

identifiziert werden können, lässt sich anschließend durch eine gezielte Feinkartierung der Resistenzlocus näher eingrenzen und ein für die Züchtung geeigneter Marker ableiten.

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### Herzog, Katja<sup>1</sup>; Flachowsky, Henryk<sup>1</sup>; Deising, Holger<sup>2</sup>; Hanke, Magda-Viola<sup>1</sup>

<sup>1</sup> Julius Kühn-Institut, Institute for Breeding Research on Horticultural and Fruit Crops, Dresden; <sup>2</sup> Martin-Luther-University, Faculty of Natural Sciences III, Institute of Agricultural and Nutritional Sciences, Phytopathology and Plant Protection, Halle (Saale)

### Ergebnisse zur Etablierung alternativer Strategien zur Erzeugung markergen-freier Apfelpflanzen mit erhöhter Resistenz

Preliminary results to generate marker-free apples (*Malus domestica* BORKH.) with increased fungal resistance

#### Abstract

The production of genetically modified (gm)-plants without selectable marker genes is one of the most important goals of genetic engineering in apple. Therefore, we started the development and establishment of an effective transformation system to generate marker-free apple plants. The system is based on a site-specific recombination of the selectable marker gene *npII* controlled by a heatshock-inducible promoter. We tested the system using a monitoring vector which combines the inducible site-specific recombinase for the precise elimination of *npIII* and a GUS encoding gene (*gusA*) to realize a histochemical monitoring of recombination events. Partial marker-free apple plants were obtained after heat shock and fully marker-free plants were generated following a second regeneration strategy. The oral presentation focused on this part of the project. Apple powdery mildew *Podosphaera leucotricha* (Ell. Et Ev) SALM. belongs to the economical important fungal pathogens in apple production and causes decreased yield as well as reduced fruit quality. To increase resistance against *Podosphaera leucotricha* we transformed apple plants with a specific construct. Transgenic plants were selected, characterized by molecular techniques and tested for their resistance to powdery mildew. Four of the five tested transgenic lines showed significantly reduced symptoms of disease compared to control plants.

Keywords: *Malus domestica*, *npIII*, marker-free, site-specific recombination system

### Admassu, Belayneh; Friedt, Wolfgang; Ordon, Frank

Julius Kühn-Institut, Institut für Resistenzforschung und Stresstoleranz (RS), Quedlinburg

### Diversity of *Puccinia graminis* f. sp. *tritici* Population in Ethiopia and Stem Rust Resistance Genes in Wheat

#### Abstract

Ethiopia is the second largest wheat producer in sub-Saharan Africa next to South Africa. It is an important food grain cultivated on ca. 1.4 million ha. The national average productivity is estimated at 1.7 tons/ha. The low productivity is attributed to a number of factors including diseases like stem rust caused by *Puccinia graminis* f. sp. *tritici* (*Pgt*). As a result of a recent spread of a new and highly virulent race called Ug99, stem rust is becoming a serious threat to wheat production in Ethiopia and other east African countries. Durable stem rust control in wheat requires detailed knowledge on virulence spectrum and genetic diversity of *Pgt*. Molecular markers were proven to be easier and more efficient than the conventional method in variety development for disease resistance. Hence, this project studied the virulence and genetic structure of *Pgt* populations in Ethiopia, and developed a genetic map of a

stem rust resistance gene (*Sr13*) that is effective against Ug99. A total of 152 isolates was analyzed and 22 races were identified. Races TTKSR, TTHSR and RRTR were predominant with frequencies of 26.6, 17.7 and 11.1%, respectively. These races were also detected in all regions. It turned out that the highly virulent race designated as Ug99 was present throughout the country and dominated in all regions except Northwest Ethiopia. Four stem rust resistance genes (*Sr13*, *Sr30*, *Sr36* and *SrTmp*) were found to confer resistance to most of the races prevalent in Ethiopia. With the exception of *Sr30*, which is not effective to Ug99, the other three genes can be used in breeding for resistance to stem rust in Ethiopia. The genetic structure of selected *Pgt* isolates was investigated using 20 SSRs. The assays showed a high level of genetic diversity within *Pgt* populations in Ethiopia. Tests for population subdivision revealed the absence of genetic differentiation among the populations on the basis of geographic separation. This study shows that the pathogen population of Ethiopia is characterized by a high genetic diversity, but absence of differentiation based on geographic origin. *Sr13* is one of the few resistance genes that are effective against wide ranging *Pgt* races, including the pestilent race Ug99. Its effectiveness to Ug99 makes it a valuable source for resistance to stem rust. Based on SSR analyses of F<sub>2</sub> individuals derived from a cross of a susceptible and resistant parents, the *Sr13* locus was mapped on chromosome 6A of wheat. Five SSR markers were also found linked to the *Sr13* gene.

