

Predicting Sorghum Hybrid Performance using Genomic and Phenomic Data



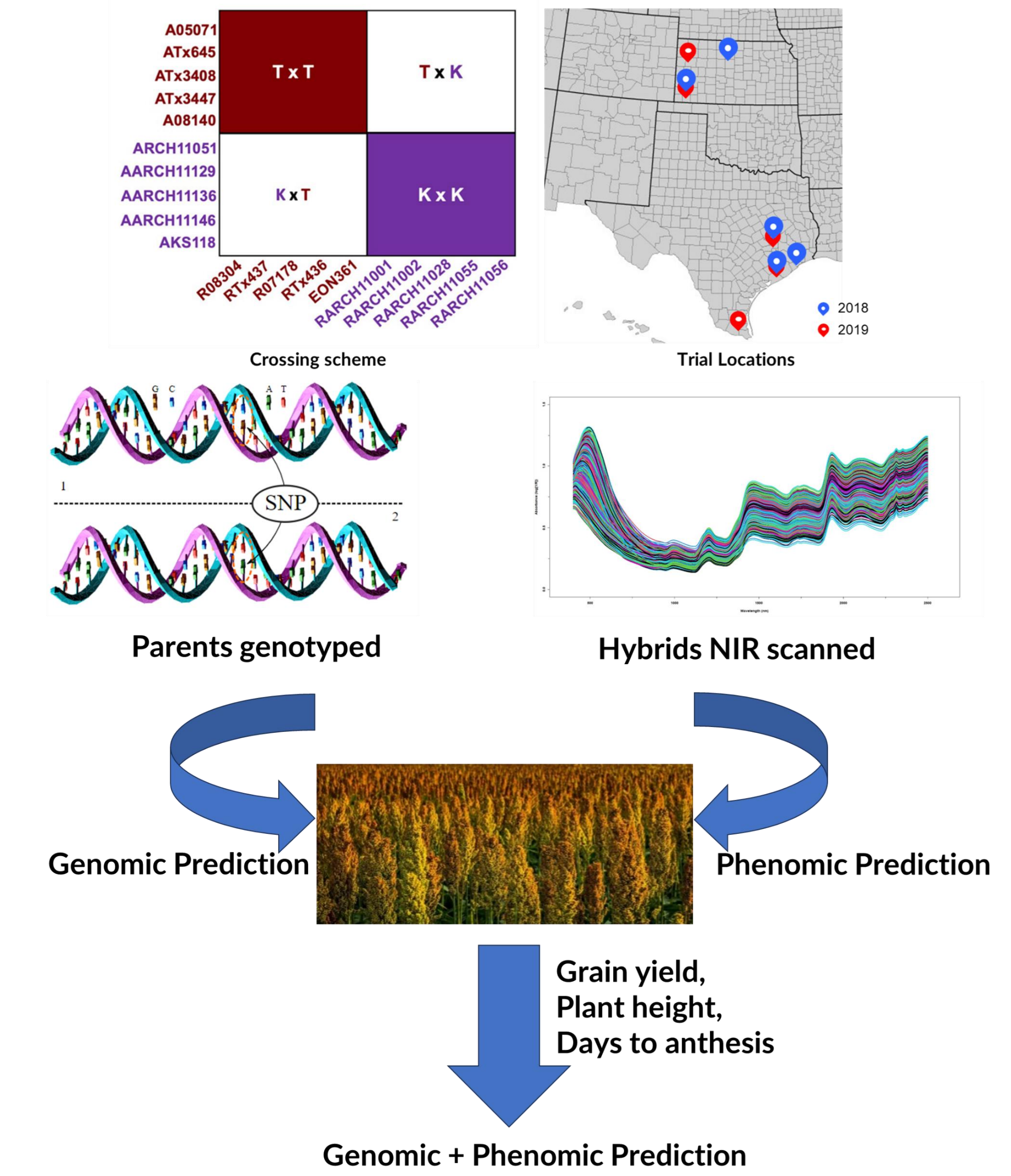
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BACKGROUND: Genomic Prediction (GP) and Phenomic Prediction (PP) could accelerate the rate of genetic gain in sorghum breeding programs. Near Infrared Spectroscopy (NIR) is widely employed to predict composition traits, however, it could also be used in the same way as genetic markers to predict agronomic performance.

Could NIR effectively predict agronomic traits of sorghum hybrids ?
Can inclusion of NIR improve prediction accuracy of genomic prediction models ?

