MAGIC-EFFICIENCY

Characterization of agronomic traits under two contrasting nitrogen regimes in the winter wheat MAGIC population WM800

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Introduction

Wheat (*Triticum aestivum* L.) takes almost one third of the world cereal production. However, wheat must be adapted and improved with regard to the climate change and the increase of global population. Especially the management of nitrogen (N) fertilization is crucial for yield and quality but, simultaneously, has a big environmental impact and its fertilization is restricted by law. Therefore, the genetic dissection of nitrogen efficiency regulation offers the opportunity to contribute to climate protection without a loss in yield and quality.

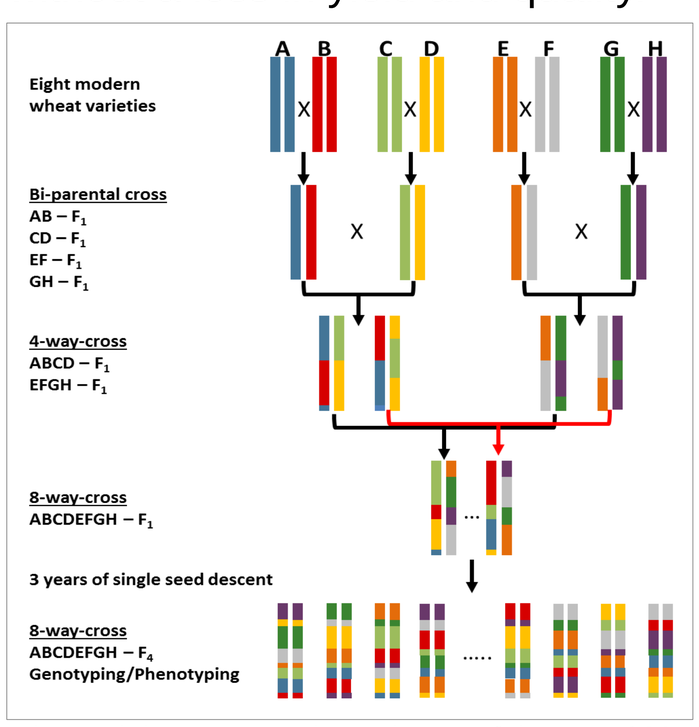

Fig.1: Eight-way crossing scheme of the WM-800 population (Sannemann et al. 2018)

UAV data (multispectral 670-980 nm & thermal) were analyzed applying a random forest model using 5 fold cross validation with 10 repeats.

Material and Method

The WM-800 population was developed in collaboration with Syngenta Seeds and RAGT by crossing the following eight German elite winter wheat cultivars (Fig. 1).

[(Patras * Meister) * (Linus * JB Asano)] * [(Tobak * Bernstein) * (Safari * Julius)]

Genotypic data of WM-800 were collected through Illumina wheat 15k SNP array and Affymetrix 135k array analyses, carried out by TraitGenetics, Gatersleben. The assays delivered 27,685 informative SNPs with physical positions according to wheat Refseq 1.0 (IWGSC 2018).

The population was investigated in a first field trial at Martin-Luther-University Halle-Wittenberg in 2019 under two contrasting nitrogen levels (N-: 100 kg N/ha, N+: 240 kg N/ha). Phenotypic data for developmental and yield traits were collected, combining classical scoring and sensor-based phenotyping with UAVs (unmanned aerial vehicles). The R package mvngGrAd (Technow, 2013) was used to adjust for within-field environmental variation.

Results and Conclusion

Highly significant differences ($p<0.001$) between the nitrogen regimes and the genotypes within the regimes could be observed for the traits yield (YLD) and grain protein content (GPC). The WM-800 shows an increased YLD under N+ treatment with a high CV (Tab. 1).

Trait	N Level	N	mean [a)]	SD [b)]	CV [%] [c)]	Rep [d)]
YLD	N-	800	59,86	6,16	10,29	0,64
	N+	800	69,37	7,35	10,59	0,61
GPC	N-	799	14,48	0,81	5,60	0,87
	N+	800	13,57	0,80	5,89	0,82

Tab. 1: Descriptive statistics of four agronomic traits evaluated in WM800. a) mean trait performance b) standard deviation c) coefficient of variation = SD/mean d) repeatability = VG/(VG+VR/r), calculated with founders and checks

