



International Conference

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A SUSTAINABLE DURUM WHEAT CHAIN
FOR FOOD SECURITY AND HEALTHY LIVES



Bologna - Italy, 19-21 September 2018

GENOME EDITING FOR IMPROVING WHEAT YIELD AND YIELD-RELATED TRAITS

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Genome editing has emerged as a disruptive technology that can be used to generate novel variation in the genomic regions affecting major agronomic traits. Our project explores the capabilities of the gene editing technology to unlock the yield potential of the complex wheat genome, and build a foundation for transformative approaches to wheat improvement. The gene editing pipeline based on the Cas9 and Cpf1 enzymes, the high-throughput screening of gRNA editing efficiency using the wheat protoplast assays, the next-generation sequencing-based detection of editing events and multiplex gene editing was established and successfully tested in wheat. For gene editing, we selected genes that have a potential to affect yield component traits in wheat. For more than 20 genes, the CRISPR/CAS9 constructs were designed and successfully tested for editing efficiency using the protoplast assay and next-generation sequencing. Transgenic plants expressing these constructs targeting either single or multiple genes were regenerated and the phenotypic effects of induced mutations are being evaluated. Our results demonstrate that the CRISPR/CAS9 system is a powerful tool for creating the beneficial combinations of homeo-allelic gene variants that can positively affect yield component traits. For example, we demonstrated that gran size and weight variation in wheat can be modulated by the dosage of *TaGW2* homoeologs with inter-cultivar differences in the magnitude of the individual homoeologue effects. The newly developed variants of some of the genes have been transferred into adapted cultivars for the field-based evaluation of the phenotypic effects of gene editing. Our study shows that gene editing technology can be used to create novel gene variants positively affecting yield component traits, and has a great potential to accelerate the development of wheat varieties with improved yield potential.

ABSTRACT