



# Exploring new alleles for frost tolerance in winter rye

Wiltrud Erath<sup>1</sup> · Eva Bauer<sup>1</sup>  · D. Brian Fowler<sup>2</sup> · Andres Gordillo<sup>3</sup> · Viktor Korzun<sup>3</sup> · Mira Ponomareva<sup>4</sup> · Malthe Schmidt<sup>3</sup> · Brigitta Schmiedchen<sup>3</sup> · Peer Wilde<sup>3</sup> · Chris-Carolin Schön<sup>1</sup>

Received: 5 April 2017 / Accepted: 10 July 2017 / Published online: 20 July 2017  
© Springer-Verlag GmbH Germany 2017

## Abstract

**Key message** Rye genetic resources provide a valuable source of new alleles for the improvement of frost tolerance in rye breeding programs.

**Abstract** Frost tolerance is a must-have trait for winter cereal production in northern and continental cropping areas. Genetic resources should harbor promising alleles for the improvement of frost tolerance of winter rye elite lines. For frost tolerance breeding, the identification of quantitative trait loci (QTL) and the choice of optimum genome-based selection methods are essential. We identified genomic regions involved in frost tolerance of winter rye by QTL mapping in a biparental population derived from a highly frost tolerant selection from the Canadian cultivar Puma and the European elite line Lo157. Lines per

se and their testcrosses were phenotyped in a controlled freeze test and in multi-location field trials in Russia and Canada. Three QTL on chromosomes 4R, 5R, and 7R were consistently detected across environments. The QTL on 5R is congruent with the genomic region harboring the *Frost resistance locus 2 (Fr-2)* in Triticeae. The Puma allele at the *Fr-R2* locus was found to significantly increase frost tolerance. A comparison of predictive ability obtained from the QTL-based model with different whole-genome prediction models revealed that besides a few large, also small QTL effects contribute to the genomic variance of frost tolerance in rye. Genomic prediction models assigning a high weight to the *Fr-R2* locus allow increasing the selection intensity for frost tolerance by genome-based pre-selection of promising candidates.

Communicated by Diane E. Mather.

**Electronic supplementary material** The online version of this article (doi:[10.1007/s00122-017-2948-7](https://doi.org/10.1007/s00122-017-2948-7)) contains supplementary material, which is available to authorized users.

✉ Eva Bauer  
e.bauer@tum.de

✉ Chris-Carolin Schön  
chris.schoen@tum.de

<sup>1</sup> TUM School of Life Sciences, Plant Breeding, Technical University of Munich, Liesel-Beckmann-Str. 2, 85354 Freising, Germany

<sup>2</sup> Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada

<sup>3</sup> KWS Lochow GmbH, Ferdinand-von-Lochow-Str. 5, 29303 Bergen, Germany

<sup>4</sup> Department of Genetics, Kazan (Volga Region) Federal University, Kremlevskaja Str. 18, Kazan 420008, Russia

## Introduction

Compared to related small grain cereals like wheat and barley, rye is more frost tolerant (Fowler and Limin 1987) and, therefore, constitutes an ideal model to investigate the genetic architecture of frost tolerance in cereals. Owing to its high degree of abiotic stress tolerance, rye is a valued crop in production areas where most small grain cereals are not profitable (Miedaner 2013). The high level of frost tolerance allows winter rye cultivation in northern and continental cropping areas of the temperate zones. As climate change proceeds, climatologists predict that cold winter extremes will occur more frequently in the northern hemisphere despite global warming (Petoukhov and Semenov 2010; Sorokina et al. 2016). In these high stress regions, winter rye production is only efficient if high yield is combined with a high level of frost tolerance.