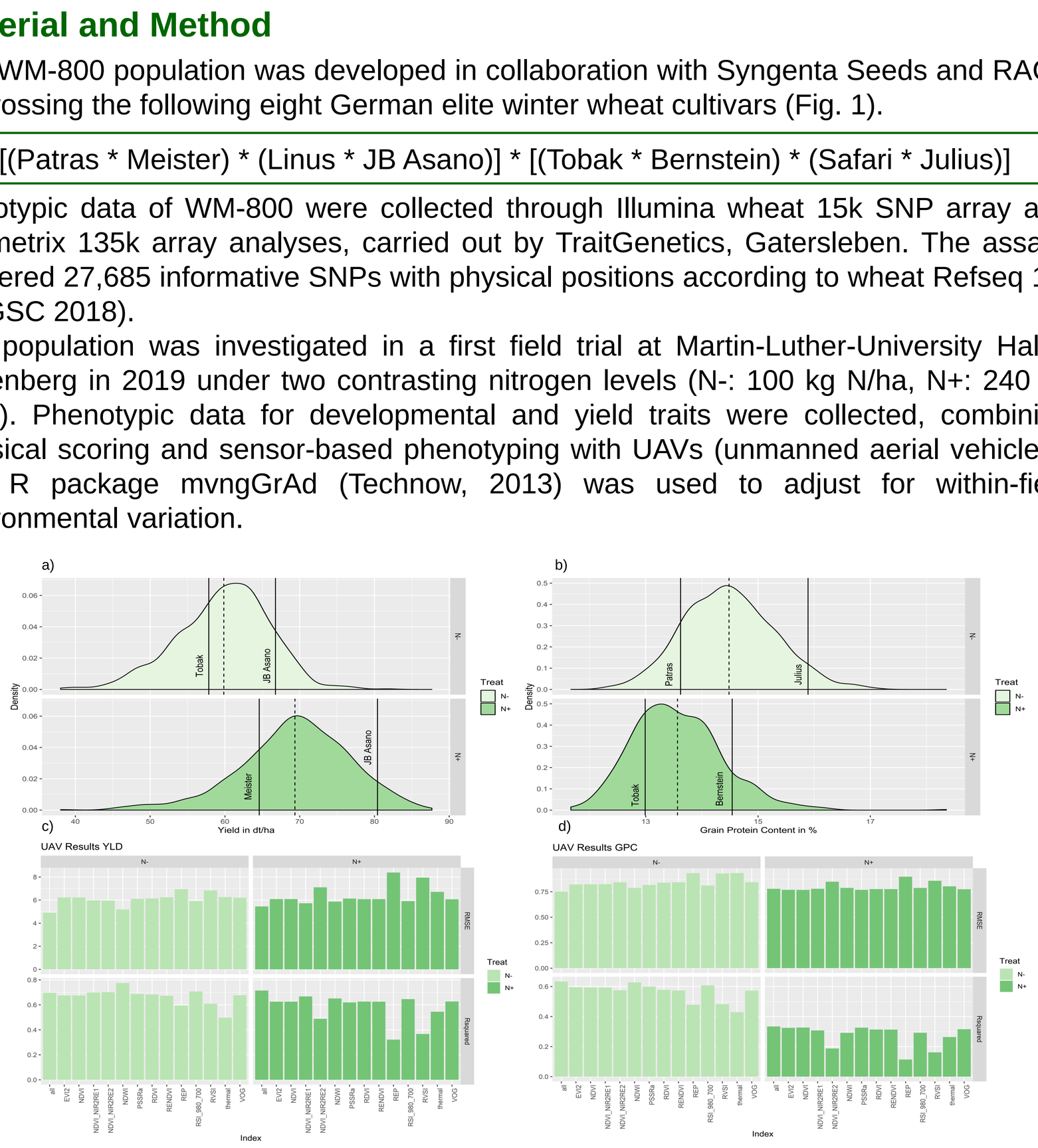

Fig. 2: Histograms illustrating frequency distribution of agronomic traits (a & b) and corresponding R^2 and RMSE values from the random forest modell from UAV data (c & d). N- indicates the treatment with nitrogen starvation, N+ indicates the one with added nitrogen. The dashed line indicates the population mean, the solid lines indicate the founder with the lowest and highest trait value. a) Yield in dt/ha. b) Grain protein content (GPC) in %. c) R^2 & RMSE for YLD. d) R^2 & RMSE for GPC.

GPC is lower in the N+ than in the N- treatment (Fig. 2). Higher YLD in N+ suggests, that GPC is lower in N+ due to a dilution effect.

Prediction of the ground truth data with multispectral UAV data results in high R^2 values and low mean prediction errors (RMSE) for YLD in both treatments. The best model is the one using all vegetation indices (all).

Prediction of GPC works well in the N- treatment but R^2 values in the N+ are low.

Outlook

The WM-800 will be phenotyped in a second field trial in Halle 2020, using UAV with RGB, multispectral and thermal cameras for further investigation of nitrogen-efficiency.

The FZ Jülich investigates root morphology under contrasting N regimes and BASF conducts a trial with high throughput phenotyping also under contrasting N regimes. A third project investigates backing quality with a hyperspectral camera and carries out elemental analysis (ICP-OES and C/N). To identify loci controlling nitrogen efficiency, genome wide association studies (GWAS) will be conduced.

Acknowledgements

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