INTRODUCTION

Barley is not only one of the major crops to feed livestock and an essential ingredient of beer, it has also gained a growing importance in food production. However, infection with fungal pathogens is one of the most devastating threats to annual yields, causing severe damage to various organs (Liu et al., 2011; Park et al., 2015; Wolfe & McDermott, 2003). To ensure sustainable and high-yield crop production, an ongoing improvement towards resistant varieties is the most important challenge for research and plant breeding.

An ecologically sustainable method of crop protection is the identification of, and breeding with, naturally occurring resistance genes that originate in related wild varieties or landraces (Dinh et al., 2020). However, many resistance genes are mainly effective against certain races of one fungal species or have already been overcome (Clifford, 1985; König et al., 2012; Niks et al., 2000).
identification of new resistance mechanisms is therefore a major future challenge. One promising approach is to eliminate the fundamental requirements for a successful pathogen infection. The availability of sugars to cover their energy demand is a major need for plant pathogens (Bezrutczyk et al., 2018). Thus, uncovering the routes of nutrient utilization by fungal pathogens and developing methods that block feeding could represent a highly promising strategy to engineer durable and broad-spectrum resistance.

Sugars are the basal energy source for living organisms and their acquisition and partitioning are key steps to conduct physiological processes. In plants, sugars are produced in photosynthetically active source tissues and distributed to supply energy to consuming sink tissues. Specialized sugar transporters are crucial players in these delivery pathways and belong to three major groups: the SWEETs (Sugars Will Eventually be Exported Transporters), SUTs (sucrose H+ co-transporters) and STPs (sugar transport proteins). Members of the SWEET family typically consist of seven transmembrane (TM) domains and transport a variety of substrates. SUTs and STPs belong to the major facilitator superfamily (MFS) with typically 10–12 TM domains (Büttner, 2010; Julius et al., 2017). Sucrose-exporting SWEETs and SUTs control the key step of phloem loading and long-distance transport. STPs, on the other hand, transport monosaccharides, like glucose or fructose, over short distances, thereby providing ready-to-use sugars to feed energy-consuming cells and cell compartments (Büttner, 2010; Eom et al., 2015; Julius et al., 2017).

As the low sugar content in the plant apoplast might constrain their growth, pathogens utilize the sugar reservoirs of their host to convert the infection area into an artificial sink (Pommerrenig et al., 2020). SWEETs are well-known targets that are exploited by diverse fungal and bacterial pathogens, for example Botrytis cinerea, Blumeria graminis, Ustilago maydis, Pseudomonas syringae, and various Xanthomonas species (Breia et al., 2020; Chen et al., 2010; Doidy et al., 2012; Sosso et al., 2019; Timilsina et al., 2020). In response, plants can activate the expression or enhance the transport activity of SUTs or STPs to counter the pathogen-induced leakage of sugars (Bezrutczyk et al., 2018; Pommerrenig et al., 2020).

One of the most prominent STPs involved in plant–pathogen interactions is STP13, but its role in the outcome of the respective infection seems a double-edged sword. On the one hand, increased STP13 activity supports basal resistance, as shown for the interaction of the necrotrophic fungus B. cinerea with Arabidopsis thaliana. Hence, it was hypothesized that increased AtSTP13 expression might remove glucose from the infection site to slow down the infection process (Lemonnier et al., 2014). Notably, AtSTP13 is also involved in interactions with bacterial pathogens. On detection of the pathogen-associated molecular pattern (PAMP) flag22 by the plant receptor FLS2, AtSTP13 is expressed and phosphorylated by BAK1 (Yamada et al., 2016). This modification enhances the sugar uptake of the transporter, possibly causing it to compete with the pathogen for sugar availability in the apoplast.

