*Article*

# Wheat *mlo* mutants show allele-specific levels of enhanced susceptibility to the hemibiotrophic fungal pathogen *Magnaporthe oryzae* pv. *Triticum*

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**Abstract:** Barley *mlo* mutants are well known for their profound resistance against powdery mildew disease. Recently, *mlo* mutant plants were generated in hexaploid bread wheat (*Triticum aestivum*) with the help of transgenic (transcription-activator-like nuclease, TALEN) and non-transgenic (targeted induced local lesions in genomes, TILLING) biotechnological approaches. While full gene knockouts in the three wheat *Mlo* (*TaMlo*) homoeologs, created *via* TALEN, confer full resistance to the wheat powdery mildew pathogen (*Blumeria graminis* f.sp. *tritici*), the currently available TILLING-derived *Tamlo* missense mutants provide only partial protection against powdery mildew attack. Here we studied the infection phenotypes of TALEN- and TILLING-derived *Tamlo* plants to the two hemibiotrophic pathogens *Zymoseptoria tritici*, causing Septoria leaf blotch in wheat, and *Magnaporthe oryzae* pv. *Triticum* (*MoT*), the causal agent of wheat blast disease. While *Tamlo* plants showed unaltered outcomes upon challenge with *Z. tritici*, we found allele-specific levels of enhanced susceptibility to *MoT*, with stronger powdery mildew resistance correlated with more invasive growth by the blast pathogen. Surprisingly, unlike barley *mlo* mutants, young wheat *mlo* mutant plants do not show undesired pleiotropic phenotypes such as spontaneous callose deposits in leaf mesophyll cells or signs of early leaf senescence. In conclusion, our study provides evidence for allele-specific levels of enhanced susceptibility of *Tamlo* plants to the hemibiotrophic wheat pathogen *MoT*.

**Keywords:** *Blumeria graminis*; hexaploid bread wheat; *Magnaporthe oryzae*; Mlo; plant disease resistance; powdery mildew; TALEN; TILLING; *Zymoseptoria tritici*

## 1. Introduction

Bread wheat (*Triticum aestivum*) is one of the world´s most important food crop species (Shiferaw et al., 2013). Like other cereals, it can suffer from a variety of microbial diseases. Common practices for disease control comprise the deployment of resistant cultivars and the application of agrochemicals (pesticides). However, genetically conditioned disease resistance, although from the

perspective of costs, practicability and sustainability highly desired, is often ephemeral due to the rapid evolution of pathogenic microbes that can overcome plant immunity (Frantzeskakis et al., 2020).

Powdery mildew is a common and widespread disease of angiosperm plants that is caused by ascomycete powdery mildew fungi (Glawe, 2008). These fungi thrive on the basis of an obligate biotrophic lifestyle, i.e. they require living host tissue for growth and reproduction (Panstruga and Schulze-Lefert, 2002). Powdery mildew also affects important food crops such as wheat and barley. The causing agent of the disease on these cereals is *Blumeria graminis* – a species that exists in various highly host-specialized variants (*formae speciales*; (Troch et al., 2014)) and has been elected one of the top 10 fungal pathogens in terms of scientific and economic importance (Dean et al., 2012).

Resistance of cereals to powdery mildew is often conditioned by dominantly inherited resistance (*R*) genes, which usually confer race-specific immunity (Alam et al., 2011; Jørgensen, 1994). Unlike prototypical *R* genes, recessively inherited loss-of-function *mlo* (*mildew locus o*) mutations give rise to race non-specific powdery mildew resistance (Jørgensen, 1992). Originally discovered as a natural mutant of barley (Piffanelli et al., 2004), *mlo*-mediated resistance has been recently shown to represent a common phenomenon in angiosperm plants (reviewed by (Kusch and Panstruga, 2017)). Typically, *mlo* resistance can be induced by loss-of-function mutations in a single *Mlo* gene, although exceptions exist such as in *Arabidopsis thaliana* where mutations in three *MLO* genes contribute to resistance *via* unequal genetic redundancy (Consonni et al., 2006). Barley *mlo* mutants have been extensively used in European agriculture and were found to confer stable, effective and long-lasting resistance (Lyngkjær et al., 2000; Brown, 2015). The molecular basis of this type of disease resistance is still incompletely understood (Acevedo-Garcia et al., 2014; Kusch and Panstruga, 2017).

In hexaploid bread wheat, three orthologs of the barley *Mlo* gene (*TaMlo* homoeologs) are present in the A, B and D genome (Elliott et al., 2002). Previous transgenic and non-transgenic approaches led to wheat mutants with genetic lesions in all three *TaMlo* homoeologs (Wang et al., 2014; Acevedo-Garcia et al., 2017b). The transgenic approach, mediated by transcription activator-like effector nucleases (TALEN), resulted in knockout mutants with apparently complete resistance to the wheat powdery mildew pathogen, *Blumeria graminis* f.sp. *tritici* (*Bgt*) (Wang et al., 2014). By contrast, the non-transgenic approach, achieved *via* targeted induced local lesions in genomes (TILLING) technology resulting in missense mutations in the *TaMlo* homoeologs, yielded mutants with residual activity and accordingly partial *Bgt* resistance (Acevedo-Garcia et al., 2017b). Recently, TILLING-derived *mlo* mutants were also reported in tetraploid durum wheat (*Triticum turgidum* (Ingvardsen et al., 2019)).

In some species (such as barley and *Arabidopsis thaliana*), powdery mildew-resistant *mlo* mutants show pleiotropic phenotypes such as the spontaneous formation of callose-containing cell wall appositions and signs of early leaf senescence (Wolter et al., 1993; Schwarzbach, 1976; Piffanelli et al., 2002; Consonni et al., 2006; Consonni et al., 2010). These phenotypes are variable and their occurrence and severity appear to depend on yet poorly characterized environmental conditions. Interestingly, powdery mildew-resistant *mlo* mutants in some plant species, such as tomato and pea, seem to lack such pleiotropic phenotypes (Bai et al., 2008; Humphry et al., 2011).

Apart from powdery mildew, for which mutations in *Mlo* genes cause durable broad-spectrum resistance, *mlo* mutants modulate the outcome of interactions with some other pathogens as well. The first report in this respect described the enhanced susceptibility of barley *mlo* mutants to the rice blast fungus *Magnaporthe oryzae*, which is also a pathogen of barley (Jarosch et al., 1999). *M. oryzae* recently emerged as a novel pathogen of wheat in Brazil, likely enabled by the extensive use of a particular wheat cultivar, which permitted a host jump as a consequence of the loss of a crucial avirulence determinant in the fungus (Inoue et al., 2017). The wheat blast disease is an upcoming threat for wheat cultivation and, thereby, for global food security (Gladieux et al., 2018). The disease was first reported in 1985 for South America and spread to Asia in 2016 (Islam et al., 2016). There is an ongoing debate whether or not isolates causing blast disease on wheat represent a novel species or a particular lineage within the *M. oryzae* species complex (Ceresini et al., 2019; Valent et al., 2019). For this study, we will follow the latter perception and refer to the pathogen as *M. oryzae* pathotype *Triticum* (*MoT*).

Here, we analyzed a set of bread wheat *Tamlo* mutants, including transgenic TALEN and non-transgenic TILLING mutants, to assess their disease phenotypes with various fungal phytopathogens. We focused on powdery mildew (*Bgt*), and the two hemibiotrophic pathogens *MoT* and *Z. tritici*. We further assessed the potential of the *Tamlo* mutants to develop undesired pleiotropic phenotypes by histochemically analyzing the formation of spontaneous callose deposits and scoring signs of early leaf senescence. Results of our experiments indicate that similar to barley *mlo* mutants, strong *Tamlo* mutants are prone to enhanced *MoT* susceptibility.

## 2. Materials & Methods

### *2.1. Plant material and growth conditions*

The hexaploid bread wheat cv. Cadenza (a British spring wheat variety) and its derived TILLING *Tamlo* lines as well as the Chinese cv. Kenong 199 (KN199, a winter wheat variety) and its derived TALEN *Tamlo* triple mutant lines were described before (Acevedo-Garcia et al., 2017b; Wang et al., 2014). Wheat plants were grown and propagated as described before (Acevedo-Garcia et al., 2017b) except for the used soil type, which was changed to SoMi513 (HAWITA, Vechta, Germany). Barley cv. Ingrid and its isogenic *mlo*-3 null mutant have been described before (Büschges et al., 1997).

### *2.2. Bgt infection assays*

The German *Bgt* field isolate JA82 was described and propagated as described before (Acevedo-Garcia et al., 2017b) with minor changes. During a later stage in the course of this study, the wheat variety used for fungal propagation was changed to the commercially available spring wheat variety KWS Sharki (https://www.kws.com/de/de/produkte/getreide/weizen/sortenuebersicht/kws-sharki/) and 7-day-old seedlings were used in a weekly propagation routine. The infection assays with *Bgt* were performed as described before (Acevedo-Garcia et al., 2017b). In brief, primary leaves of 10-day-old seedlings were fixed on a polycarbonate platform, emerging secondary leaves were cut short, and the primary leaves were equally inoculated with *Bgt* conidiospores. For evaluation of *Bgt* host cell entry rates, inoculated leaves were harvested 3 days later and fixed in a destaining solution. Epiphytic fungal structures on the destained leaves were visualized with Coomassie Brillant Blue R-250 (Carl Roth GmbH, Karlsruhe, Germany) and evaluated under the microscope by scoring at least 200 interaction sites (attacked cells with haustoria/hyphae *versus* attacked cells with appressoria). Macroscopic evaluation of the leaves was undertaken at 6 dpi.