METHODS



Prediction Models

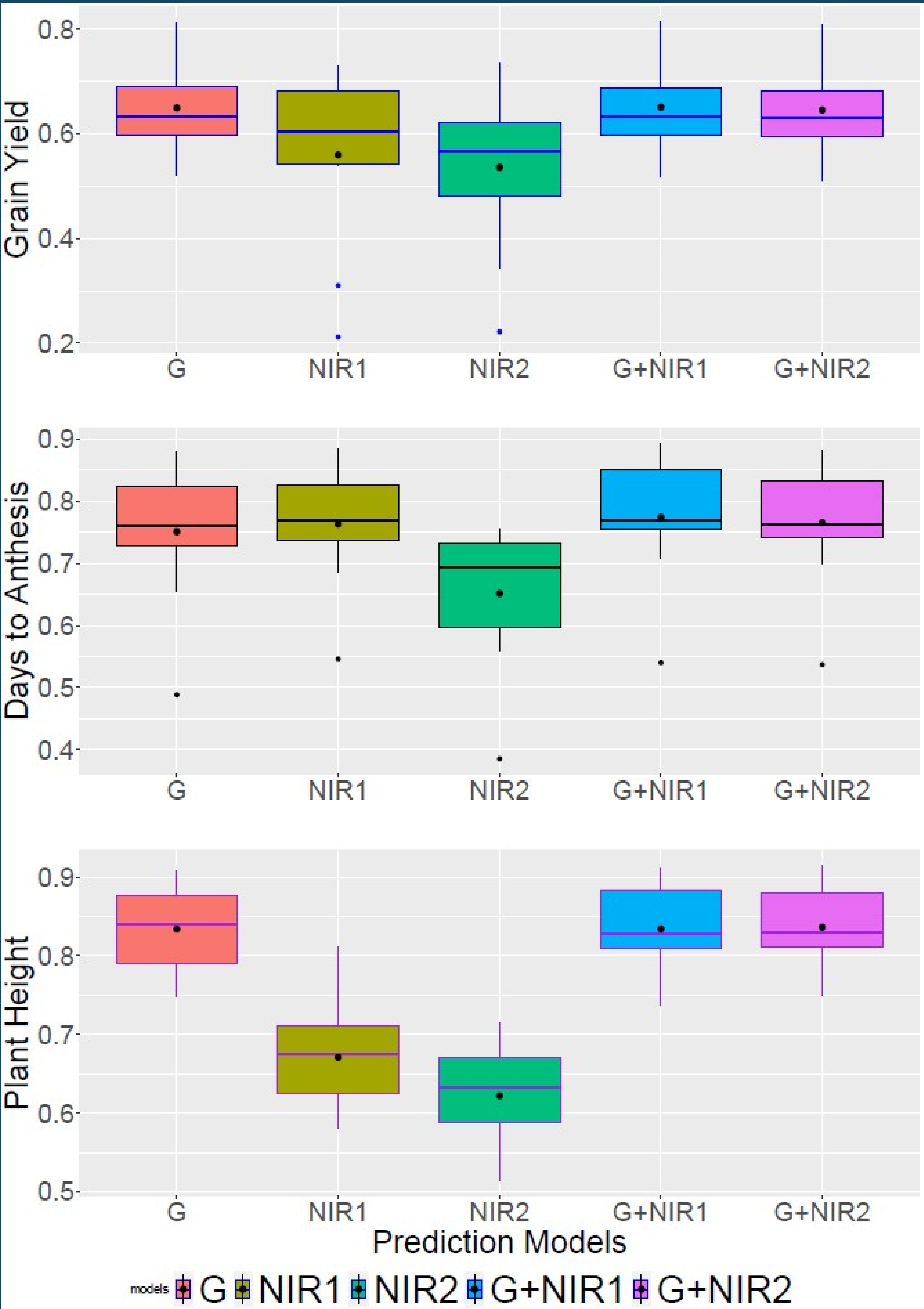
- G : Genomic markers
- NIR1 : First derivative of NIR
- NIR2 : Second derivative of NIR
- G + NIR1: markers + NIR1
- G + NIR2: markers + NIR2
- ❖ Kernel based GBLUP models with 70:30 were run with 20 repetitions

MAJOR FINDINGS

- ❖ NIR has the potential to predict agronomic traits in sorghum when there are grain samples from a range of environments
- ❖ NIR1 performs better than NIR2 in general showing data smoothing of spectra with first derivative is reliable
- ❖ NIR offers an opportunity to improve prediction accuracy

Phenomic prediction performed statistically as good as genomic prediction for traits related to grain physiochemical properties i.e. grain yield, and days to anthesis