In contrast, an overexpression of the glucose transporter TaSTP13 supports the virulence of biotrophic fungi in wheat and Arabidopsis whereas silencing of TaSTP13 in wheat increases resistance (Huai et al., 2020). Because biotrophic fungi feed from living cells, an increased STP13 activity might enhance the glucose availability in the plant cytoplasm and thereby feed the pathogens via their haustoria. In line with this assumption is the observation that the glucose transport-deficient TaLr67res (G144 to R144 exchange, hereafter named TaSTP13GR) variant from wheat increases the resistance of wheat and TaSTP13GR-transgenic barley against the biotrophic fungi Puccinia hordei and B. graminis (Milne et al., 2019; Moore et al., 2015). Moreover, recently it was shown that a nonfunctional MtSTP13 G to R variant also enhances the resistance of Medicago truncatula to the biotrophic powdery mildew fungus Erysiphe pisi (Gupta et al., 2021). This suggests that an impeded glucose import from the plant apoplast to the cytoplasm might starve the fungal haustoria, thus preventing progression of a severe infection.

The barley ortholog HvSTP13 harbouring the G144 to R144 mutation (hereafter named HvSTP13GR) also lacks glucose transport activity but whether this mutant can confer resistance against biotrophic pathogens in barley has not been analysed, as was observed for TaSTP13GR (Milne et al., 2019). If that were the case, it would open the way for barley plants that are resistant against a broad spectrum of biotrophic fungi.

In this study we analysed the expression pattern of the barley hexose transporter HvSTP13 during various biotic stresses. We observed that HvSTP13 was induced in response to several fungal and bacterial pathogens as a result of the recognition of certain PAMPs. By using β-glucuronidase (GUS) reporter studies, we dissected the HvSTP13 promoter and identified a region that is probably responsible for the induced expression. With transgenic plants we analysed the effect of the HvSTP13GR mutant and found that it confers resistance against an economically relevant biotrophic rust fungus. In summary, our study contributes new insights into the molecular trigger for HvSTP13 expression and its potential to confer broad-spectrum resistance against biotrophic pathogens.

## RESULTS

### 2.1 The expression of HvSTP13 is induced by fungal and bacterial PAMPs

In barley, HvSTP13 is induced on treatment with the leaf rust fungus P. hordei (Ph) and the powdery mildew fungus B. graminis pv. hordei (Bgh) (Milne et al., 2019). To further dissect the HvSTP13 expression pattern under diverse biotic pressures, we infected barley seedlings with the biotrophic fungi Ph, Bgh, and Puccinia striiformis f. sp. hordei (Psh), or with the necrotrophic fungus Pyrenophora teres pv. teres (Pt). Leaf samples were harvested at 24, 48, and 72 hr postinoculation (hpi) and total RNA was extracted for reverse transcription quantitative PCR (RT-qPCR). The infection was confirmed by analysing the expression of a plant chitinase (HvPR3) that is known to respond to fungal infection (Figure S1; Ali et al., 2018). In contrast to mock-inoculated plants, all four fungal pathogens elicited an increase in HvSTP13 expression between 24 and 72 hpi (Figure 1a). To analyse whether HvSTP13 is also induced on bacterial...
treatment, we inoculated the host pathogen *Xanthomonas translucens pv. hordei* UPB820 (Xth) as well as the nonhost pathogen *Pseudomonas syringae pv. tomato* DC3000 (Pto) into barley and found an increase of *HvSTP13* expression for both bacterial pathogens (Figure 1b). A detailed time curve, performed with Xth, indicated that *HvSTP13* induction started between 1 and 4 hpi (Figure S2a). Next, we analysed the expression of *HvSTP13* in barley after inoculation with the PAMPs chitin, flg22, β-1,3-glucan, and laminarin. An increase of *HvSTP13* transcript was detected with flg22 and chitin treatment not later than 4 hpi (Figure 1c). In contrast, laminarin and β-1,3-glucan did not activate the expression of *HvSTP13* (Figure S2b). These results confirm not only that *HvSTP13* is induced as a consequence of fungal and bacterial PAMP-signalling, but also suggest a potential role in PAMP-triggered immunity (PTI)-related processes.