### *2.3. Z. tritici infection assays*

The Dutch *Z. tritici* isolates IPO323 (local ID: Zt244) is available from the Westerdijk Institute (Utrecht, The Netherlands) with the accession numbers CBS115943. *Z. tritici* strains Zt05 (ID: MgDk09_U34) (Thygesen et al., 2009) and Zt153 (ID: Zt_Ger_13_5_1_1) (Grandaubert et al., 2019) were isolated in Denmark and Germany, respectively and are available upon request. Strains were maintained on either liquid yeast malt sucrose (YMS) broth (4 g $L^{-1}$ yeast extract, 4 g $L^{-1}$ malt extract, 4 g $L^{-1}$ sucrose) at 18 °C on an orbital shaker or on solid YMS medium (supplemented with 20 g $L^{-1}$ agar) at 18 °C.

Infection phenotypes were determined as described before (Habig et al., 2017). Briefly, seeds of the seven tested wheat genotypes (cv. Cadenza, four TILLING *Tamlo* triple mutant lines, KN199 and the TALEN *Tamlo* triple mutant line) were germinated on wet Whatman paper for four days before potting. Wheat seedlings were further grown for seven days before inoculation. The *Z. tritici* strains were grown on YMS solid medium for 5 days at 18 °C before the cells were scraped from the plate surface. A ~5 cm long section on the secondary leaf of each plant was infected by brushing a cell suspension with $10^7$ cells $mL^{-1}$ in 0.1% Tween 20 on the abaxial and adaxial side of leaf. Plants were placed into sealed bags containing ~1 L of water for 48 h to facilitate infection at maximum air humidity. Plants were grown under constant conditions with a day-night cycle of 16 h light (~200 µmol $m^{-2}$ $s^{-1}$) and 8 h darkness in growth chambers at 20 °C. Infected leaf areas were harvested at 21

dpi, pressed for five days at 4 °C and then scanned using a flatbed scanner (HP Photosmart C4580, HP, Böblingen, Germany). Pycnidia density and percentage of the leaf area covered by lesions were determined using automated image analyses as described previously (Habig et al., 2017; Stewart et al., 2016).

*2.4. MoT infection assays*

Wheat plants were pre-germinated for 24 h on wet filter paper and then germlings were transferred to standard soil (type ED73, Balster Einheitserdewerk GmbH, Froendenberg, Germany). Plastic pots (7×7×8 cm) with five germlings each were kept in a growth chamber at a 16 h light (200–250 µmol $s^{-1}$ $m^{-2}$)/8 h dark rhythm at 20 °C and 65% relative humidity.

The *Magnaporthe* isolates BR32 (Faivre-Rampant et al., 2008) and Br116.5 (Tanaka et al., 2009) were kindly provided by Didier Tharreau (CIRAD Montpellier, France) and by Yukio Tosa (Kobe University, Japan), respectively. Inoculations of wheat plants with these isolates were performed as described previously (Strugala et al., 2015; Delventhal et al., 2017). In brief, fungal cultures were maintained on oatmeal agar (20 g $l^{-1}$ agar, 2 g $l^{-1}$ yeast extract, 10 g $l^{-1}$ starch, 30 g $l^{-1}$ oat flakes) at 23 °C in the dark. Sporulation was induced by keeping fungal cultures for two weeks at a 16 h light/8 h dark regime under black light at 22 °C. After two weeks, conidia were harvested by rinsing plates with water and filtering through three layers of gauze. For inoculation, the conidia suspension was initially adjusted to 400,000 spores $ml^{-1}$, then diluted 1:2 with surfactant (2 g $l^{-1}$ gelatin, 1 ml $l^{-1}$ Tween) to a final concentration of 200,000 conidia $ml^{-1}$ and finally spray-inoculated onto plants. After incubation at 24-26 °C and 100% relative humidity for 24 h in the dark, inoculated plants were covered with a plastic hood and kept under growing conditions described above.

*2.5. Scoring of spontaneous callose deposition*

Primary leaves of wheat and barley plants were harvested at a plant age of 31 and 24 days, respectively. In both cases, the upper 3 cm of the leaves were removed, and the following 3 cm sections were analyzed. Barley leaf samples were cleared and fixed in ethanol/chloroform (3:1) with 0.15 % (w/v) trichloroacetic acid as described before (Wolter et al., 1993), while wheat leaf sections were cleared in ethanol/acetic acid (3:1). For staining, all samples were incubated in 0.067 M potassium-phosphate buffer (pH 5.8) with 0.05 % (w/v) aniline blue for at least 12 h (adapted from (Wolter et al., 1993)). Leaf sections were analyzed by epifluorescence microscopy using the Keyence BZ-9000 microscope (DAPI filter set; excitation wavelength: 370 nm, detection at 509 nm) and pictures captured using the BZ-II viewer software with exposure times between 1/2 and 1/9 s as well as high black balance to reduce background fluorescence. Subsequently, micrographs of wheat samples were analyzed using CellProfiler software (version 3.1.9; (Jones et al., 2008)) for batch analysis, while the barley samples were scored manually due to high background fluorescence of the leaf veins.

*2.6. Assessment of leaf chlorosis/necrosis*

As for the scoring of spontaneous callose depositions, primary leaves of wheat and barley plants were removed for analysis at a plant age of 31 and 24 days, respectively. Leaves were fixed on a light panel (Kaiser Slimlite, Kaiser Fototechnik GmbH & Co. KG, Buchen, Germany) and pictures of the upper 5 cm of the leaves were taken. The contrast of the photographs was increased to further reduce the background and the pictures were analyzed with the "leaf necrosis classifier" software (https://lnc.proteomics.ceitec.cz/home).

*2.7. Statistical analysis of the data*

Statistical analyses and graph generation were performed using the GraphPad Prism software (GraphPad Prism Software Inc., San Diego, CA, USA). In boxplot graphs, the center lines show the medians and upper and lower box limits indicate the 25$^{th}$ and 75$^{th}$ percentiles, respectively, with all data points represented by colored dots. Statistical analyses were performed using either a regular two-way analysis of variance (ANOVA; $p<0.05$) or a one-way ANOVA test with Tukey's method for

multiple comparisons (multi-paired ANOVA; $p<0.05$) as indicated. The latter was used to generate significance groups represented as letters above the boxplots in the respective graphs.

## 3. Results

### *3.1. Tamlo lines show allele-dependent levels of powdery mildew resistance*

We first complemented our previously initiated, yet at the time incomplete, collection of four TILLING *Tamlo* triple mutant lines bearing different allele combinations and thus mutational events in the *TaMlo* homoeologs of the wheat A, B and D genomes ((Acevedo-Garcia et al., 2017b) and Supplemental Figure 1). In addition, we expanded the set of the two triple mutant lines described before (designated lines 1 and 2; (Acevedo-Garcia et al., 2017b)), harboring *Tamlo* alleles with experimentally determined medium to very strong effects, by selecting independent progenies with the same allele combination. This resulted in three extra independent segregants for triple mutant line 1 and two additional independent segregants for triple mutant line 2. We further selected two new triple mutant lines (designated lines 3 and 4; with two and three independent segregants, respectively) that are based on *Tamlo* alleles with experimentally determined weak to strong effects (Supplemental Figure 1). Therefore, we expected lines 3 and 4 to exhibit lower levels of powdery mildew resistance than observed for lines 1 and 2 (Acevedo-Garcia et al., 2017b). In addition to the four TILLING triple mutant lines, we identified all corresponding single and double mutant combinations related to the four triple mutant lines. In summary, we retrieved a complete set of single, double and triple mutant combinations of the four TILLING triple mutant lines (line 1-4) harboring different *Tamlo* allele combinations with expected differential powdery mildew infection phenotypes (Acevedo-Garcia et al., 2017b), and with each of the respective triple mutant lines represented by two to four independent segregants (Supplemental Figure 1). This comprehensive collection provides a valuable genetic resource to study the effect of different *Tamlo* mutant alleles on the severity of various wheat diseases.

We challenged the four sets of single, double and triple TILLING mutants and their respective wild-type (cv. Cadenza; spring wheat variety) with *Bgt* by inoculating fixed primary leaves of 10-day-old seedlings with conidiospores and assessed fungal host cell entry rates at 3 days post inoculation (dpi) as well as the corresponding macroscopic phenotype at 6 dpi. For comparison, we included the previously described TALEN *Tamlo* triple mutant (Wang et al., 2014) together with the respective wild-type genotype (cv. KN199; winter wheat variety). While cv. Cadenza was fully susceptible to *Bgt* with a median host cell entry rate of 78%, representatives of the four TILLING triple mutant lines showed a gradual decrease in their *Bgt* susceptibility, with line 4 revealing the weakest (56% entry rate) and line 1 the strongest effect (16% entry rate). Lines 2 and 3 exhibited intermediate phenotypes, with 32% and 37% entry rates, respectively (Figure 1A). By contrast, the TALEN triple mutant was nearly completely resistant to *Bgt* (5% host cell entry) while the respective parental wild-type line, cv. KN199, had an entry rate (71%) comparable to cv. Cadenza (Figure 1A). The microscopically assessed levels of host cell entry rates of all wheat genotypes correlated well with the observed macroscopic infection phenotype (Figure 1). Leaves of cv. Cadenza and cv. KN199 wild-type plants were densely covered by profusely sporulating powdery mildew colonies (Figure 1B). *Bgt* colony density gradually decreased from TILLING triple mutant line 4 to mutant line 1, indicative of the highest degree of resistance in line 1. In accordance with the low *Bgt* entry rates, the TALEN line was essentially free of macroscopically visible colonies, signifying a very high level of resistance (Figure 1B).

