



# MAGIC-EFFICIENCY

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

Laura Schmidt<sup>1</sup>, U. Seifert<sup>2</sup>, K. Nagel<sup>3</sup>, J. Jacobs<sup>4</sup>, E. Kazman<sup>5</sup>, H. Cöster<sup>6</sup>, J. Holzapfel<sup>7</sup>, E. Ebmeyer<sup>8</sup>, T. Gerjets<sup>9</sup>, Klaus Pillen<sup>1</sup>, W. Sannemann<sup>1</sup>

<sup>1</sup>Chair of Plant Breeding, Martin-Luther-University Halle-Wittenberg, Germany; <sup>2</sup>IFF Magdeburg, <sup>3</sup>Forschungszentrum Jülich; <sup>4</sup>BASF; <sup>5</sup>Syngenta Seeds;

<sup>6</sup>RAGT 2n; <sup>7</sup>Secobra Saatzauch GmbH; <sup>8</sup>KWS Lochow; <sup>9</sup>GFPi.

E-Mail: laura.schmidt@landw.uni-halle.de

### 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 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.

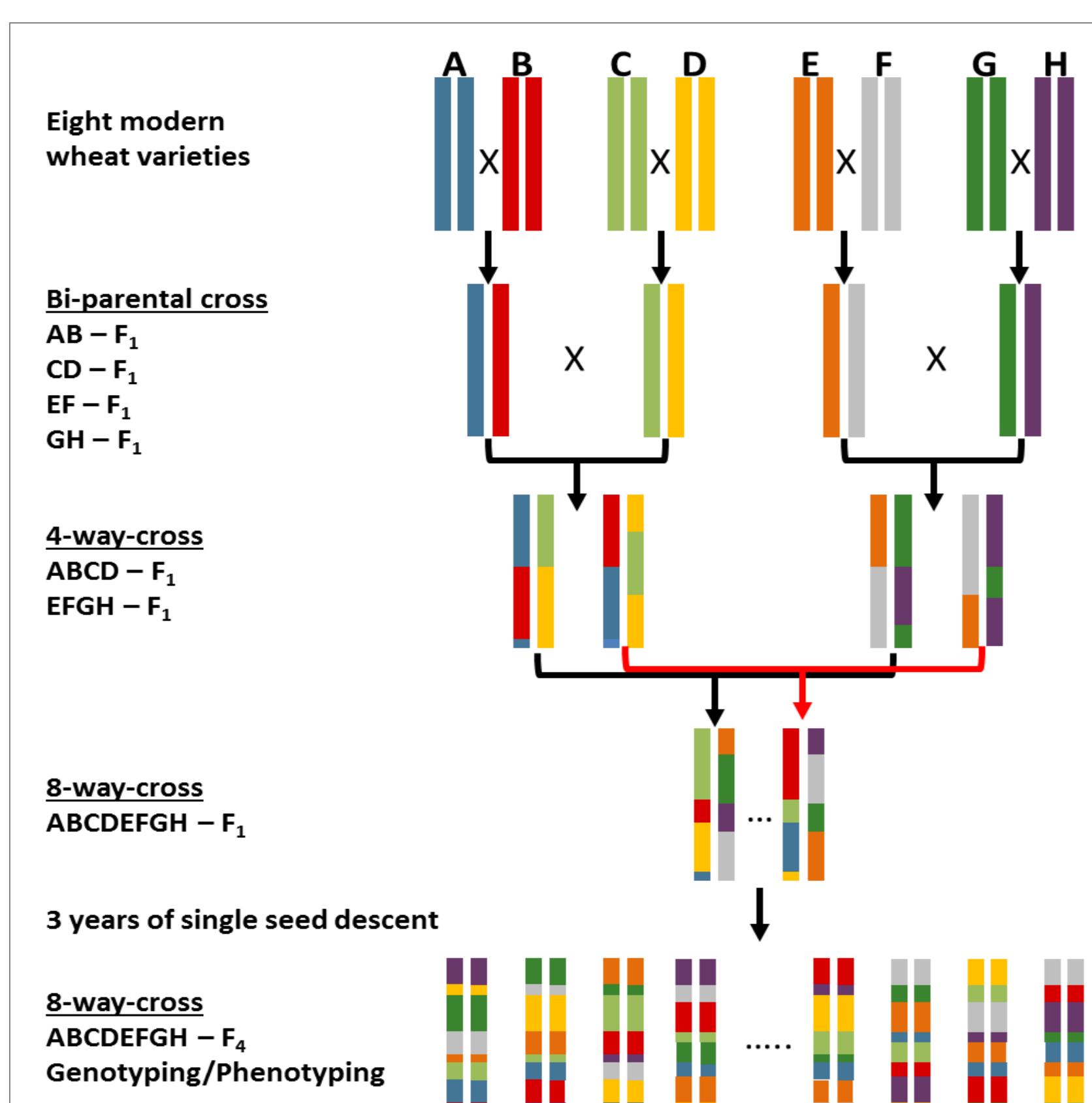


Fig.1: Eight-way crossing scheme of the WM-800 population (Sannemann et al. 2018)

### 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 analysis, 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.