### 2.2 The promoter of *HvSTP13* harbours PAMP-responsive elements

To identify elements that might be required for the pathogen-mediated transcriptional activation, we used PLACE and PlantCARE to predict *cis*-regulatory elements (CREs) in an approximately 2 kb region upstream of the *HvSTP13* coding sequence. The analysis revealed several putative cis-regulatory elements that are known to be involved in the regulation of plant defence responses.
region of the HvSTP13 promoter (Higo et al., 1998; Lescot et al., 2002). In accordance with the response of the STP13 expression to multifaceted biotic and abiotic factors, the in silico analysis predicted a variety of different CREs within the HvSTP13 promoter region (Tables S1 and S2). Abscisic acid (ABA) has been shown to activate the expression of STP13 in Arabidopsis, barley, wheat, grapevine, and M. truncatula (Gupta et al., 2021; Hayes et al., 2010; Huai et al., 2020; Milne et al., 2019; Yamada et al., 2011). Consistent with this, the prediction revealed the presence of several ABA-responsive elements (ABREs) in the HvSTP13 promoter. Additionally, the in silico prediction identified several promising binding sites for WRKY transcription factors (W-box) and one sugar-responsive element (SURE), two CRE types that are involved in immunity and sugar signalling pathways (Tables S1 and S2, and Figure S3a; Chen et al., 2019; Sun et al., 2003).

To analyse which promoter regions are required for the PAMP-triggered induction of HvSTP13, we amplified four truncated HvSTP13 promoter variants that lack certain CREs. We labelled them according to the number of nucleotides upstream of the transcription start site (TSS). This results in promoter fragments p-887, p-445, p-222, and p-93. All used promoter fragments additionally included the 301 bp of the 5′ untranslated region (UTR) (Figures 2a and S3a). The promoter variants were fused to a promoterless β-glucuronidase (GUS) reporter gene and transformed into barley embryos to generate transgenic GUS reporter lines. For each construct, three independent T1 lines, with six plants each, were analysed. The presence of the transgene was verified by PCR. Negative siblings (indicated with −), as well as wild-type Golden Promise plants, were used as negative controls. Leaf discs were infiltrated with flg22, chitin, or MgCl₂. The resulting GUS activity was analysed after 24 h. The two fragments p-887 and p-445 displayed an increase in GUS activity after treatment with flg22 and chitin, indicating an induction after PAMP signalling. For the two shorter fragments, p-222 and p-93, no difference in GUS activity was observed between transgenic and nontransgenic siblings after flg22 or chitin treatment (Figure 2b). This indicates that the region between −445 and −222 bp upstream of the TSS possibly contains important cis-regulatory elements, which could be bound by regulatory transcription factors and thus allow for PAMP-mediated induction.

### 2.3 The glucose transport-deficient HvSTP13GR mutant is localized in the plasma membrane in N. benthamiana

The HvSTP13 wild type and the HvSTP13GR mutant were cloned into yeast expression vectors and transformed into the yeast strain EBY.
and respective genomes, thus conferring resistance in wheat, barley, a dominant negative effect on the wild-type HvSTP13 GR transporter and the positive control HvSTP13, both including the pHvSTP13 5’ UTR, under control of a short 35S promoter and monitored the subcellular localization after transient expression in Nicotiana benjamina leaves (Figure 3a). As positive control OsSWEET4, a plasma membrane-localized sugar transporter from rice, was used (Sosso et al., 2015), while free eGFP served as negative control. Free eGFP localized unspecifically into the nucleus and the cytoplasm, whereas OsSWEET4 exhibited a distinct localization at the edges of each cell that is typical for plasma membrane proteins (Figure 3b). The wild-type HvSTP13 displayed a clear localization to the plasma membrane comparable to OsSWEET4. The expression of the HvSTP13GR mutant appeared more patchy compared to the HvSTP13 wild type, but also localized predominantly to the plasma membrane (Figure 3b). This suggests that the lost glucose transport activity of the HvSTP13GR mutant is not due to mislocalization or protein degradation. Consequently, we used the HvSTP13GR variant for resistance analysis.

2.4 | The barley HvSTP13GR mutant confers resistance to a biotrophic fungus

In previous studies the transport-deficient TaSTP13GR or MtSTP13GR mutants were introduced as a transgene and exerted a dominant negative effect on the wild-type STP13 copies in the respective genomes, thus conferring resistance in wheat, barley, and M. truncatula (Gupta et al., 2021; Milne et al., 2019; Moore et al., 2015). Presumably, the barley HvSTP13GR mutant would also confer resistance to biotrophic fungi when introduced as a transgene. However, this has not been analysed yet.

