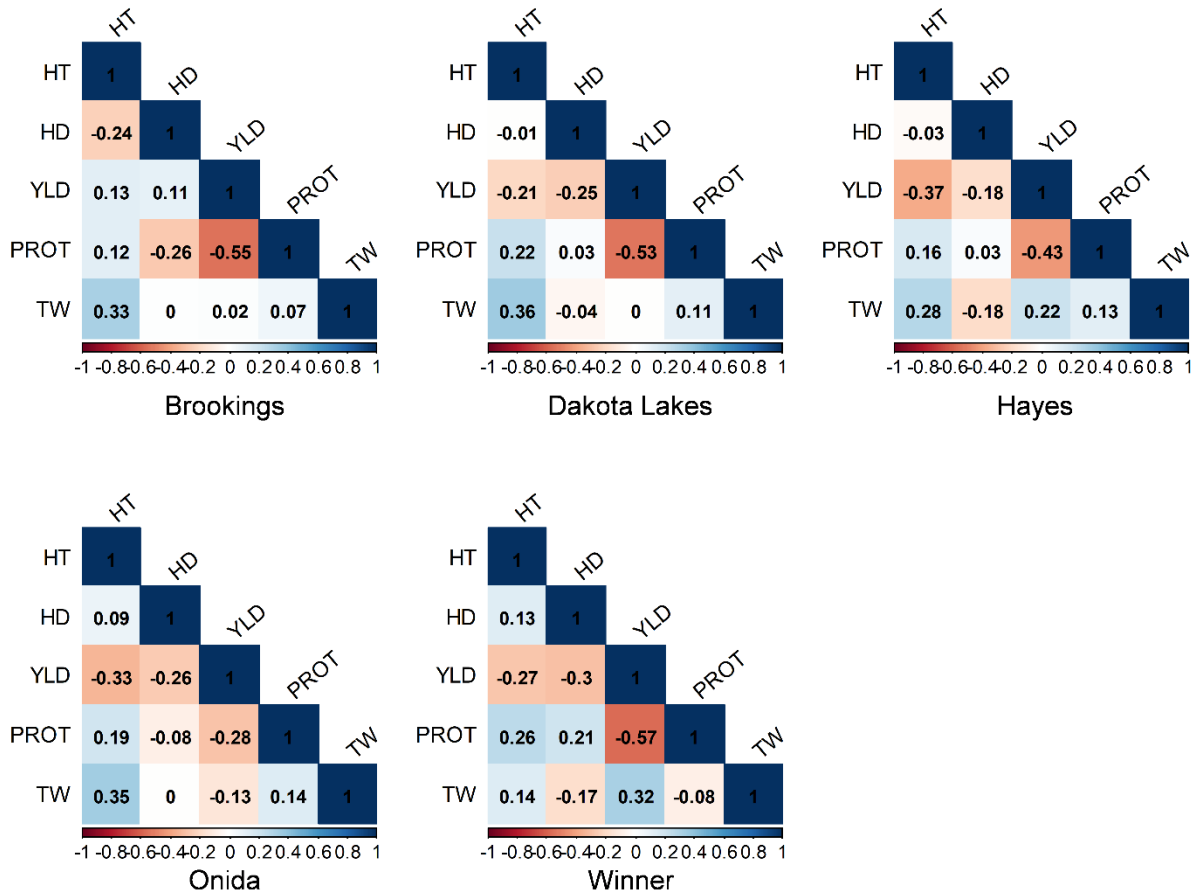
	Training set								Testing set		
Trait 1	YLD	YLD	YLD	YLD	YLD	YLD	YLD	YLD	PRED	PRED	ST-CV1
Trait 2											
Trait 3											
Trait 4											
Trait 5											
Trait 1	YLD	YLD	YLD	YLD	YLD	YLD	YLD	YLD	PRED	PRED	MT-CV1
Trait 2	PROT	PROT	PROT	PROT	PROT	PROT	PROT	PROT			
Trait 3	TW	TW	TW	TW	TW	TW	TW	TW			
Trait 4	HT	HT	HT	HT	HT	HT	HT	HT			
Trait 5	HD	HD	HD	HD	HD	HD	HD	HD			
Trait 1	YLD	YLD	YLD	YLD	YLD	YLD	YLD	YLD	PRED	PRED	MT-CV2
Trait 2	PROT	PROT	PROT	PROT	PROT	PROT	PROT	PROT	PROT	PROT	
Trait 3	TW	TW	TW	TW	TW	TW	TW	TW	TW	TW	
Trait 4	HT	HT	HT	HT	HT	HT	HT	HT	HT	HT	
Trait 5	HD	HD	HD	HD	HD	HD	HD	HD	HD	HD	

Supplementary Figure S2. Correlation coefficients among five agronomic traits recorded at five locations in 2018-19. Evaluated traits include YLD, grain yield; PROT, grain protein content; TW, test weight; HT, plant height; and HD, days to heading.