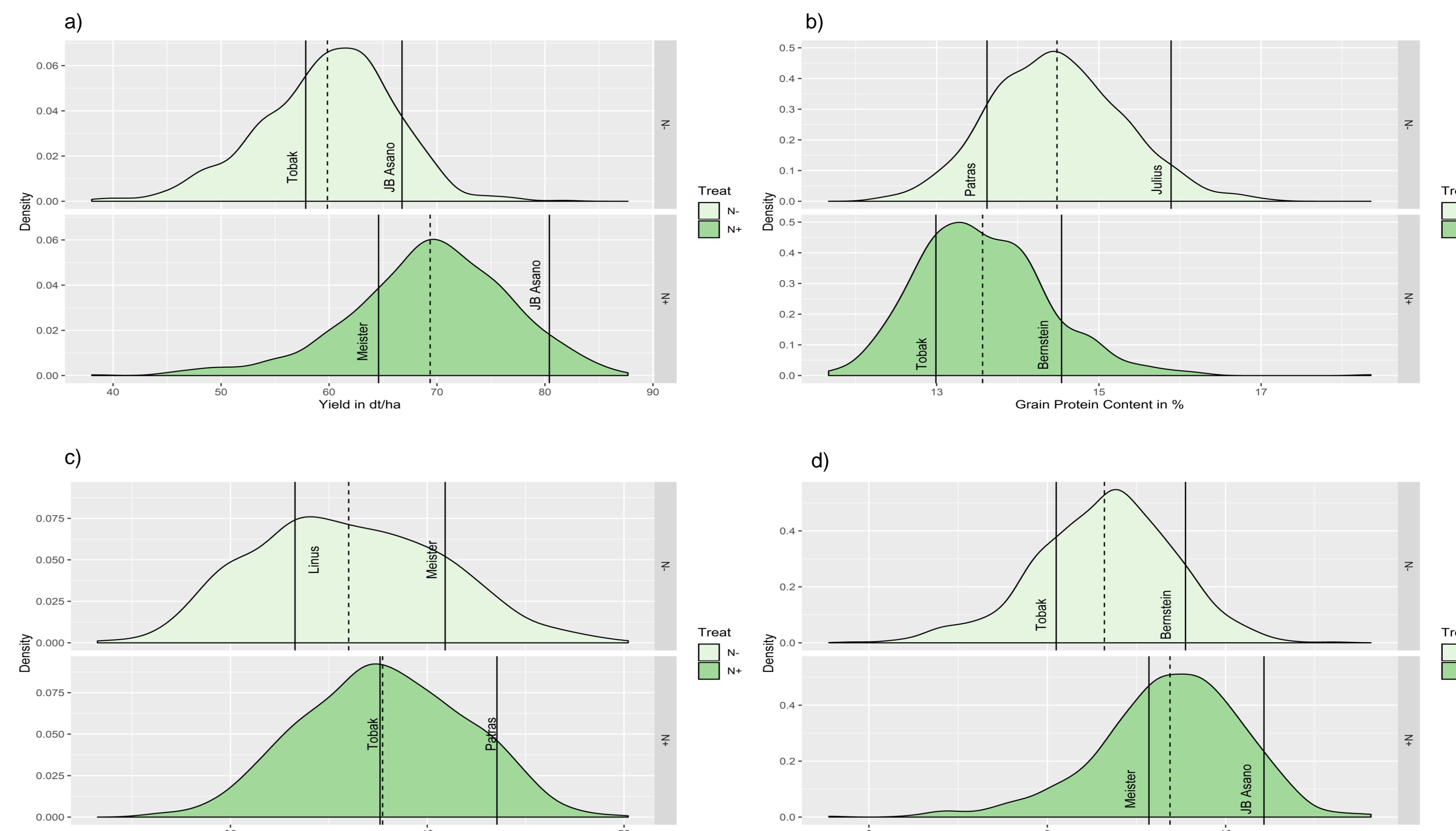


Fig. 2: Histograms illustrating frequency distribution of agronomic traits. N- indicates the treatment with nitrogen starvation, N+ indicates the one with added nitrogen. The dashed line indicates the population mean, the solid lines indicate the founder with the lowest and highest trait value. a) Yield in dt/ha. b) Grain protein content (GPC) in %. c) Thousand kernel weight in g. d) Protein-Yield as a product of yield and GPC in dt/ha.

### 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), grain protein content (GPC), thousand kernel weight (TKW) and protein-yield (PYLD). The WM-800 showed an increased YLD, PYLD and TKW under N+ treatment with a high CV for all three traits (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
TKW	N-	799	36,01	4,78	13,27	0,94
	N+	800	37,83	4,13	10,91	0,77
PYLD	N-	799	8,64	0,76	8,85	0,72
	N+	800	9,38	0,82	8,72	0,63

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 founder and checks

GPC is lower in the N+ treatment than in the N- treatment. Higher YLD and PYLD in N+ suggests, that GPC is lower in N+ due to a dilution effect. For all four traits there are WM-800 lines showing higher or lower trait values than the best and worst founder (Fig. 2).

### Acknowledgements

This work is supported by BMEL

syngenta  
SEEDS

BASF  
The Chemical Company

Fraunhofer  
IAP

JÜLICH

Bundesministerium für  
Ernährung, Landwirtschaft und Verbraucherschutz  
SECOBRA  
recherches  
GFPi

This indicates transgressive segregation in the WM800.

### Outlook

The WM-800 will be phenotyped in a second field trial in Halle 2020. Data from the UAV with RGB, multispectral 670-980nm and thermal cameras will be used for further investigation of nitrogen-efficiency. The Forschungs-

zentrum 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 conducted.

### References

- Sannemann et al. 2018. Adaptive selection of founder segments and epistatic control of plant height in the MAGIC winter wheat population WM-800. *BMC Genomics* 19.
- International Wheat Genome Sequencing Consortium (IWGSC) 2018. Shifting the limits in wheat research and breeding using a fully annotated reference genome. *Science*, 361(6403), [eaar7191].
- Technow 2015. R package mvngGrAd: moving grid adjustment in plant breeding field trials. R package version 0.1.5