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**Figure 1**

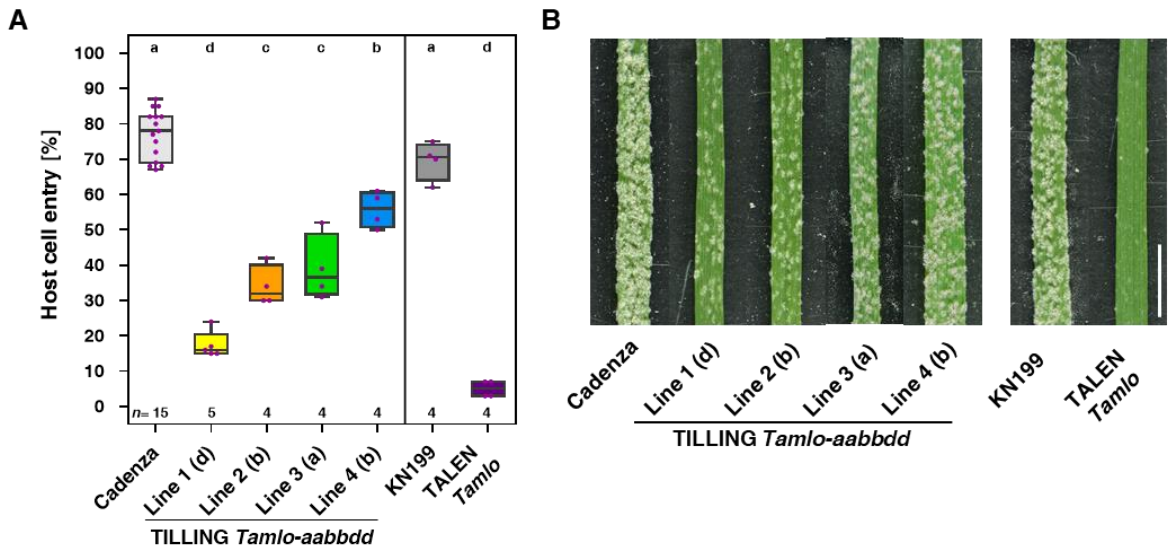


**Figure 1.** *Bgt* infection phenotypes of wheat TILLING and TALEN *Tamlo* triple mutants. Primary leaves of 10-day-old TILLING and TALEN *Tamlo* triple mutants and the corresponding wild-type genotypes, cv. Cadenza and cv. KN199, respectively, were inoculated with conidiophores of *Bgt* isolate JA82. Leaf samples were either harvested at 3 dpi for scoring host cell entry rates (**A**) or photographed at 6 dpi to illustrate macroscopic infection phenotypes (**B**). (**A**) Host cell entry rates for the indicated wheat genotypes were assessed microscopically and are represented as boxplots. Data of individual biological replicates per genotype are displayed as colored dots, and the total number of biological replicates is given as *n* above the *x*-axis. Each biological replicate represents the mean of four evaluated leaves per genotype, with at least 200 *Bgt* interaction sites scored per leaf. Letters above the boxplots denote different significance groups according to statistical analysis (multi-pared ANOVA test; $p<0.05$). (**B**) Macroscopic *Bgt* infection phenotypes of wheat primary leaves of the indicated wheat genotypes at 6 dpi. The white scale bar represents 1 cm.

To gain a complete picture regarding the powdery mildew susceptibility/resistance of the TILLING lines, we also assessed the *Bgt* host cell entry rates of the newly selected mutants (summarized in Supplementary Figure 1). We combined and jointly evaluated the respective data with previous results obtained for some of the single, double and triple mutants of lines 1 and 2 (Acevedo-Garcia et al., 2017b). This comprehensive meta-analysis revealed that none of the single mutant lines had a host cell entry rate that is statistically different from cv. Cadenza (Supplemental Figure 2). By contrast, several double mutant combinations exhibited significantly reduced entry rates, which is indicative of functional redundancy between the three *TaMlo* homoeologs. Notably, in accordance with our earlier report (Acevedo-Garcia et al., 2017b), in particular the *AAbbdd* double mutant combinations reached host cell entry rates comparable to the respective triple mutant lines, i.e., not significantly different from the triple mutant lines according to statistical analysis (Supplemental Figure 2). In summary, we established a set of TILLING *Tamlo* triple mutants with differential, allele-specific degrees of powdery mildew resistance, reaching from strong but incomplete resistance in line 1 to rather weak resistance in line 4 (Figure 1).

### *3.2. Tamlo triple mutants show unaltered infection by the fungal pathogen Zymoseptoria tritici*

With the aim to characterize the *Tamlo* mutants further, we next assessed the infection phenotypes of representatives of the four TILLING and the TALEN triple mutants together with their respective parental lines (cv. Cadenza and cv. KN199, respectively) upon challenge with the hemibiotrophic wheat pathogen *Z. tritici*. To take into account the broad genetic diversity of this

pathogen we used three field isolates of *Z. tritici* - the reference isolate IPO323 (here termed Zt244), originating from the Netherlands, and the isolates Zt05 and Zt153, sampled in Denmark and Germany, respectively. We determined the macroscopic infection phenotype and quantified the density of pycnidia and the extent of necrotic leaf area upon challenge with these three isolates. *Z. tritici* isolates Zt05 and Zt244 caused no characteristic disease symptoms on the tested wheat lines (Supplemental Figure 3), and the density of pycnidia produced by these two isolates was negligible (Figure 2A and B). We thus conclude that cv. Cadenza and cv. KN199 both carry one or more *Septoria tritici blotch* (*Stb*) resistance gene(s) that are effective against isolates Zt05 and Zt244, preventing successful colonization. Isolate Zt153 caused little disease symptoms on cv. KN199 and its derived TALEN *Tamlo* line (Supplemental Figure 3), which was associated with a moderate density of pycnidia (Figure 2C) and an intermediate level of necrotic leaf area (Figure 3D). In general, the TALEN line appeared to be more resistant to *Z. tritici* than its parental line, though the difference was not visible in terms of asexual reproduction (sporulation). Only the extent of the necrotic leaf area showed a statistically significant difference (Figure 3D). Cv. Cadenza and its derived TILLING *Tamlo* lines were fully susceptible to isolate Zt153, with severe disease symptoms (Supplemental Figure 3), as evidenced by near-complete leaf necrosis, and a considerable density of pycnidia. However, there was no statistically significant difference between the five wheat genotypes tested regarding these two parameters (Figure 3C and D). We thus conclude that the *Tamlo* mutations, which condition allele-specific weak to strong disease resistance against the biotrophic powdery mildew pathogen *Bgt* (Figure 1), do not markedly affect the outcome of infection with the hemibiotroph *Z. tritici*.

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## Figure 2

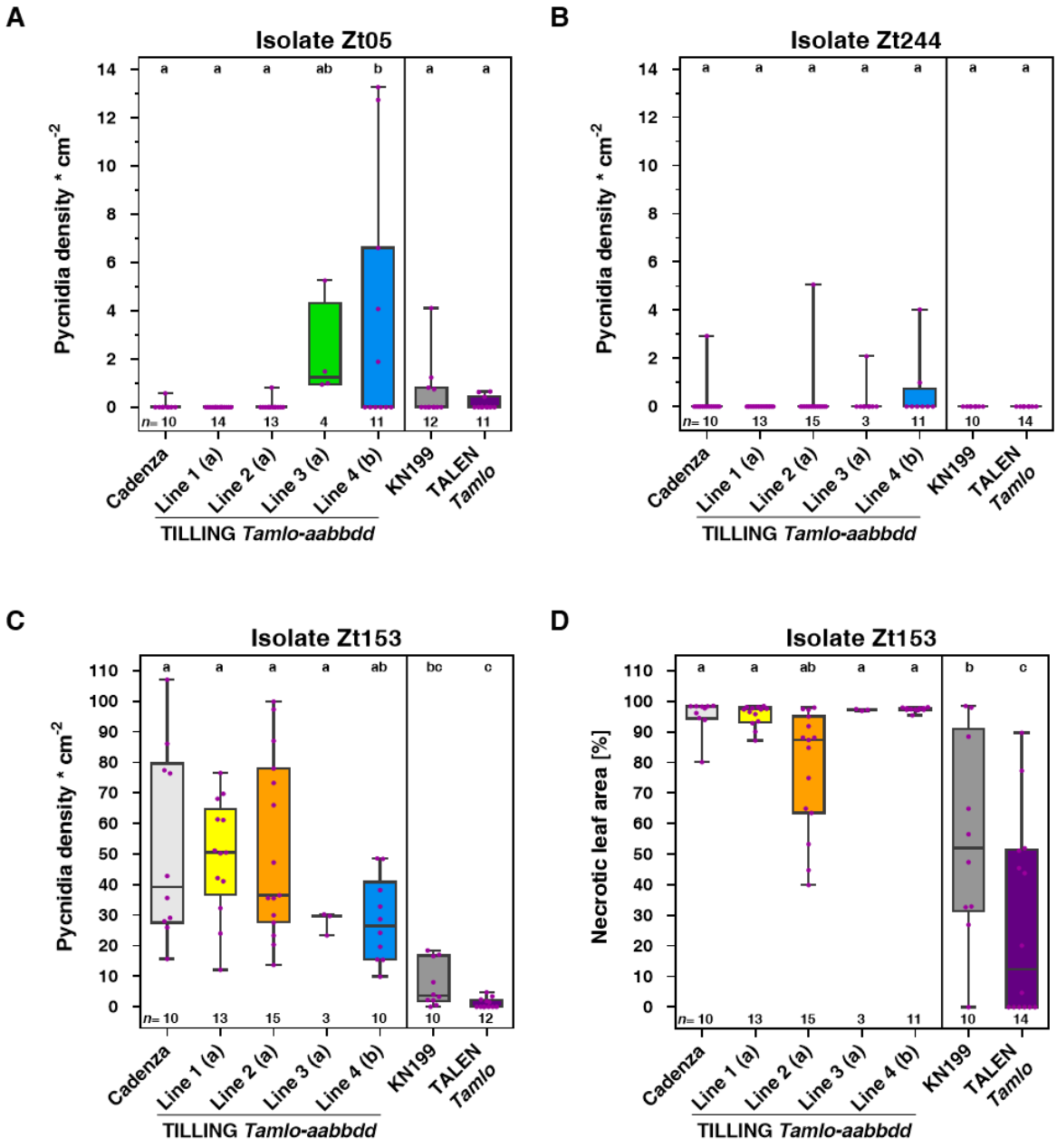


**Figure 2.** ***Tamlo*** **triple mutant lines show unaltered infection by the fungal pathogen** ***Z. tritici*****.** (**A-C**) Boxplots showing the pycnidia density produced by the three *Z. tritici* isolates Zt05 (**A**), Zt244 (**B**) and Zt153 (**C**) at 21 dpi on leaves of the different wheat lines. (**D**) Boxplot of another disease parameter, necrosis, is shown for the isolate Zt153. Necrosis is quantified as % necrotic tissue measured at 21 dpi in a designated leaf area infected with spores. Data shown are from one biological replicate with the number of analyzed leaves given as *n* above the *x*-axis. Letters above the boxplots denote different significance groups according to statistical analysis (multi-pared ANOVA test; $p<0.05$).

