

Diseminarea informatiilor

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- Michel, S., Ametz, C., Gungor, H., Akgöl, B., Epure, D., Grausgruber, H., Buerstmayr, H. (2017). Genomic assisted selection for enhancing line breeding: merging genomic and phenotypic selection in winter wheat breeding programs with preliminary yield trials. *TAG. Theoretical and Applied Genetics. Theoretische Und Angewandte Genetik*, 130(2), 363–376. <http://doi.org/10.1007/s00122-016-2818-8>.
- Epure, D., Becheritu, M., Cioineag, C. (2017) Prediction of drought resistant lines of winter wheat using canopy temperature depression and chlorophyll content analysis. *Agrolife Scientific Journal, Volume 6 (1)*, 104-111.
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Genomic assisted selection for enhancing line breeding: merging genomic and phenotypic selection in winter wheat breeding programs with preliminary yield trials

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Abstract

Key message Early generation genomic selection is superior to conventional phenotypic selection in line breeding and can be strongly improved by including additional information from preliminary yield trials.

Abstract The selection of lines that enter resource-demanding multi-environment trials is a crucial decision in every line breeding program as a large amount of resources are allocated for thoroughly testing these potential varietal candidates. We compared conventional phenotypic selection with various genomic selection approaches across multiple years as well as the merit of integrating phenotypic

information from preliminary yield trials into the genomic selection framework. The prediction accuracy using only phenotypic data was rather low ($r = 0.21$) for grain yield but could be improved by modeling genetic relationships in unreplicated preliminary yield trials ($r = 0.33$). Genomic selection models were nevertheless found to be superior to conventional phenotypic selection for predicting grain yield performance of lines across years ($r = 0.39$). We subsequently simplified the problem of predicting untested lines in untested years to predicting tested lines in untested years by combining breeding values from preliminary yield trials and predictions from genomic selection models by a heritability index. This genomic assisted selection led to a 20% increase in prediction accuracy, which could be further enhanced by an appropriate marker selection for both grain yield ($r = 0.48$) and protein content ($r = 0.63$). The easy to implement and robust genomic assisted selection gave thus a higher prediction accuracy than either conventional phenotypic or genomic selection alone. The proposed method took the complex inheritance of both low and high heritable traits into account and appears capable to support breeders in their selection decisions to develop enhanced varieties more efficiently.

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Introduction

Selection and development of new varieties of autogamous crops relies on a number of different breeding schemes including the pedigree and bulk methods as well as breeding acceleration using doubled haploids or single seed descent with off-season generations. Notwithstanding, they all share a step of conventional phenotypic selection based on preliminary yield trials in their methodology. These preliminary yield trials are for the larger part unreplicated

Improving the baking quality of bread wheat by genomic selection in early generations

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Abstract

Key message Genomic selection shows great promise for pre-selecting lines with superior bread baking quality in early generations, 3 years ahead of labour-intensive, time-consuming, and costly quality analysis.

Abstract The genetic improvement of baking quality is one of the grand challenges in wheat breeding as the assessment of the associated traits often involves time-consuming, labour-intensive, and costly testing forcing breeders to postpone sophisticated quality tests to the very last phases of variety development. The prospect of genomic selection for complex traits like grain yield has been shown in numerous studies, and might thus be also an interesting method to select for baking quality traits. Hence, we focused in this

study on the accuracy of genomic selection for laborious and expensive to phenotype quality traits as well as its selection response in comparison with phenotypic selection. More than 400 genotyped wheat lines were, therefore, phenotyped for protein content, dough viscoelastic and mixing properties related to baking quality in multi-environment trials 2009–2016. The average prediction accuracy across three independent validation populations was $r = 0.39$ and could be increased to $r = 0.47$ by modelling major QTL as fixed effects as well as employing multi-trait prediction models, which resulted in an acceptable prediction accuracy for all dough rheological traits ($r = 0.38$ – 0.63). Genomic selection can furthermore be applied 2–3 years earlier than direct phenotypic selection, and the estimated selection response was nearly twice as high in comparison with indirect selection by protein content for baking quality related traits. This considerable advantage of genomic selection could accordingly support breeders in their selection decisions and aid in efficiently combining superior baking quality with grain yield in newly developed wheat varieties.

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Introduction

The genetic improvement of baking quality is one of the grand challenges in winter wheat breeding due to its complex inheritance pattern, which is governed mainly by wheat storage proteins, foremost the prolamins gliadin and glutenin (Payne 1987; Shewry et al. 1995, 2003) as well as their interaction with other fractions like the puroindolins that confer grain hardness (Bekes 2012a; Quayson et al. 2016; Würschum et al. 2016). The quality of these wheat storage proteins can be determined by various measurements, amongst others by dough rheological tests that assess the viscoelastic and mixing properties during dough preparation