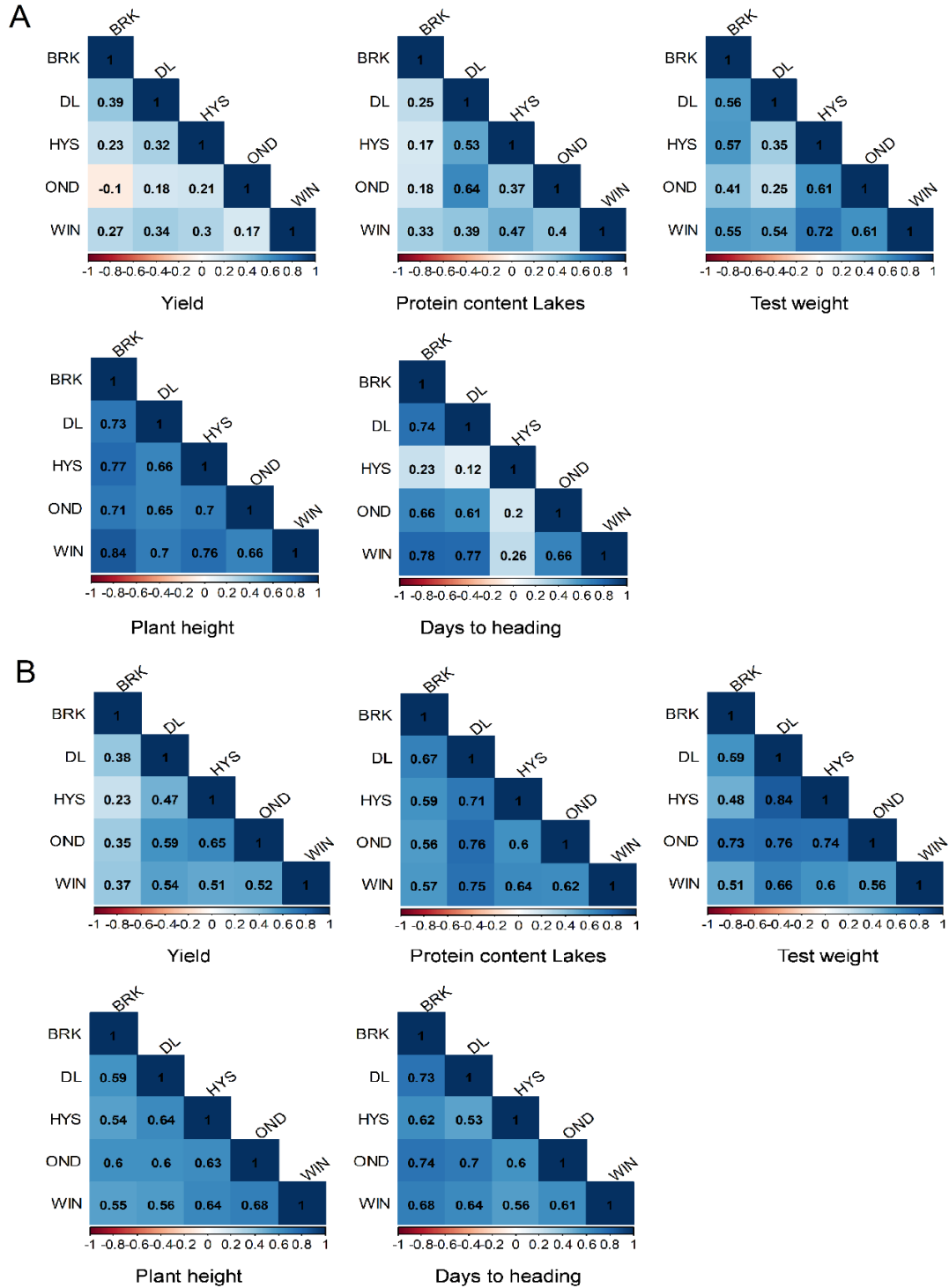




Supplementary Figure S3. Correlation coefficients for five agronomic traits evaluated at five locations in 2019-20. Evaluated traits include grain yield (YLD); grain protein content (PROT); test weight (TW); plant height (HT); and days to heading (HD).



Supplementary Figure S4. Correlation coefficients among five environments (Brookings, BRK; Dakota Lakes, DL; Hayes, HYS; Onida, OND; and Winner, WIN) for five traits evaluated in (A) 2018-19 and (B) 2019-20.



Supplementary Figure S5. Heatmap of the kinship matrix using 10,294 SNPs (**A**) for 151 lines evaluated in the growing season of 2018-19, and (**B**) for 156 lines evaluated in the growing season of 2019-20.