### *3.3. Tamlo triple mutant lines show allele-dependent levels of enhanced susceptibility to the fungal pathogen Magnaporthe oryzae pv. Triticum*

To explore whether wheat *mlo* mutants like barley *mlo* mutants show altered infection phenotypes in response to blast pathogens, we next assessed the disease phenotypes of the four

TILLING and TALEN *Tamlo* triple mutants together with their respective parental wild-type lines following challenge with the wheat blast pathogen *MoT*. All wheat genotypes were inoculated with either *MoT* isolate BR32 (Faivre-Rampant et al., 2008) or *MoT* isolate Br116.5 (Tanaka et al., 2009), two Brazilian isolates with differential virulence spectrum, and the resulting disease symptoms were macroscopically assessed at 7 dpi (Figure 3). We noted the occurrence of characteristic blast lesions on all wheat genotypes upon challenge with *MoT* isolate Br116.5, however, disease severity varied in a genotype-dependent manner. While cv. Cadenza and the four TILLING lines also exhibited varying degrees of blast lesions upon challenge with *MoT* isolate BR32, cv. KN199 and the TALEN line did not show any disease symptoms in response to this isolate. We thus conclude that KN199 and its derived TALEN line might display genotype-specific (*R* gene-mediated) resistance against isolate BR32. In the following, we thus excluded cv. KN199 and its derived TALEN line from further evaluation regarding this *MoT* isolate.

Macroscopic comparison of disease severity of cv. Cadenza and TILLING lines 1-4 revealed that line 1 was more severely affected by both *MoT* isolates than the wild-type or any of the other TILLING lines (Figures 3A and B). Similar results with both tested *MoT* isolates indicate that this outcome is isolate-independent. Similar to TILLING line 1, the TALEN line showed a higher degree of disease symptoms than its parental wild-type line cv. KN199 upon challenge with *MoT* isolate Br116.5 (Figure 3B). Interestingly, TILLING lines 3 and 4 exhibited slightly fewer disease symptoms than cv. Cadenza with both *MoT* isolates (Figures 3A and B).

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## Figure 3

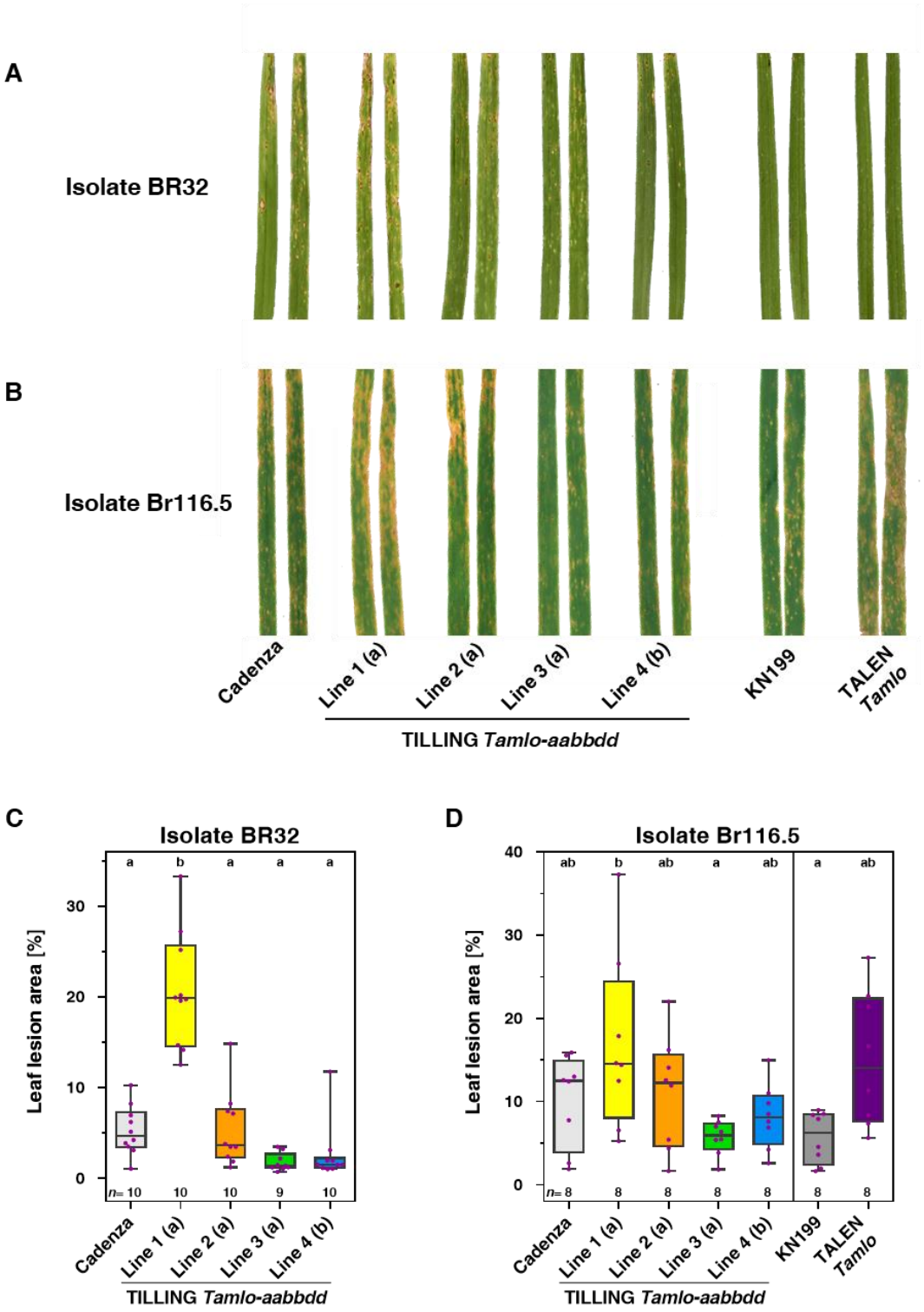


**Figure 3. Macroscopic disease symptoms of wheat lines upon challenge with *Mot*.** (**A** and **B**) Plants of cv. Cadenza and TILLING-lines 1, 2, 3 and 4 and cv. KN199 and the TALEN line, respectively, were inoculated with *MoT* isolate BR32 (**A**) or Br116.5 (**B**). Inoculation was performed on either primary leaves of 14-day-old-plants (**A**) or on secondary leaves of 18-day-old-plants (**B**). Displayed are two representative leaves for each interaction and treatment at 7 dpi. (**C** and **D**) Quantification of diseased leaf areas (blast symptoms) on different wheat genotypes after inoculation with *MoT*. The average

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diseased leaf areas were calculated based on photographs from eight to ten leaves using the software tool Assess 2.0. Results depicted in **C** and **D** are from combinations of plant genotypes and fungal isolates corresponding to leaves shown in **A** and **B**, respectively. Leaves of cv. KN199 and the TALEN line showed no visible disease symptoms after inoculation with *MoT* isolate BR32 and were therefore omitted in panel **C**. Data shown in panels **C** and **D** are from one biological replicate with the number of analyzed leaves given as *n* above the *x*-axis. Letters above the boxplots denote different significance groups according to statistical analysis (multi-paired ANOVA test; $p<0.05$).

To substantiate the results of the macroscopic evaluation, we performed quantitative assessment of the diseased leaf areas using the software APS Assess 2.0 on photographs of infected leaves. Results obtained by this measurement essentially confirmed the visual impressions and revealed a statistically significant difference in the diseased leaf areas between cv. Cadenza and TILLING line 1 in case of the *MoT* isolate BR32 (Figure 3C). The data further in tendency indicate an increase in the leaf lesion area for the TILLING line 1 as compared to cv. Cadenza and of the TALEN mutant in comparison to cv. KN199 in case of the *MoT* isolate BR116.5, although these differences were not significant according to stringent statistical analysis (Figure 3D).

To explore the basis for the different levels of disease susceptibility of the wheat genotypes against *MoT* isolate Br116.5, we microscopically analyzed interaction sites of cv. Cadenza and TILLING line 1 as well as of cv. KN199 and the TALEN line. Therefore, we harvested respective leaf samples at 24 and 96 hours post inoculation (hpi) and examined them by consecutive bright-field (to assess the presence of either epiphytical infection structures or bulbous hyphal in epidermal cells) and epifluorescence microscopy (to evaluate the deposition of autofluorescent material). We assigned each interaction site to one of the following six categories (Supplemental Figure 4): (1) presence of epiphytic fungal infection structures such as conidia or appressoria and absence of autofluorescence; (2) presence of bulbous infection hyphae within epidermal cells; (3) presence of autofluorescent deposits underneath appressoria; (4) whole cell autofluorescence of the attacked epidermal cell; (5) autofluorescence of intact, globularly-shaped mesophyll cells in close contact to attacked epidermal cells; and (6) autofluorescence of collapsed mesophyll cells.

