

Transgenic barley in applied research and biotechnology

Goetz Hensel¹, Cornelia Marthe¹, Anne Kusserow¹, Axel Himmelbach², Nikolai Borisjuk⁵, Stefanie Goedeke¹, Eszter Kapusi¹, Ingrid Otto¹, Catrin Kaydamov¹, Sylvia Broeders^{1,6}, Tobias Czauderna³, Nils Stein⁴, Isolde Saalbach¹, Patrick Schweizer² and Jochen Kumlehn¹

¹ Leibniz Institute of Plant Genetics and Crop Plant Research, Plant Reproductive Biology, Gatersleben, Germany

² Leibniz Institute of Plant Genetics and Crop Plant Research, Transcriptome Analysis, Gatersleben, Germany

³ Leibniz Institute of Plant Genetics and Crop Plant Research, Pattern Recognition, Gatersleben, Germany

⁴ Leibniz Institute of Plant Genetics and Crop Plant Research, Genome Diversity, Gatersleben, Germany

⁵ Thomas-Jefferson-University, Philadelphia, PA, USA

⁶ EU, JRC, Institute for Reference Materials and Measurements, RM Unit, Geel, Belgium

Barley belongs to the most important crops worldwide. For this species, numerous tools and resources such as specific cDNA libraries, EST databases and physical and genetic maps have been developed. As a result, many DNA-sequences are available for which a detailed functional analysis is desirable. Therefore, a powerful cereal transformation platform based on the use of *Agrobacterium tumefaciens* has been established in our laboratory. Either immature embryos or isolated microspores stimulated to undergo androgenetic development have been routinely used as gene transfer targets. The employment of these methods have resulted in the transformation of various spring and winter type cultivars of barley. Functional gene analyses and biotechnological approaches further require cell-specific promoters. In this respect, we are facing the general problem that most promoters from dicotyledons are not useful in monocotyledonous plants. The identification and employment of several monocot-compatible promoters have resulted in the establishment of a number of useful expression systems for barley, including those with specificities to the epidermis, the endosperm or the egg cell. Examples are presented for approaches to the functional analysis of genes involved in interactions between barley and pathogenic fungi as well as to the production of recombinant proteins in barley grains.