J. Verbr. Lebensm. 1 (2006) Supplement 1: 117
1661-5751/06/040117-1
DOI 10.1007/s00003-006-0084-3

Journal für Verbraucherschutz und Lebensmittelsicherheit
Journal of Consumer Protection and Food Safety

High throughput RNAi to study the interaction between barley and powdery mildew fungi

D. Douchkov, W. Dong, U. Zierold, D. Nowara, U. Seiffert and P. Schweizer

Institute of Plant Genetics and Crop Plant Research (IPK), D-06466 Gatersleben, Germany.

Correspondence to: P. Schweizer, Institute of Plant Genetics and Crop Plant Research (IPK), D-06466 Gatersleben, Germany,
E-mail: schweiz@ipk-gatersleben.de

Received: September 5, 2005

Barley is one of the most important feed and food crops worldwide. Despite its agronomic importance and excellent, available genetic resources, tools for genome-wide analysis of barley have only recently been initiated and include high-resolution genetic maps, physical gene mapping, highly efficient protocols for genetic transformation, insertion mutagenesis, TILLING platforms, a large EST collection as well as gene arrays for expression profiling. We have contributed to extending this genomics toolbox in barley by establishing 22,000 EST sequences from powdery mildew-attacked barley epidermis, a 10K cDNA array as well as a high-throughput RNAi system for assessing gene function in attacked barley epidermal cells. The RNAi system for transient-induced gene silencing (TIGS) based on biolistic transgene delivery is being used to study the function of approximately 900 barley candidate genes including 693 up-regulated genes, 101 resistance-gene analogues expressed in barley epidermis as well as 58 proteasome component genes. The library of RNAi constructs was built up by a new, cost-efficient method that combines highly efficient ligation and recombination by the GATEWAY cloning system into a final RNAi destination vector that was found to direct highly efficient RNAi. The full RNAi construct library was tested in a TIGS screening for breakdown of nonhost resistance against wheat powdery mildew. Approximately 200 up-regulated host genes were also tested for breakdown of *mlo*-mediated host resistance or modulation of host susceptibility. Forty-three candidate genes producing a susceptible or resistant phenotype in one or several of the first-round TIGS screening are being analyzed in greater detail. Until present, ten genes were found to alter (non)host responses of barley to powdery mildews in a reproducible manner.