In the barley/*M. oryzae* interaction, the beforehand mentioned categories are correlated with the successive invasion of the pathogen from epidermal to mesophyll tissue. For simplicity, we focus here on the most relevant categories 1, 2 and 6, with category 6 being an indicator of advanced mesophyll colonization by the pathogen (Jarosch et al., 2003; Jarosch et al., 2005). Inspection of leaf samples revealed that, irrespective of the wheat genotype analyzed, there was hardly any autofluorescence detectable underneath appressoria at 24 hpi (corresponding to category 1), and no collapsed, autofluorescent mesophyll cells (category 6) were detectable in any of the interactions. However, cv. KN199 and the TALEN line showed presence of some fungal hyphae in epidermal cells (category 2), with the TALEN line permitting more hyphal growth than its respective wild-type (Figure 4A). At 96 hpi, the frequency of interaction sites without autofluorescence decreased to 46% and 18% for cv. Cadenza and cv. KN199, respectively. Concomitantly, we recorded 12% (cv. Cadenza) and 43% (cv. KN199) of sites with collapsed, autofluorescent mesophyll cells (category 6), which specify successful fungal mesophyll invasion. Bright-field microscopy revealed that fungal hyphae were present in epidermal cells (category 2) at all of these infection sites. In contrast to the corresponding wild-type genotypes cv. Cadenza and cv. KN199, TILLING line 1 and the TALEN mutant showed considerably higher proportions of collapsed mesophyll cells at 96 hpi (category 6; 52% and 69%, respectively; Figure 4). These results are indicative of enhanced mesophyll invasion of the pathogen in the *Tamlo* genotypes, which is consistent with the more pronounced disease symptoms observed for both genotypes in comparison to the parental lines (Figure 3). In summary, we conclude that *Tamlo* triple mutant lines exhibit allele-dependent increased disease susceptibility to *MoT*, with the stronger *Tamlo* mutant alleles present in TILLING line 1 and the TALEN mutant affecting the outcome of the interaction the most.

## Figure 4

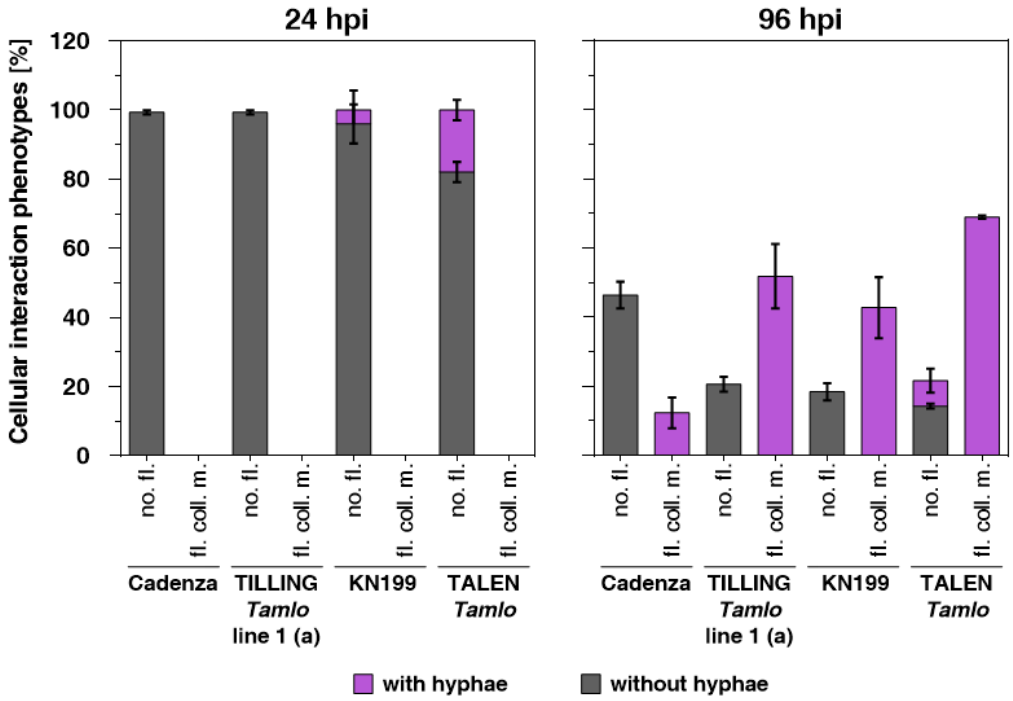


**Figure 4. Quantitative assessment of cellular *MoT* interaction phenotypes.** Primary leaves of the specified wheat lines were inoculated with *M. oryzae* isolate BR32 or Br 116.5 and harvested at 24 hpi (**A**) or 96 hpi (**B**). After removal of leaf pigments, samples were subjected to bright-field and epi-fluorescence microscopy and each fungal infection site was assigned to the category no fluorescence at the infection site (no. fl.; category 1; A1 in Supplemental Figure 4) or fluorescence associated with collapsed mesophyll cells (fl. coll. m.; category 6; A5 in Supplemental Figure 4). The proportion of infection sites at which invasion of bulbous fungal hyphae in epidermal tissue occurred additionally (category 2; B in Supplemental Figure 4) are marked for each category in magenta. At least 100 interaction sites were evaluated per leaf and genotype. Mean and standard deviation were calculated from three (cv. Cadenza and the TILLING line) or two (cv. KN199 and the TALEN line) leaves for each time point.

### *3.4. Tamlo triple mutants do not exhibit signs of early leaf senescence*

In barley and Arabidopsis, *mlo* mutations are associated with signs of premature leaf senescence and spontaneous callose deposition (Consonni et al., 2006; Consonni et al., 2010; Wolter et al., 1993; Piffanelli et al., 2002). To explore whether this is also the case for the *Tamlo* mutants, we grew cv. Cadenza, representatives of the TILLING triple mutant lines 1 and 2, cv. KN199 and the TALEN line in controlled conditions. At the age of 31 days, we scored the spontaneous occurrence of callose deposits and macroscopically assessed the extent of leaf chlorosis and necrosis in the primary leaves of the plants. As a control, we included a barley wild-type genotype (cv. Ingrid) and a corresponding isogenic *mlo* null mutant (backcross (BC) Ingrid *mlo*-3; (Büschges et al., 1997)) in these experiments, which were scored at the age of 24 days. Consistent with a previous report (Wolter et al., 1993), the BC Ingrid *mlo*-3 mutant developed substantially more callose deposits than cv. Ingrid (median of 1027 versus 548 deposits $cm^{-2}$; Figure 5A) and showed extensive signs of leaf chlorosis and necrosis, covering approximately 17% of the leaf area (cv. Ingrid: 2%; Figure 5B and C). By contrast, the number of spontaneous callose deposits did not differ significantly between the two tested TILLING lines and cv. Cadenza (median of 143, 107 and 166 deposits $cm^{-2}$, respectively; Figure 5D). The same was true

for cv. KN199 and the TALEN line (595 and 442 deposits $cm^{-2}$; Figure 5D), though these two genotypes had in tendency higher numbers of callose deposits than cv. Cadenza and the two TILLING lines, which likely was caused by an effect of the different genetic backgrounds of these two wheat varieties. None of the five analyzed wheat lines showed obvious signs of early leaf chlorosis and necrosis in our experimental conditions (Figure 5E and F).

Peer-reviewed version available at Genes 2020, 11, 517; doi:10.3390/genes11050517