Keywords: Wheat, stem rust, Sr resistance gene, Ethiopia, SSR markers

**König, J.; Perovic, D.; Kopahnke, D.; Przulj, N.; Romeis, T.; Ordon, F.**

Julius Kühn-Institut, Institut für Resistenzforschung und Stresstoleranz (RS), Quedlinburg

### **Kartierung der Zwergrostresistenz der Gerste MBR1012**

Genetic mapping of leaf rust resistance in barley accession MBR1012

#### **Zusammenfassung**

Der Zwergrost gehört zu den wichtigsten Krankheitserregern der Gerste und kann im gemäßigten Klima Ertragsverluste von über 60 % verursachen. Auf der Suche nach neuen Resistenzquellen wurde in der aus Serbien Montenegro stammenden Landrasse MBR1012 eine wirksame Resistenz gegenüber Zwergrost identifiziert. Um die Vererbung der Resistenz dieser Landrasse aufzuklären, wurden 76 DH-Linien aus der Kreuzung der resistenten Landrasse MBR1012 mit der anfälligen Sorte Scarlett mit der hochvirulenten Zwergroststamme I80 künstlich inokuliert. Die Spaltung der DH-Population nach der Inokulation mit I80 zeigte, dass die Resistenz monogenetisch vererbt wird. Basierend auf den Ergebnissen der bulked segregant analysis konnte die Resistenz dem Chromosom 1H zugeordnet werden und eng gekoppelte molekulare Marker entwickelt werden, welche eine beschleunigte Übertragung dieser Resistenz in adaptierte Sorten erlauben. Die Suche nach neuen Resistenzen gegen *Puccinia hordei* ist von besonderer Bedeutung, da die Rostpilze durch Mutation und Rekombination zahlreiche physiologische Rassen bilden, wodurch Resistenzen relativ schnell überwunden werden können.

Stichwörter: Gerste (*Hordeum vulgare* L.), Zwergrost (*Puccinia hordei* Oth), Resistenz, bulked segregant analysis (BSA), DH-Linien (doubled-haploid).

#### **Abstract**

Leaf rust (*Puccinia hordei* Oth) is an economically important disease of barley in temperate regions, causing considerable yield losses up to about 60 %. Resistance to leaf rust has been detected in a landrace derived from Serbia Montenegro (MBR1012). To obtain information on the genetics of resistance of MBR1012 to leaf rust, 76 DH-lines derived from a cross of MBR1012 to the susceptible cv. Scarlett were inoculated using the highly virulent leaf rust isolate I80. It turned out that resistance is inherited in a monogenic manner and by bulked segregant analysis resistance was assigned to chromosome 1H. Next closely linked molecular markers were developed facilitating an efficient introgression into adapted cultivars. Broadening the genetic base of resistance to leaf rust is of special importance as this pathogen is able to overcome resistances quickly due to mutation and recombination.

Keywords: Barley (*Hordeum vulgare* L.), leaf rust (*Puccinia hordei* Oth), resistance, bulked segregant analysis (BSA), DH-lines (doubled-haploid)

#### **Einleitung**

Der Pilz *Puccinia hordei* Oth ist der Erreger des Zwergrosts der Gerste (*Hordeum vulgare*) und gehört zu den obligaten Parasiten. Der Wirtswechsel erfolgt beim Zwergrost zwischen *Hordeum* und *Ornithogalum* Arten. Der Schaderreger *P. hordei* ist ein wirtschaftlich wichtiges Gerstenpathogen, das in gemäßigten Breiten bei anfälligen Kulturen Ertragseinbußen von bis zu 60 % verursachen kann (Cotterill et al 1992). Aus wirtschaftlichen und ökologischen Gründen ist der Einsatz von Fungiziden nach Möglichkeit zu beschränken, so dass resistente Sorten die beste Alternative für einen gesunden Bestand sind. Doch gestaltet sich die Züchtung dauerhaft rostresistenter Sorten schwierig, da bei den Rosten eine große Zahl morphologisch meist nicht unterscheidbarer physiologischer Rassen auftritt, die durch Mutation und Neukombination entstehen (Bresinsky et al 2008). Aus diesem Grund ist die Identifikation neuer Resistenzträger und deren genetische Analyse von besonderer Bedeutung. In diesem