Overall prediction accuracy of prediction models across all the environments



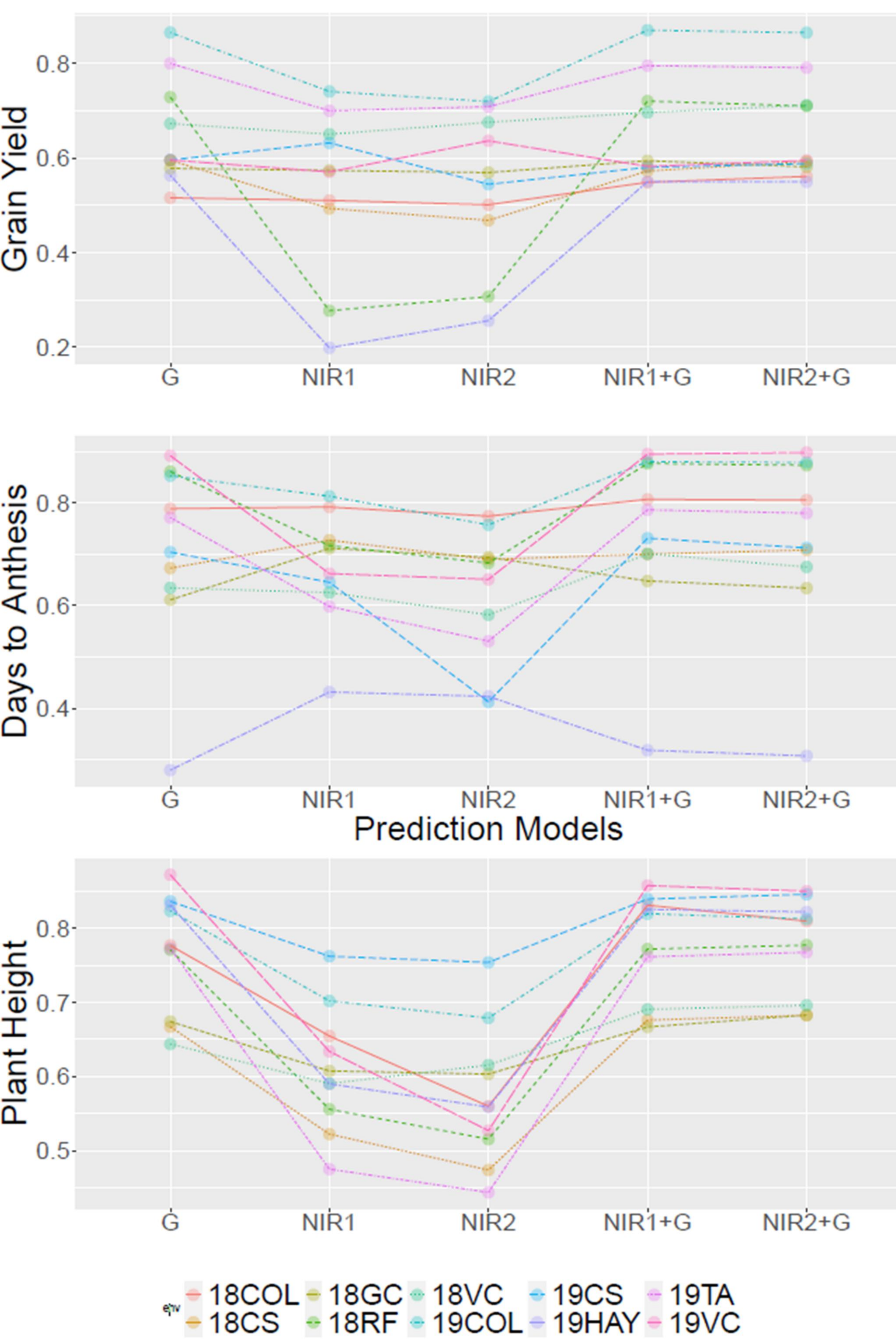
Statistical groupings of models at $\alpha = 0.05$

Models	GY	DA	PH
G	0.649 ^{NS}	0.751 ^a	0.834 ^a
NIR1	0.560 ^{NS}	0.763 ^a	0.671 ^b
NIR2	0.536 ^{NS}	0.651 ^b	0.622 ^b
G+NIR1	0.650 ^{NS}	0.775 ^a	0.835 ^a
G+NIR2	0.645 ^{NS}	0.766 ^a	0.837 ^a

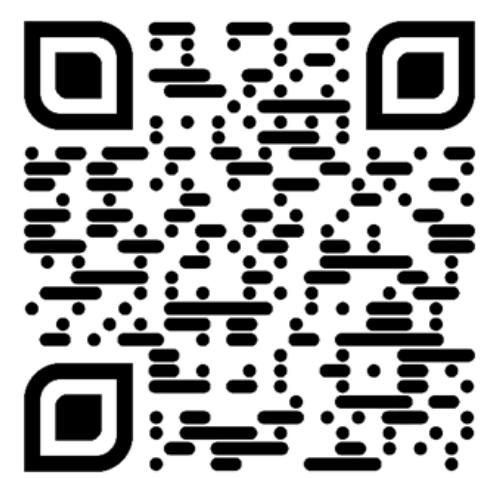
NS: Non-significant; a and b represent different statistical groups
GY: grain yield, DA: Days to Anthesis, PH: Plant Height

- ❖ Markers and NIR have similar predictability for grain yield
- ❖ Markers and NIR1 have similar predictability for DA
- ❖ Markers outperformed NIR in predicting PH

Prediction accuracy of different prediction models within environments



- ❖ NIR could supplement/complement genomic prediction models depending on traits of interest
- ❖ Characterizing spectra to capture G X E would be interesting when grain samples from range of environments are available



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