To analyse the impact of the HvSTP13GR mutant on various pathogen infections, we generated transgenic barley plants that carry the genomic sequence of either the HvSTP13 wild type or the HvSTP13GR mutant under control of the native HvSTP13 promoter. To analyse their resistance phenotype, we infected T1 plants of three independent transgenic HvSTP13 or HvSTP13GR lines as well as the wild-type Golden Promise with the biotrophic rust fungus Ph and monitored the infection progress. Two and 4 days after infection, we harvested leaf sections and stained the fungal structures. At 2 days postinfection (dpi) all plants showed an even dispersion of spores on the leaf surface and only minimal differences in their overall developmental stage (Figure S5). Strikingly, at 4 dpi, significant differences in the Ph infection development became apparent between HvSTP13 and HvSTP13GR transgenic plants (Figures 4 and 5). Plants from the HvSTP13 transgenic lines displayed a comparable size of infection sites as the wild type, with a branched hyphal net, indicating a successful infection (Figure 4). For HvSTP13GR transgenic lines, on the other hand, we observed a retarded infection progress, with infection sites being significantly smaller compared to the wild type or the HvSTP13 transgenic lines (Figure 4). Moreover, the infection sites never exceeded the formation of only a few haustorial mother cells (Figure 5). Ten days after infection, the leaves of the remaining plants were evaluated regarding their rust pustule formation (Figure 6). For the HvSTP13-transgenic and wild-type Golden Promise plants a heavy formation of pustules was observed on the surface of the infected leaves. In contrast, for the HvSTP13GR transgenic plants, only chlorotic spots but no pustules were observed (Figure 6). We confirmed an adequate induction of HvSTP13 at 48 hpi via RT-qPCR, indicating that the resistance phenotype, observed for the HvSTP13GR transgenic plants, is not based on an impaired expression of either the genomic or the transgenic copy of HvSTP13 (Figure S6a,b). Instead, it is conceivable that the presence of the transport-deficient HvSTP13GR mutant dominantly affects the function of the wild-type HvSTP13, comparable to the reported resistance mechanism for TaSTP13GR and MtSTP13GR.

3 | DISCUSSION

In wheat the presence of the glucose transport-deficient TaSTP13GR mutant confers resistance against the two rust fungi Puccinia triticina and P. striiformis f. sp. tritici as well as against the powdery mildew fungus B. graminis f. sp. tritici (Moore et al., 2015). Transferring the TaSTP13GR transgene into barley mediated resistance against the respective barley rust fungus Ph and the powdery mildew fungus Bgh (Milne et al., 2019). The barley ortholog HvSTP13 has already been cloned and an equivalent HvSTP13GR mutant has been described as glucose transport-deficient in heterologous yeast studies (Milne et al., 2019). However, it has not been analysed whether the HvSTP13GR mutant confers resistance to biotrophic fungi comparable to TaSTP13GR. Here we
demonstrated that the glucose transport-deficient HvSTP13GR variant confers resistance against the economically relevant rust fungus Ph, thus behaving in a similar way to the previously described TaSTP13GR variant (Milne et al., 2019). Because this resistance is not based on a gene-for-gene relationship, but possibly on the reduced availability of nutrients for the pathogen, or on increased defence signalling, the manipulation of the STP13 glucose transporter might present a promising way for the generation of a durable and broad-spectrum resistance, not only for barley but also for other important crops.