## Figure 5

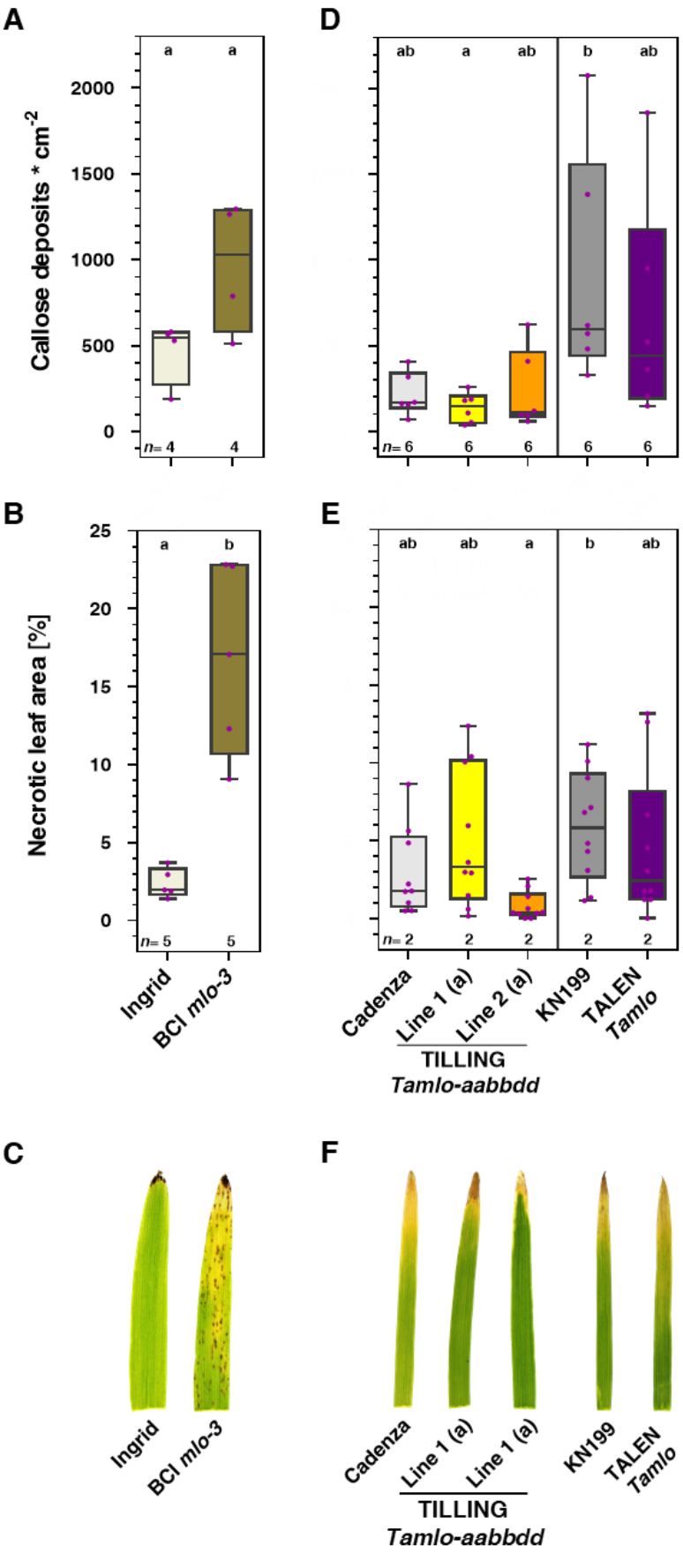

**Figure 5. *Tamlo* triple mutant lines do not exhibit signs of early leaf senescence.** (**A-C**) Spontaneous callose deposits and leaf necrosis in a barley *mlo* mutant as compared to the isogenic *Mlo* wild-type (cv. Ingrid). **A**) Callose deposits in 24-day-old primary barley leaves. Data of individual biological replicates per genotype are displayed as colored dots in the boxplots, and the number of replicates (*n*) is indicated below each boxplot. Each biological replicate represents the mean of three to ten evaluated leaves. Letters above the boxplots denote significantly different groups ($p<0.05$) according to a regular two-way ANOVA test. (**B**) Quantitative assessment of the extent of macroscopically visible necrosis in primary leaves of 24-day-old barley plants. Data of individual biological replicates per genotype are displayed as colored dots in the boxplots, and the number of replicates (*n*) is indicated below each boxplot. Each biological replicate represents the mean of three to five evaluated leaves. Letters above the boxplots denote different significance groups according to statistical analysis (regular two-way ANOVA; $p<0.05$). (**C**) Macroscopic phenotype of primary leaves of 24-day-old barley plants. (**D-F**) Spontaneous callose deposits and leaf necrosis in wheat *mlo* mutants as compared to the respective isogenic *Mlo* wild-type (cv. Cadenza or cv. KN199). (**D**) Callose deposits in 31-day-old primary wheat leaves. Data of individual biological replicates per genotype are displayed as colored dots in the boxplots, and the number of replicates (*n*) is indicated below each boxplot. Each biological replicate represents the mean of ten evaluated leaves. Letters above the boxplots denote significantly different groups ($p<0.05$) according to a one-way ANOVA test with Tukey's multiple comparisons. (**E**) Quantitative assessment of the extent of macroscopically visible necrosis in primary leaves of 31-day-old wheat plants. The colored dots represent ten evaluated leaves from two independent experiments ($n=2$; five leaves each). Letters above the boxplots denote different significance groups according to statistical analysis (one-way ANOVA with Tukey's multiple comparisons; $p<0.05$). (**C**) Macroscopic phenotype of primary leaves of 31-day-old wheat plants.

## 4. Discussion

We selected and analyzed a set of wheat TILLING-derived *mlo* mutants with various allele combinations (Supplemental Figure 1). These included novel segregants of two previously characterized *Tamlo* triple mutant lines (lines 1 and 2) as well as several segregants of two new *Tamlo* triple mutants (lines 3 and 4). All mutants are based on missense mutations in the three *TaMlo* homoeologs that were previously found to exhibit different levels of residual functionality in a barley single cell transient expression assay (Acevedo-Garcia et al., 2017b). According to this knowledge, the four TILLING *Tamlo* lines were predicted to reveal different degrees of powdery mildew resistance, which was experimentally confirmed by the results of our bioassays (Figure 1 and Supplemental Figure 2). The novel segregants corroborated a high level of resistance to *Bgt* in lines 1 and 2, with line 2 being somewhat more susceptible in the current experiments than reported before (Acevedo-Garcia et al., 2017b). As predicted, lines 3 and 4 showed markedly higher *Bgt* entry rates and exhibited more sporulating colonies on the leaf surface (Figure 1 and Supplemental Figure 2). We noted that intriguingly in most cases *Tamlo* double mutants of the *AAbbdd* genotype showed a similar level of resistance as the corresponding triple mutants harboring the same allele combination (Supplemental Figure 2), which is consistent with our previous findings (Acevedo-Garcia et al., 2017b). We conclude that irrespective of the mutated homoeologs a *Tamlo* double mutant of the *AAbbdd* genotype might be sufficient to obtain almost full protection against *Bgt* infection. We further confirmed the previously reported near-complete resistance of the TALEN *Tamlo* triple mutant against *Bgt* (Wang et al., 2014) with our German field isolate JA82 (Figure 1). Altogether, the four TILLING lines, the TALEN line and the corresponding wild-types (cv. Cadenza and cv. KN199) cover a huge spectrum of susceptibility/resistance, ranging from near-complete resistance in the TALEN line to full susceptibility in the wild-types (Figure 1). The wheat *mlo* lines thus recapitulate the situation known from barley, where *mlo* mutant alleles conferring differential levels of powdery mildew resistance have been reported (Habekuss and Hentrich, 1988; Hentrich, 1979; Hentrich and Habekuss, 1993; Piffanelli et al., 2002). This set of plants is therefore well suited to study the effect of *Tamlo* mutations on the outcome of interactions with other pathogens and the occurrence and strength of putative pleiotropic phenotypes. A similar panel of TILLING-based *mlo* mutants covering

a broad range of powdery mildew susceptibility/resistance was recently described for tetraploid durum wheat (*T. turgidum*; (Ingvardsen et al., 2019)).

We tested representatives of the four TILLING lines as well as the TALEN mutant and the respective parental wild-types with two hemibiotrophic pathogens (*Z. tritici* and *M. oryzae*) that differ in life-style from powdery mildew. *Z. tritici* has a long latent phase before it switches to a necrotrophic lifestyle (Sánchez-Vallet et al., 2015). *M. oryzae* is also classified as a hemibiotrophic pathogen but its initial biotrophic phase is considerably shorter than that of *Z. tritici* (Fernandez and Orth, 2018). Of the three tested *Z. tritici* isolates, only Zt153 was virulent on the examined wheat genotypes. However, upon challenge with Zt153, the wheat *mlo* mutants did not differ from the respective wild-types regarding the macroscopic infection phenotype (Supplemental Figure 3) or the density of pycnidia and the extent of the necrotic area (Figure 2). By contrast, TILLING line 1 and the TALEN mutant showed more severe disease symptoms (characteristic blast lesions) upon challenge with *MoT* isolate Br116.5, and TILLING line 1 also upon challenge with *MoT* isolate BR32 (Figure 3). The stronger symptoms correlated with enhanced invasive fungal growth in these lines (Figure 4). The fact that this outcome was only seen with TILLING line 1 and the TALEN mutant, which exhibit the highest level of powdery mildew resistance (Figure 1), indicates that allele strength may play a decisive role for the establishment of this phenotype. Putative anticorrelation between the degree of powdery mildew resistance and its associated pleiotropic phenotypes depending on *mlo* allele strength has been proposed before (Kusch and Panstruga, 2017).

The enhanced susceptibility of wheat *mlo* mutants against *MoT* is reminiscent of the enhanced susceptibility of barley *mlo* mutants against *M. oryzae* (Jarosch et al., 1999). More generally, powdery mildew-resistant barley and Arabidopsis *mlo* mutants were reported to have altered infection phenotypes to some additional pathogenic and beneficial microorganisms. Besides their enhanced susceptibility to *M. oryzae*, barley *mlo* mutants were reported to have tissue-dependent enhanced disease resistance against the oomycete pathogen *Phytophthora palmivora* (Le Fevre et al., 2016) as well as increased sensitivity to toxin-containing culture filtrates of the fungal pathogen *Bipolaris sorokiniana* (Kumar et al., 2001). By contrast, existing data regarding the fungal pathogens *Fusarium graminearum* and *Ramularia collo-cygni* as well as mycorrhizal fungi are controversial. For spike infections of barley *mlo* mutants with *F. graminearum*, both enhanced susceptibility (Jansen et al., 2005) and unaltered infection phenotypes (Hofer et al., 2015) have been noticed. Similarly, both enhanced leaf susceptibility (McGrann et al., 2014) and unaltered spike infection (Hofer et al., 2015) have been observed for barley *mlo* mutants against *R. collo-cygni*, possibly pointing to tissue- or development-specific differences as in in case of *P. palmivora* where infection was only attenuated in young leaves of an *mlo* mutant (Le Fevre et al., 2016). Finally, contrasting outcomes were also seen in experiments studying root colonization by symbiotic fungi. While previously reduced colonization intensity and arbuscule abundance of the mycorrhizal fungus *Funnelliformis mosseae* (former *Glomus mosseae*) was described for a barley *mlo* mutant (Ruiz-Lozano et al., 1999), a recent study did not find such differences for this fungus, but instead reduced colonization with the root-colonizing endophyte *Serendipita indica* (Hilbert et al., 2020). However, another recent report describes reduced colonization by the arbuscular mycorrhizal fungus *Rhizophagus irregularis* in the case of *mlo* mutants in barley, wheat and *Medicago truncatula* (Jacott et al., 2020). The in part contradictory outcomes with barley *mlo* mutants in these studies could be conditioned by experimental differences and environmental factors such as growth conditions, employed microbial isolates and inoculation procedures. The actual methods used for the scoring of infection phenotypes may likewise affect the outcome. Of note, most studies in barley were performed with a single (backcrossed) *mlo* mutant (harboring the *mlo*-5 null allele) and its isogenic parental line. The usage of multiple independent *mlo* alleles would greatly improve the credibility of such comparative analyses. Similar to barley *mlo* mutants, Arabidopsis powdery mildew-resistant *mlo* mutants show in part altered infection phenotypes to a range of other microorganisms (Acevedo-Garcia et al., 2017a; Consonni et al., 2010; Consonni et al., 2006). However, no clear pattern regarding lifestyle, tissue preference or mode of colonization emerged from these assays. It has been speculated previously that the tendency of *mlo* mutants to undergo spontaneous mesophyll cell death might be generally beneficiary for pathogens that engage in a hemibiotrophic

(Jarosch et al., 1999) or necrotrophic lifestyle (McGrann et al., 2014; Kumar et al., 2001). However, the unaltered infection phenotypes of barley, Arabidopsis and wheat *mlo* mutants with some hemibiotrophic/necrotrophic pathogens (for example our data with *Z. tritici*; Figure 2 and Supplemental Figure 3) argue against this generalized simplistic explanation. It thus remains to be explored which factor(s) of *mlo* mutants contribute to the modulation of infection phenotypes against a subset of pathogens.

