



Genetic dissection of ingredients in grains determined by hyperspectral imaging (HSI) associated with yield-related traits in a wild barley NAM population

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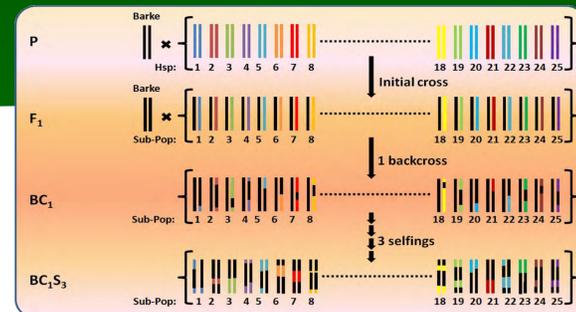
Introduction

Breeding for increased yield leads to a reduction in grain quality, resulting in a conflict between calories and nutritional value of cereal grains. About 30% of the world population are estimated to suffer from Fe or Zn deficiency, especially in developing countries. To overcome the problem of hidden hunger cereal grains have to be fortified with essential minerals. Genetic biofortification offers promising potential to improve grain nutrient concentration. As genetic variation is mandatory for this kind of approach, we used the barley NAM population ‘Halle Exotic Barley’ (HEB-25) to study phenotypic variation in genetic resources (Maurer et al. 2015). HEB-25 consists of 1,420 BC₁S₃ lines, subdivided into 25 families with up to 75 individuals. Each line resulted from initial crosses between the German barley cultivar ‘Barke’ and one of the

25 highly divergent wild barley accessions from the Fertile Crescent.

Methods

Field trials in 2014 and 2015 were conducted at the experimental station ‘Kühnfeld’ of Halle University (Herzig et al. 2018). Four yield component traits and total grain yield, as well as 15 macro & micro ingredients have been investigated. These were spectroscopically determined by hyperspectral imaging (HSI) and linked to grain nutrient concentrations (ICP-OES) by means of multivariate data processing and trained neural networks. Subsequently, we carried out a genome-wide association study (GWAS) with 5,398 informative SNPs. GWAS results were verified in 20 replications of 5-fold cross-validation.



Results

Overall, we observed a broad phenotypic variation for most of the investigated traits, with broad-sense heritabilities of 19.8–89.7%. Eight grain ingredients could be grouped with very similar positive correlations among each other (Fig. 1). Predominantly negative correlations between YLD, TGW, GNE and EAR and grain ingredients were found.

The accuracy of ingredient determination by HSI was sufficient for subsequent GWAS analysis in the diverse wild barley NAM population HEB-25. For most ingredient traits the full GWAS model revealed reliable results and explained 63–75% of the phenotypic variance. Decreasing and increasing wild allele effects compared to the reference parent ‘Barke’ could be identified. In addition, genomic regions comprising *Ppd-H1*, *HvCEN* and *HvGA20ox2*, which accelerate flowering in HEB-25, seem to increase grain ingredient concentrations (Fig. 2). For instance, the *HvGA20ox2* region increased Fe, GPC and Zn by 5.5–6.9% without any yield loss and is a promising target for introgression of exotic alleles into barley elite breeding material.