Our detailed microscopic analysis of the infection progress for Ph demonstrated that the presence of the HvSTP13GR transgene does not disturb the initial phase of fungal development until the first haustorial mother cells (HMCs) are formed. However, while the development of Ph progresses in HvSTP13 transgenic and wild-type plants, the fungus revealed an arrested development in the presence of the nonfunctional HvSTP13GR transporter. Based on our and other findings, different scenarios are conceivable to explain the impact of the glucose transport-deficient STP13GR variant on resistance. On the one hand, the glucose that is imported by STP13 could be an essential carbon source for the fungus, especially in the beginning of the infection. After a spore attaches to the plant surface it germinates and forms infectious structures. In this first developmental phase biotrophic fungi feed from their own nutrient store, but internal stores are limited and the host plant is needed as nutrient source to energize further developmental processes (Divon & Fluhr, 2007). For this, biotrophic fungi form specialized organs called haustoria that invaginate the plant cell membrane and form a tight contact to the plant cytoplasm. There is emerging evidence that the composition of these organs is unique and provides all components needed for an efficient nutrient or signal transfer between the fungus and the plant (Bozkurt & Kamoun, 2020; Kwaaitaal et al., 2017; Polonio et al., 2020). Thus, the establishment of this tight interaction platform to gain nutrients from the host might be a key step that decides the failure or success of the disease. Support for this scenario comes from the observation that diverse fungal pathogens express one or several haustorial glucose transporters that are important for fungal virulence. Furthermore, it was hypothesized that glucose is not only used as an energy source but also functions as a signal molecule for fungal growth (Chang et al., 2020; van der Linde & Göhre, 2021; Sosso et al., 2019; Voegele et al., 2001). Additionally, fungi secrete invertases, whose activity might further increase the supply of monosaccharides at the interaction surface (Chang et al., 2017; Voegele et al., 2006). If this glucose supply is

![Figure 3](image-url)
hampered by the presence of the transport-deficient STP13GR variant, the fungus starves and lacks energy to develop further. Such a disruption of fundamental requirements would also explain the broad-spectrum resistance conferred by the STP13GR mutant against different biotrophic fungi and in different host plants (Gupta et al., 2021; Milne et al., 2019; Moore et al., 2015). On the other hand, various sugars have been shown to regulate cellular processes at multiple levels, including immunity reactions (Bezrutczyk et al., 2018). Hence, a blocked glucose import might change the relative glucose concentrations in the apoplast and the cytosol, and activate sugar signalling pathways. This shift might be sensed by the intracellular hexokinase 1 or the extracellular G-protein-coupled receptor RGS1 (regulator of G-protein signalling protein 1). Both proteins are reported to be involved in the activation of defence pathways, including signal transduction, gene expression, stomatal closure, cell wall restructuring, or reactive oxygen species (ROS) production (Grigston et al., 2008; Jing et al., 2020; Morkunas & Ratajczak, 2014; Xiao et al., 2000; Zhong et al., 2019). Here, the inactive STP13GR mutant might result in the activation of those sugar signalling pathways and promote the plant stress response. Furthermore, an altered or gain of function of the TaSTP13GR mutant was discussed by Milne et al. (2019) as the basis for the resistance mechanism. Indeed, the G144 to R144 mutation adds an additional positively charged amino acid in close proximity to the proton donor-acceptor pair D41 and R140 (Paulsen et al., 2019). This might result in rearrangements of the binding pocket and allow for the binding of an altered substrate that activates an immune response. However, as Huai et al. (2020) demonstrated, silencing of the TaSTP13 transporter increased the resistance against stripe rust; therefore, it is still under debate whether or not the loss of the glucose transport activity, a gain of function, or a combination of both is the basis for the resistance phenotype of the STP13GR mutants. In future, alternative mutants and analysis are needed to elucidate the underlying resistance mechanism.
In wheat, the expression of the closely related ortholog TaSTP13 is induced by pathogen infection as well as abiotic treatments, including ABA (Huai et al., 2020; Moore et al., 2015). The comparison of the HvSTP13 promoter with an equivalent portion of the TaSTP13 promoter resulted in an identity of 65%–68% (Figure S3b) and it would be interesting in future to analyse if certain CREs are shared by TaSTP13 and HvSTP13. We demonstrated that the expression of HvSTP13 is increased on recognition of bacterial and fungal PAMPs, and we identified a promoter region that is probably required for the induced expression. In this promoter region two interesting CREs were predicted, namely two ABREs and a cluster of four W-boxes. ABA, which activates the binding of transcription factors to ABREs, is mainly related to the abiotic stress response, but emerging evidence suggests a cross-talk of ABA with pathogen infection. The role of ABA to support or repress immunity reactions largely depends on the pathogen and the phase of infection (Cao et al., 2011). Notably, in grapevine, the promoter of the STP13 ortholog VvHT5 also employs a unique cluster of ABREs that connects the expression of VvHT5 to ABA signalling pathways, thus linking it to both wounding and pathogen infection (Hayes et al., 2010). However, whether this observation is connected to PAMP recognition or other effects of pathogen infection is unknown. In comparison, the presence of a W-box cluster in the HvSTP13 promoter indicates an intriguing link to a PAMP-induced response, as WRKY transcription factors are key players in downstream processes of the PTI (Chen et al., 2019). The interaction of AtSTP13 with FLS2 and its phosphorylation via BAK1 further supports such a connection between STP13 activity and PTI signalling, thus rendering WRKYs as promising agents for HvSTP13 induction (Yamada et al., 2016). Increasing research characterized WRKY transcription factors in important crops as wheat and barley, and different roles for