Spontaneous deposition of callose and the occurrence of leaf chlorosis and necrosis have been reported in barley and Arabidopsis *mlo* mutants (Wolter et al., 1993; Consonni et al., 2006). These phenotypes, which also involve the catabolism of leaf pigments (Piffanelli et al., 2002; Consonni et al., 2010), reduced photosynthetic performance (Consonni et al., 2010) and the occurrence of mesophyll cell death (Peterhänsel et al., 1997), have been interpreted as a type of premature leaf senescence (Consonni et al., 2010; Piffanelli et al., 2002). Notably, similar undesired phenotypes were not seen in the case of tomato and pea *mlo* mutants (Bai et al., 2008; Humphry et al., 2011). In the present work, we also failed to detect elevated levels of spontaneous callose deposition or early leaf chlorosis/necrosis in the tested wheat *mlo* mutants (Figure 5). For the TALEN *mlo* line this outcome contrasts results from our previous study, where we noticed a premature leaf senescence phenotype for this mutant but not for the TILLING *mlo* lines (Acevedo-Garcia et al., 2017b). This seeming discrepancy might be explained by the different developmental stages (seedlings *versus* mature plants) and/or growth conditions used in the experiments. It is known that the appearance and extent of pleiotropic phenotypes is variable in barley *mlo* mutants and depends on the genetic background and possibly yet unidentified environmental factors (Wolter et al., 1993). Further experiments will be required to unravel the exact conditions that either promote or protract the development of pleiotropic phenotypes in *mlo* mutants in general and in wheat *mlo* mutants in particular. In summary, we feel that our results are of high relevance for agricultural practice, and we recommend caution regarding the employment of *mlo* wheat genotypes in geographical regions where *MoT* is prevalent.

**Acknowledgements:** We are thankful to Prof. Caixia Gao and Prof. Jin-Long Qiu from the State Key Laboratories (Chinese Academy of Sciences, Beijing, China) for providing seeds of the transgenic TALEN-derived *Tamlo* mutant and its parental line KN199, and to Prof. Hans Thordal-Christensen (University of Copenhagen, Denmark) for facilitating the delivery of the seeds. Didier Tharreau (CIRAD Montpellier, France) and Yukio Tosa (Kobe University, Japan) are acknowledged for providing *Magnaporthe* isolates. This work was funded by a shared grant of the German Federal Ministry of Food and Agriculture (BMEL; project management via the Specialist Agency for Renewable Resources; grant number 22030411) and the German Society for the Advancement of Plant Innovation (GFPi; grant number G 135/12 NR), respectively.

**Author contributions**: RP, ES and US conceived the study. KG, TE, JAG, MF, MH and RS and performed the experiments and analyzed the data. KG designed the Figures. RP drafted the manuscript; ES, KG und US edited the manuscript.

**Conflicts of interest**: The authors declare no conflict of interest.

**Abbreviations**

| | |
|---|---|
| Bgt | Blumeria graminis f.sp. tritici |
| cv. | cultivar |
| dpi | days post inoculation |
| hpi | hours post inoculation |
| Mlo | Mildew locus o |
| MoT | Magnaporthe oryzae pv. Triticum |
| TALEN | Transcription activator-like effector nuclease |
| TILLING | Targeted induced local lesions in genomes |

**References**

**Acevedo-Garcia J, Gruner K, Reinstädler A, Kemen A, Kemen E, Cao L, Takken FLW, Reitz MU, Schäfer P, O'Connell RJ, Kusch S, Kuhn H, Panstruga R** (2017a) The powdery mildew-resistant Arabidopsis *mlo2 mlo6 mlo12* triple mutant displays altered infection phenotypes with diverse types of phytopathogens. Sci. Rep. **7**: 27.

**Acevedo-Garcia J, Kusch S, Panstruga R** (2014) Magical mystery tour - MLO proteins in plant immunity and beyond. New Phytol. **204**: 273–281.

**Acevedo-Garcia J, Spencer D, Thieron H, Reinstadler A, Hammond-Kosack K, Phillips AL, Panstruga R** (2017b) *mlo*-based powdery mildew resistance in hexaploid bread wheat generated by a non-transgenic TILLING approach. Plant Biotechnol. J. **15**: 367–378.

**Alam MA, Xue F, Wang C, Ji W** (2011) Powdery mildew resistance genes in wheat: identification and genetic analysis. J. Mol. Biol. Res. **1**: 20–39.

**Bai YL, Pavan S, Zheng Z, Zappel NF, Reinstädler A, Lotti C, Giovanni C** de, **Ricciardi L, Lindhout P, Visser R, Theres K, Panstruga R** (2008) Naturally occurring broad-spectrum powdery mildew resistance in a central American tomato accession is caused by loss of *Mlo* function. Mol. Plant-Microbe Interact. **21**: 30–39.

**Brown JKM** (2015) Durable resistance of crops to disease: A Darwinian perspective. Annu. Rev. Phytopathol. **53**: 513–539.

**Büschges R, Hollricher K, Panstruga R, Simons G, Wolter M, Frijters A, van Daelen R, van der Lee T, Diergaarde P, Groenendijk J, Töpsch S, Vos P, Salamini F, Schulze-Lefert P** (1997) The barley *Mlo* gene: A novel control element of plant pathogen resistance. Cell **88**: 695–705.

**Ceresini PC, Castroagudín VL, Rodrigues FÁ, Rios JA, Aucique-Pérez CE, Moreira SI, Croll D, Alves E, Carvalho G** de, **Maciel JLN, McDonald BA** (2019) Wheat blast: From its origins in South America to its emergence as a global threat. Mol. Plant Pathol. **20**: 155–172.

**Consonni C, Bednarek P, Humphry M, Francocci F, Ferrari S, Harzen A, van Themaat EVL, Panstruga R** (2010) Tryptophan-derived metabolites are required for antifungal defense in the Arabidopsis *mlo2* mutant. Plant Physiol. **152**: 1544–1561.

**Consonni C, Humphry ME, Hartmann HA, Livaja M, Durner J, Westphal L, Vogel J, Lipka V, Kemmerling B, Schulze-Lefert P, Somerville SC, Panstruga R** (2006) Conserved requirement for a plant host cell protein in powdery mildew pathogenesis. Nat. Genet. **38**: 716–720.

**Dean R, van Kan JAL, Pretorius ZA, Hammond-Kosack KE, Di Pietro A, Spanu PD, Rudd JJ, Dickman M, Kahmann R, Ellis J, Foster GD** (2012) The Top 10 fungal pathogens in molecular plant pathology. Mol. Plant Pathol. **13**: 414–430.

**Delventhal R, Rajaraman J, Stefanato FL, Rehman S, Aghnoum R, McGrann GRD, Bolger M, Usadel B, Hedley PE, Boyd L, Niks RE, Schweizer P, Schaffrath U** (2017) A comparative analysis of nonhost resistance across the two *Triticeae* crop species wheat and barley. BMC Plant Biol. **17**: 232.

**Elliott C, Zhou FS, Spielmeyer W, Panstruga R, Schulze-Lefert P** (2002) Functional conservation of wheat and rice Mlo orthologs in defense modulation to the powdery mildew fungus. Mol. Plant-Microbe Interact. **15**: 1069–1077.

**Faivre-Rampant O, Thomas J, Allègre M, Morel J-B, Tharreau D, Nottéghem J-L, Lebrun M-H, Schaffrath U, Piffanelli P** (2008) Characterization of the model system rice--Magnaporthe for the study of nonhost resistance in cereals. New Phytol. **180**: 899–910.

**Fernandez J, Orth K** (2018) Rise of a cereal killer: The biology of *Magnaporthe oryzae* biotrophic growth. Trends Microbiol. **26**: 582–597.

**Frantzeskakis L, Di Pietro A, Rep M, Schirawski J, Wu C-H, Panstruga R** (2020) Rapid evolution in plant-microbe interactions - a molecular genomics perspective. New Phytol. **225**: 1134–1142.

**Gladieux P, Condon B, Ravel S, Soanes D, Maciel JLN, Nhani A, Chen L, Terauchi R, Lebrun M-H, Tharreau D, Mitchell T, Pedley KF, Valent B, Talbot NJ, Farman M, Fournier E** (2018) Gene

flow between divergent cereal- and grass-specific lineages of the rice blast fungus *Magnaporthe oryzae*. mBio **9**: e01219-17.

**Glawe DA** (2008) The powdery mildews: A review of the world's most familiar (yet poorly known) plant pathogens. Annu. Rev. Phytopathol. **46**: 27–51.

**Grandaubert J, Dutheil JY, Stukenbrock EH** (2019) The genomic determinants of adaptive evolution in a fungal pathogen. Evol. Lett. **3**: 299–312.

**Habekuss A, Hentrich W** (1988) Charakterisierung funktionell verschiedener ml-o-Mutanten durch Primärinfektion, Pustelwachstum, Inkubation und Befallsverlauf. Tag.-Ber. Akad. Landwirtsch.-Wiss. **272**: 229–237.

**Habig M, Quade J, Stukenbrock EH** (2017) Forward genetics approach reveals host genotype-dependent importance of accessory chromosomes in the fungal wheat pathogen *Zymoseptoria tritici*. mBio **8**: e01919-17.

