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TILLING AS A RENEWABLE SOURCE OF MUTATIONS FOR FUNCTIONAL GENOMICS AND PRACTICAL BREEDING

TILLING (Targeting Induced Local Lesions IN Genomes) was first described in 2000 as a reverse genetics tool that combines classical mutagenesis and high-throughput mutation screening. In this presentation the current status of TILLING platforms in different species will be summarized. The lecture will focus on latest achievements of TILLING in functional genomics and in practical plant breeding. The advantages and limitations of this strategy will be compared to other reverse genetic approaches, first of all to CRISPR/Cas 9 based RNA guided genome editing. We will present our HorTILLUS (*Hordeum vulgare* –TILLING –University of Silesia) population, that is TILLING population developed for barley spring variety 'Sebastian' after double treatment with two mutagens: MNU and sodium azide. The average mutations density in this population, estimated as 1 mutations per 477 kbp, is relatively high. HorTILLUS platform has proved to be a useful tool for functional genomic studies, as well as for forward selection of mutants with desired phenotypes. We have used this population to study the function of genes related to many aspects of barley growth and development, such as brassinosteroid and strigolactone metabolism, abiotic stress response (drought, aluminum) and DNA repair processes. HorTILLUS population comprises more than 9,600 M2 plants (and progenies) and is being constantly renewed. We would like to share this population within barley community in a cooperative manner.

Country or International Organization

Poland

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