**Figure 5** Histological analysis of *Puccinia hordei* development in wild-type and transgenic plants at 4 days postinoculation. Wild-type Golden Promise (WT) and three independent HvSTP13 or HvSTP13GR transgenic lines (L1–L3) were infected with *P. hordei*. The stained fungal structures were visualized with a Leica S8 confocal microscope at 5× (a), 10× (b; Z-stack), and 40× (c; Z-stack) magnification and GFP fluorescence settings. The respective enlarged area is marked with a grey square. The images are representatives of two biological replicates with at least three independent infection areas each. SP, spore; GT, germ tube; A, appressorium; SV, substomatal vesicle; IH, infection hypha; HMC, haustorial mother cell; H, haustorium.
WRKY transcription factors in modulating resistance or susceptibility were presented. For example, HvWRKY10, HvWRKY19, and HvWRKY28 have been shown to act as positive regulators in the resistance response of barley to Bgh (Meng & Wise, 2012). For wheat it has been shown that the transient expression of the barley WRKYs HvWRKY6, HvWRKY40, and HvWRKY70 increases resistance against the biotrophic leaf rust fungus *P. triticina* and a follow-up study confirmed the resistance of wheat expressing HvWRKY6 and HvWRKY70 against *P. striiformis* f. sp. *tritici* and *B. graminis* f. sp. *tritici* (Gao et al., 2018; Li et al., 2020). Furthermore, HvWRKY23 is activated on PAMP recognition by HvCERK1 and probably supports resistance against the hemibiotrophic head blight pathogen *Fusarium graminearum* (Karre et al., 2017, 2019). These examples support the hypothesis that the PAMP-dependent activation of the HvSTP13 promoter is a result of PTI signalling via WRKY transcription factors to combat the artificial sink that is generated by pathogens (Pommerrenig et al., 2020).

In conclusion, HvSTP13 might be an important regulatory checkpoint in the multifaceted response of the plant on both biotic and abiotic stresses.

Our experimental approaches confirm the potential of the HvSTP13GR mutant for resistance breeding and identified promoter regions that are relevant for regulating transcription factors. Consequently, our work contributed to further decode the complex regulation network in which STP13 is probably a major player.

### EXPERIMENTAL PROCEDURES

#### 4.1 Bacterial infection of barley

Pto strain DC3000 and Xth strain UPB820<sup>R</sup> were grown for 2 days at 28°C using peptone sucrose agar (PSA) plates. The strains were resuspended in 10 mM MgCl<sub>2</sub>, adjusted to OD<sub>600</sub> of 0.2 and inoculated in 7-day-old barley plants. The plants were cultivated in a phytochamber with 16/8 h light and 18/12°C day/night conditions.

#### 4.2 Fungal infection for HvSTP13 expression analysis

Fungal infection experiments for HvSTP13 expression analysis were performed at the Institute for Resistance Research and Stress Tolerance (Federal Research Centre for Cultivated Plants, Julius Kühn Institute, Quedlinburg, Germany).