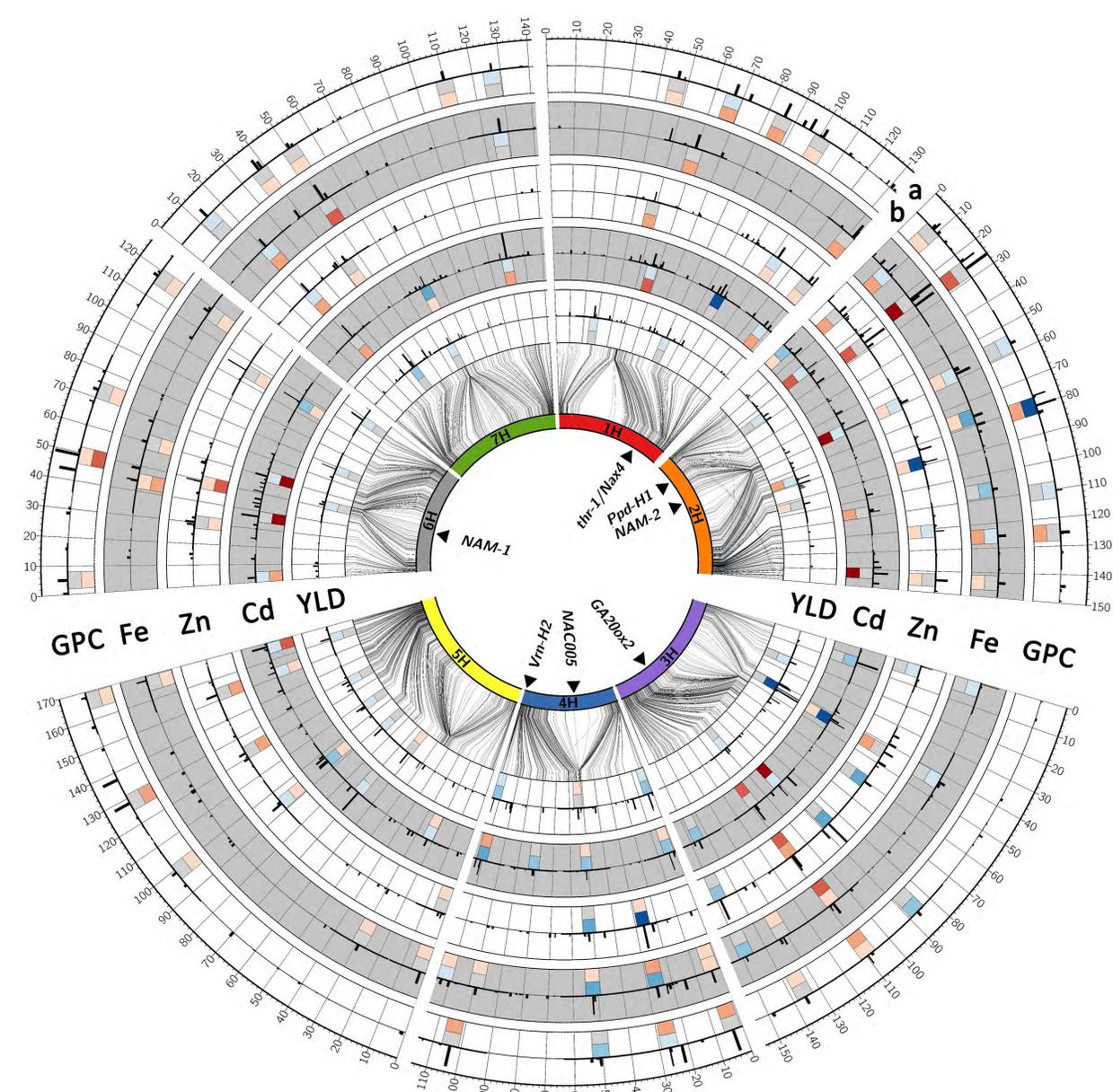


Fig. 2: GWAS results for four grain ingredients and YLD.

Barley chromosomes are shown as coloured bars on the inner circle. Connector lines represent the translation between the physical position (inside) and genetic map position in cM (outside) of each marker. (a) Height of black bars indicate the QTL detection rate (DR) in 100 cross-validation runs during GWAS procedure. QTLs with a detection rate ≥ 25 are defined as reliable. Below those, family-specific effects are indicated as coloured boxes (b). The minimum and the maximum effects across the 25 families are represented as heat map in the upper and lower part of the box, respectively.

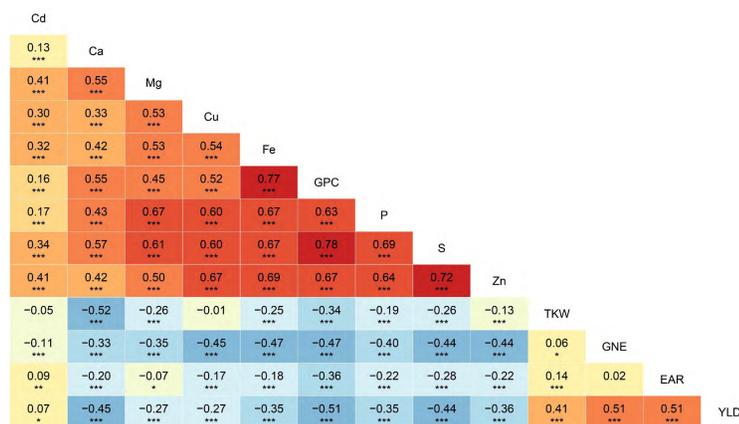


Fig. 1. Pearson's correlation coefficients.

Cadmium (Cd), Calcium (Ca), Magnesium (Mg), Copper (Cu), Iron (Fe), Grain Protein Content (GPC), Phosphorus (P), Sulfur (S), Zinc (Zn), Thousand Grain Weight (TGW), Grain Number per Ear (GNE), Ears per m² (EAR), Plot Yield (YLD). Significant correlation coefficients are indicated with: * P < 0.05, ** P < 0.01 and *** P < 0.001

References

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Acknowledgements

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