

Phenotypic and genetic analysis of biomass and grain yield in hybrid rye

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Abstract

Winter rye (*Secale cereale* L.) is becoming increasingly important as substrate for biogas production in Central Europe and contributes to diversify crop rotation systems in agricultural bioenergy production. Dry matter yield has evolved as a novel breeding goal comparably important than traditional grain yield. In this study, we aimed at the identification of indirect phenotypic and molecular selection parameters for dry matter yield to increase the genetic gain of this parameter.

The study was conducted with 258 elite testcross progenies for dry matter yield harvested at late milk stage and grain yield harvested at full ripening at three to four locations in Germany in 2011 and 2012. Further, we collected data for heading time, plant height in three stages and number of spikes per square meter. We observed a wide range of dry matter yield (10-24 t·ha⁻¹) and grain yield (6-15 t·ha⁻¹) among testcross progenies. Genetic variances were significantly ($P < 0.01$) different from zero for all traits. High entry-mean heritabilities ($H^2 = 0.76-0.94$) were found for three plant height measurements and moderate heritabilities ($H^2 = 0.52$ and 0.49 , respectively) for grain and dry matter yield. We observed a moderate correlation between plant height at EC 51-55/ EC 73 and dry matter yield ($r = 0.64$, $r = 0.52$, respectively, $P < 0.01$) and a low correlation between grain yield and dry matter yield ($r = 0.33$, $P < 0.01$). Expected gain from direct selection for dry matter yield was 0.15 t·ha⁻¹ per year. Indirect selection for dry matter yield

using plant height at EC 51-55 was more effective (0.19 t·ha⁻¹ per year). Indirect selection of dry matter yield by grain yield was less effective (0.08 t·ha⁻¹ per year).

For the construction of the genetic map, we used a total of 911 SSR- and DArT-markers covering 964 cM of the rye genome. In total, we observed 23 QTL based on adjusted entry means using software PLABMQTL of the assessed agronomic traits. Most QTL were found for heading time (7) followed by plant height at EC 73 (6). Single QTL explained between 46% (plant height at EC 51-55) and 5% (third plant height at EC 73) of the genotypic variance. We have identified co-localized QTL for plant height and dry matter yield on chromosomes 2R and 5R, which supports the strong phenotypic correlation between both traits.

Indirect selection for dry matter yield using plant height at EC 73 should be successful to improve dry matter yield in rye. However, additionally improved lodging resistance should be selected. QTL with high effects on plant height were found that allow to improve selection gain by marker-assisted selection. The observed broad genetic variation for biomass yield in elite experimental hybrids gives good prospects for breeding improved hybrid rye as a renewable source of biogas production.

Keywords

Biogas, dry matter yield, indirect selection, plant height, *Secale cereale*

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References

HAFFKE S, KUSTERER B, FROMME FJ, ROUX S, HACKAUF B, MIEDANER T, 2014: Analysis of covariation of grain yield and

dry matter yield for breeding dual use hybrid rye. Bioenerg Res, in press. doi: 10.1007/s12155-013-9383-7.

MIEDANER T, HÜBNER M, KOCH S, SEGGL A, WILDE P, 2010: Biomass yield of selfincompatible germplasm resources and their testcrosses in winter rye. Plant Breed 129, 369-375.

ROUX SR, WORTMANN H, 2010: Züchterisches Potenzial von Roggen (*Secale cereale* L.) für die Biogaserzeugung. J Kulturpfl 62, 173-182.

UTZ HF, 2011: PlabMQTL - Software for meta-QTL analysis with composite interval mapping. Version 0.9. Institute of Plant Breeding, Seed Science, and Population Genetics, University of Hohenheim, Stuttgart, Germany.

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