least as safe as conventionally bred plants, or plants from induced translocation breeding or mutation breeding. Therefore we propose to add cisgenesis of plants to the list of GM technologies that are exempted from the GMO regulation in the European Union (Annex 1B of Directive 2001/18/EC).

The number of functionally analysed genes in fruit trees is increasing, and will be boosted further by combining whole genome sequences with known genetic loci for interesting traits, gene expression data, and ESTs. Also technologies are available for either introduction of alleles without use of marker genes, or for later excision of marker genes, such as kanamycin resistance gene, the so called "marker-free" technologies. Cisgenesis combines the knowledge of gene sequences and their functions with marker-free technologies.

Cisgenesis is an approach for utilizing the growing wealth of knowledge of plant genes to the benefit of the society in a fast, safe and acceptable way.

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# Parallel sessions Session Resistance

## *Finding more resistance sources to septoria tritici blotch of wheat*


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Septoria tritici blotch (STB) is caused by *Mycosphaerella graminicolla* and is among the most devastating worldwide foliar blights of wheat. STB consistently reduces yields by 10-15% and under conducive conditions up to 50%. Fungicide control of the disease is not sustainable due to abrupt (strobilurins) or gradual (azoles) fungicide resistance development. Therefore, breeding for resistance is the most effective control strategy to this disease. Up to 15 major resistance genes and QTLs, *Stb1-Stb15*, were recently identified and are being used in breeding programs. However, the resources to combat this disease are still very limited and we therefore started a survey to identify new sources of resistance. Candidate genes are being mapped and molecular markers to facilitate application in breeding programs will be developed. We explored STB resistance in 48 hexaploid wheat lines, including synthetic hexaploids, using a global panel of 18 *M. graminicola* isolates. New *Stb* genes were postulated and are currently being characterized and mapped. It was of particular interest that synthetic hexaploid lines showed a broad resistance to the entire *M. graminicola* panel.





## *Efficient targeting of barley genes for basal resistance to Puccinia hordei*


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Basal resistance is the complement of the term "basic compatibility". Evidence suggests basal resistance to be a weak form of non-host resistance, resulting from the partial failure of the microbe to deal effectively with the defence that plant species mount against maladapted microbial intruders. With rust and mildew fungi, basal resistance hampers the formation of fungal haustoria and is due to genes with relatively small, quantitative effects, located on so called quantitative trait loci (QTL).
The barley populations Steptoe/Morex and Oregon Wolfe Barleys vary quantitatively, without hypersensitive reaction, in their level of resistance to the biotrophic leaf rust fungus *Puccinia hordei*. Each population segregates for a different set of QTLs from which the most effective QTL-alleles for resistance that have been detected in seedlings are *Rphq11* in Steptoe and *Rphq16* in Dom. *Rphq11* and *-16* are not effective in adult plants grown in greenhouse or in the field. Steptoe and Dom were crossed and backcrossed with a susceptible barley line and individual F3 or BC1 plants were selected that contain the resistance allele of *Rphq11* or *-16* but none of the other resistance QTLs that the donors possess. The effect of each QTL was confirmed in $F_4$ or $BC_1S_1$ families and their precise position determined by substitution mapping.

The strategy followed allowed a quick fine-mapping of the genes underlying two resistance QTLs at a sub-centiMorgan level without the tedious need of developing near-isogenic lines and required using only a handful of molecular markers flanking the QTLs. This work will permit to identify soon the physical location of those two genes on the barley genome.

## *Resistance testing and occurrence of pathotypes in Synchytrium endobioticum: an overview.*


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In EU Directive 69/464/EEG it is mentioned that each country should yearly publish a list of potato cultivars resistant to pathotypes of *S. endobioticum*. Hereto, it is compulsory to do a laboratory test, of which two tests are extensively described in the literature: the Spieckermann-test (Spieckermann & Kothoff, 1924) and the Lemmerzahl-test (Lemmerzahl, 1930). In the Netherlands the Spieckermann-test is used in official resistance testing. Inoculum consists of winter sporangia (resting spores) mixed with sand. Eye pieces of potato are covered with this mixture, and subsequently moistened. Zoospores released after germination of the winter sporangia are responsible for infection. Susceptible cultivars react with wart formation (no defense), those resistant react with forming a necrotic region surrounding the infection site. In the Lemmerzahl-method, fresh wart tissue is used to infect eye pieces of potato. Then, summersporangia freely releasing zoospores cause infection. It is believed that the Lemmerzahl–test is more sensitive, i.e. more cultivars are rated 'susceptible' after testing, this in comparison with the Spieckermann-test.