**Hentrich W** (1979) Multiple Allelie, Pleiotropie und züchterische Nutzung mehltauresistenter Mutanten des mlo-Locus der Gerste. Tag.-Ber. Akad. Landwirtsch.-Wiss. **175**: 191–202.

**Hentrich W, Habekuss A** (1993) Untersuchungen an heteroallelen Mutanten des ml-o Locus der Sommergerste. Schriftenreihe VAFB Thüringen **1/1993**: 61–69.

**Hilbert M, Novero M, Rovenich H, Mari S, Grimm C, Bonfante P, Zuccaro A** (2020) *MLO* differentially regulates barley root colonization by beneficial endophytic and mycorrhizal fungi. Front. Plant Sci. **10**: 9319.

**Hofer K, Linkmeyer A, Textor K, Hückelhoven R, Hess M** (2015) *MILDEW LOCUS O* mutation does not affect resistance to grain infections with *Fusarium* spp. and *Ramularia collo-cygni*. Phytopathology **105**: 1214–1219.

**Humphry M, Reinstädler A, Ivanov S, Bisseling T, Panstruga R** (2011) Durable broad-spectrum powdery mildew resistance in pea *er1* plants is conferred by natural loss-of-function mutations in *PsMLO1*. Mol. Plant Pathol. **12**: 866–878.

**Ingvardsen CR, Massange-Sánchez JA, Borum F, Uauy C, Gregersen PL** (2019) Development of *mlo*-based resistance in tetraploid wheat against wheat powdery mildew. Theor. Appl. Genet. **132**: 3009–3022.

**Inoue Y, Vy TTP, Yoshida K, Asano H, Mitsuoka C, Asuke S, Anh VL, Cumagun CJR, Chuma I, Terauchi R, Kato K, Mitchell T, Valent B, Farman M, Tosa Y** (2017) Evolution of the wheat blast fungus through functional losses in a host specificity determinant. Science **357**: 80–83.

**Islam MT, Croll D, Gladieux P, Soanes DM, Persoons A, Bhattacharjee P, Hossain MS, Gupta DR, Rahman MM, Mahboob MG, Cook N, Salam MU, Surovy MZ, Sancho VB, Maciel JLN, NhaniJúnior A, Castroagudín VL, Reges JTdA, Ceresini PC, Ravel S, Kellner R, Fournier E, Tharreau D, Lebrun M-H, McDonald BA, Stitt T, Swan D, Talbot NJ, Saunders DGO, Win J, Kamoun S** (2016) Emergence of wheat blast in Bangladesh was caused by a South American lineage of *Magnaporthe oryzae*. BMC Biol. **14**: 84.

**Jacott CN, Charpentier M, Murray JD, Ridout CJ** (2020) Mildew Locus O facilitates colonization by arbuscular mycorrhizal fungi in angiosperms. New Phytol.

**Jansen C, Wettstein D** von, **Schäfer W, Kogel K-H, Felk A, Maier FJ** (2005) Infection patterns in barley and wheat spikes inoculated with wild-type and trichodiene synthase gene disrupted *Fusarium graminearum*. Proc. Natl. Acad. Sci. U.S.A. **102**: 16892–16897.

**Jarosch B, Collins NC, Zellerhoff N, Schaffrath U** (2005) *RAR1*, *ROR1*, and the actin cytoskeleton contribute to basal resistance to *Magnaporthe grisea* in barley. Mol. Plant-Microbe Interact. **18**: 397–404.

**Jarosch B, Jansen M, Schaffrath U** (2003) Acquired resistance functions in *mlo* barley, which is hypersusceptible to *Magnaporthe grisea*. Mol. Plant-Microbe Interact. **16**: 107–114.

**Jarosch B, Kogel KH, Schaffrath U** (1999) The ambivalence of the barley *Mlo* locus: Mutations conferring resistance against powdery mildew (*Blumeria graminis* f. sp. *hordei*) enhance susceptibility to the rice blast fungus *Magnaporthe grisea*. Mol. Plant-Microbe Interact. **12**: 508–514.

**Jones TR, Kang IH, Wheeler DB, Lindquist RA, Papallo A, Sabatini DM, Golland P, Carpenter AE** (2008) CellProfiler Analyst: data exploration and analysis software for complex image-based screens. BMC Bioinformatics **9**: 482.

**Jørgensen JH** (1992) Discovery, characterization and exploitation of Mlo powdery mildew resistance in barley. Euphytica **63**: 141–152.

**Jørgensen JH** (1994) Genetics of powdery mildew resistance in barley. Crit. Rev. Plant Sci. **13**: 97–119.

**Kumar J, Hückelhoven R, Beckhove U, Nagarajan S, Kogel KH** (2001) A compromised Mlo pathway affects the response of barley to the necrotrophic fungus *Bipolaris sorokiniana* (teleomorph: *Cochliobolus sativus*) and its toxins. Phytopathology **91**: 127–133.

**Kusch S, Panstruga R** (2017) *mlo*-based resistance: An apparently universal "weapon" to defeat powdery mildew disease. Mol. Plant-Microbe Interact. **30**: 179–189.

**Le Fevre R, O'Boyle B, Moscou MJ, Schornack S** (2016) Colonization of barley by the broad-host hemibiotrophic pathogen *Phytophthora palmivora* uncovers a leaf development-dependent involvement of *Mlo*. Mol. Plant-Microbe Interact. **29**: 385–395.

**Lyngkjær MF, Newton AC, Atzema JL, Baker SJ** (2000) The barley *mlo* gene: an important powdery mildew resistance source. Agronomie **20**: 745–756.

**McGrann GRD, Stavrinides A, Russell J, Corbitt MM, Booth A, Chartrain L, Thomas, William T B, Brown, James K M** (2014) A trade off between *mlo* resistance to powdery mildew and increased susceptibility of barley to a newly important disease, Ramularia leaf spot. J. Exp. Bot. **65**: 1025–1037.

**Panstruga R, Schulze-Lefert P** (2002) Live and let live: insights into powdery mildew disease and resistance. Mol. Plant Pathol. **3**: 495–502.

**Peterhänsel C, Freialdenhoven A, Kurth J, Kolsch R, Schulze-Lefert P** (1997) Interaction analyses of genes required for resistance responses to powdery mildew in barley reveal distinct pathways leading to leaf cell death. Plant Cell **9**: 1397–1409.

**Piffanelli P, Ramsay L, Waugh R, Benabdelmouna A, D'Hont A, Hollricher K, Jørgensen JH, Schulze-Lefert P, Panstruga R** (2004) A barley cultivation-associated polymorphism conveys resistance to powdery mildew. Nature **430**: 887–891.

**Piffanelli P, Zhou FS, Casais C, Orme J, Jarosch B, Schaffrath U, Collins NC, Panstruga R, Schulze-Lefert P** (2002) The barley MLO modulator of defense and cell death is responsive to biotic and abiotic stress stimuli. Plant Physiol. **129**: 1076–1085.

**Ruiz-Lozano JM, Gianinazzi S, Gianinazzi-Pearson V** (1999) Genes involved in resistance to powdery mildew in barley differentially modulate root colonization by the mycorrhizal fungus *Glomus mosseae*. Mycorrhiza **9**: 237–240.

**Sánchez-Vallet A, McDonald MC, Solomon PS, McDonald BA** (2015) Is *Zymoseptoria tritici* a hemibiotroph? Fungal Genet. Biol. **79**: 29–32.

**Schwarzbach E** (1976) The pleiotropic effects of the *ml-o* gene and their implications in breeding. In: Barley Genetics III, Karl Thiemig Verlag, München: 440–445.

**Shiferaw B, Smale M, Braun H-J, Duveiller E, Reynolds M, Muricho G** (2013) Crops that feed the world 10. Past successes and future challenges to the role played by wheat in global food security. Food Sec. **5**: 291–317.

**Stewart EL, Hagerty CH, Mikaberidze A, Mundt CC, Zhong Z, McDonald BA** (2016) An improved method for measuring quantitative resistance to the wheat pathogen *Zymoseptoria tritici* using high-throughput automated image analysis. Phytopathology **106**: 782–788.

**Strugala R, Delventhal R, Schaffrath U** (2015) An organ-specific view on non-host resistance. Front. Plant Sci. **6**: 526.

**Tanaka M, Nakayashiki H, Tosa Y** (2009) Population structure of *Eleusine* isolates of *Pyricularia oryzae* and its evolutionary implications. J. Gen. Plant Pathol. **75**: 173–180.

**Thygesen K, Jørgensen LN, Jensen KS, Munk L** (2009) Spatial and temporal impact of fungicide spray strategies on fungicide sensitivity of *Mycosphaerella graminicola* in winter wheat. Eur. J. Plant Pathol. **123**: 435–447.

**Troch V, Audenaert K, Wyand RA, Haesaert G, Höfte M, Brown, James K M** (2014) *Formae speciales* of cereal powdery mildew: close or distant relatives? Mol. Plant Pathol. **15**: 304–314.

**Valent B, Farman M, Tosa Y, Begerow D, Fournier E, Gladieux P, Islam MT, Kamoun S, Kemler M, Kohn LM, Lebrun M-H, Stajich JE, Talbot NJ, Terauchi R, Tharreau D, Zhang N** (2019) *Pyricularia graminis-tritici* is not the correct species name for the wheat blast fungus: Response to Ceresini et al. (MPP 20:2). Mol. Plant Pathol. **20**: 173–179.

**Wang Y, Cheng X, Shan Q, Zhang Y, Liu J, Gao C, Qiu J-L** (2014) Simultaneous editing of three homoeoalleles in hexaploid bread wheat confers heritable resistance to powdery mildew. Nat. Biotechnol. **32**: 947–951.

**Wolter M, Hollricher K, Salamini F, Schulze-Lefert P** (1993) The *mlo* resistance alleles to powdery mildew infection in barley trigger a developmentally controlled defense mimic phenotype. Mol. Gen. Genet. **239**: 122–128.