#### 4.2.1 Rust infection

Fresh uredospores for Ph isolate l-80 were propagated by using the highly susceptible barley cultivar Großklappige as previously described in Fazlikhani et al. (2019). Seven-day-old Golden Promise plants were

---

**FIGURE 6** Disease phenotypes of *Puccinia hordei*-infected barley plants at 10 days postinoculation. Wild-type Golden Promise (WT) and three independent HvSTP13 or HvSTP13GR transgenic lines (L1–L3) were infected with *P. hordei*. The pictures are representative of three independent infection experiments.
infected with Ph according to Wehner et al. (2019) and cultivated with 16/8 hr light and 20/17°C. Psh isolate 24 was propagated by using Hakal. The infection of Golden Promise plants was performed as described for Ph and plants were cultivated with 16/8 h light and 16/13°C day/night conditions in a greenhouse.

4.2.2 | Powdery mildew infection

Infection was performed as described in Šurlan-Momirović et al. (2016) with the isolate Freising, which was propagated on leaf segments of the susceptible cultivar Igri. Whole plants were infected in the settling tower. Pots with infected plants were placed in a tray with moist sand and covered with transparent plastic boxes. After 3 days, the air supply was increased by placing small clay pots under the rim of the plastic boxes. Incubation took place at 18/15°C, 16/8 h day/night cycle.

4.2.3 | Net blotch infection

The mycelium was propagated on potato dextrose agar (PDA) plates. One gram of the conidia-bearing mycelium was scraped off the agar plates and 100 ml of sterile water, containing 0.01% Tween 20, was added. The suspension was homogenized for 3 min with a stick blender, filtered through gauze, and sprayed evenly onto 3-week-old plants. The plants were covered with a plastic hood moistened with water for 48 h. Three days after infection, the plants were exposed to light (16/8 h day/night cycle, 60% humidity) and the temperature was raised from 18°C to 20°C according to Novakazi et al. (2019).

4.3 | Ph infection for resistance analysis in transgenic barley plants

Ph infections for resistance analysis were performed at the Department of Plant Biotechnology in Hanover. Fresh uredospores of Ph were propagated in climatic chambers (Polyklima) as described before and mixed with activated (10 min at 42°C, 1 h at room temperature) frozen spores in a 1:5 ratio. The spores were mixed with clay in a 1:3 ratio. Ten-day-old plants were sprayed with 0.02% Tween 20 using the GANZTON SP180K airbrush system. The spores were applied using a pipe cleaner. Plastic cups were moistened with 0.02% Tween 20 and used to cover the plants for 48 h. The plants were kept in climatic chambers in darkness for 24 h followed by a 16/8 h day/night cycle at 20°C for Ph. The infection experiment was repeated three times with 30 plants per transgenic line and 30 wild-type plants each (120 plants per infection).

4.4 | PAMP treatment of barley seedlings

Seven-day-old barley seedlings were inoculated with the PAMPs laminarin (200 µg/µl; Sigma-Aldrich), β-1,3-glucan (200 µg/µl; Sigma-Aldrich), chitin (100 µg/ml; Sigma-Aldrich), and flg22 (2 µM; Genscript). All PAMPs were dissolved in 10 mM MgCl2. The negative control was 10 mM MgCl2. Plants were cultivated in a phytochamber (16/8 h light, 18/12°C day/night). Inoculations were done in biological triplicate.

4.5 | RNA extraction and gene expression analysis

Total RNA was isolated using a RNeasy Plant Mini Kit (Qiagen). Leaf material was disrupted using a TissueLyser II (Qiagen). On-column DNase digestion was performed using a RNase-Free DNase Set (Qiagen). RNA concentration and purity were determined by using a Spark 10M (Tecan). cDNA was synthesized from 2 µg of RNA using a Maxima First Strand cDNA Synthesis Kit (Thermo Scientific). All qPCR analyses were performed in technical replicates, including no-RT controls, using the CFX Connect Real-Time PCR Detection System (Bio-Rad). Reactions contained Luna Universal qPCR Master Mix (NEB), 0.25 µM of each primer, and 100 ng of template cDNA in 20 µl final volume. Primers used for RT-qPCR are listed in Table S3. The ubiquitin-protein ligase (HORVU4HrG004090) served as a reference gene (Hua et al., 2015). HvPR3 (HORVU1Hr1G052430; Scheler, Schnepf, et al., 2016) served as infection control. Primer efficiencies were determined using a serial cDNA dilution. The fold induction was calculated to the mock control for each time point. Each experiment includes at least two biological replicates and was repeated at least twice.

4.6 | Construction of STP13 modules

The generated level 0 MoClo modules are shown in Figure S7a. The HvSTP13 (HORVU1Hr1G052430) modules were amplified from Golden Promise cDNA or gDNA (Table S3). The yeast pPMA1 promoter, ADH2 terminator, and Hxt1 coding sequences were amplified from EBY.VW4000 or already existing constructs (authors’ unpublished results). Level 1 transcription units were cloned into pICH47742 (plants; Weber et al., 2011; Werner et al., 2012) or in pAGT572 or pAGT573 (yeast; Scheler, Brandt, et al., 2016). For GUS reporter constructs the MoClo module pICH75111 was used (Engler et al., 2014). All multigene constructs for the generation of transgenic plants contained a hygromycin resistance gene and were generated using the destination vector pAGMB031. For transient expression in N. benthamiana, HvSTP13 and HvSTP13GR were cloned under control of the short CaMV 35S promoter and included the HvSTP13 5' UTR.

4.7 | Generation of transgenic plants and transgene analysis

Immature embryos of the barley cultivar Golden Promise were transformed with Agrobacterium tumefaciens AGL1 according to
the protocol of Harwood et al. (2009) with the following modifications. The selection period was reduced to 30 days, and 800 mg/L L-cysteine (Hensel et al., 2007) and 0.1 mM acetosyringone were added to the cocultivation medium. After a 10-day transition period, calli were placed on transition medium containing a 50% reduced hygromycin concentration (25 mg/L) for 4 days. The hygromycin concentration of the regeneration medium was also reduced to 50%. The transgene status of all regenerated T0 plants and following generations (T1, T2) was analysed by extracting the gDNA with either innuPREP Plant DNA Kit (Analytik Jena; T1, T2) or REDExtract-N-AMP plant Kit (Sigma Aldrich; T1, T2). The transgene was detected by amplifying the Ocs terminator of the hygromycin resistance gene cassette (Table S3).

4.8 | Analysis of promoter variants via GUS assay

For each GUS reporter construct, three independent T1 transgenic lines with six plants each were used. Two leaf discs (5 mm) were harvested from 10-day-old plants and vacuum infiltrated with 10 mM MgCl2, 1 μM flg22, or 100 μg/ml chitin. The leaf discs were incubated in the phytochamber as described before. After 24 h the leaf discs were frozen in liquid nitrogen and ground using the TissueLyser II. The GUS activity was measured in the Spark 10M reader as described previously (Kay et al., 2007). The measurements were performed in technical replicates. The experiment was performed twice.

4.9 | In planta localization studies

Four- to 6-week-old N. benthamiana plants were inoculated with A. tumefaciens GV3101 strains using a needleless syringe and an OD600 of 0.4. The localization of the resulting proteins was analysed at 2 dpi using a Leica True Confocal Scanner SP8 microscope equipped with an HC PL APO CS2 40x/1.10 water immersion objective (Leica Microsystems). Pictures for GFP fluorescence were taken with a HyD detector (488 nm, 502–516 nm) and pictures for chlorophyll autofluorescence with a PMT2 detector (658–708 nm). Detailed pictures were taken with a Leica True Confocal Scanner SP8 microscope using the HyD detector settings for GFP. Z-stacks represent up to 30 panels depending on the growth depth of the fungal structures.

ACKNOWLEDGEMENTS

We thank Anna Marthe, Christine Hoppe, and Ilona Renneberg for technical assistance and Sebastian Becker and Annekatrin Richter for helpful discussions on the manuscript. We are grateful to Claude Bragard and Ralf Koebnik for providing Xth UPB820® and Alain Tissier for providing yeast MoClo plasmids. This work was supported by university core funding only.

CONFLICT OF INTEREST

The authors declare that they have no competing interests.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon reasonable request.

ORCID

Jana Streubel https://orcid.org/0000-0001-8155-511X

REFERENCES


**SUPPORTING INFORMATION**

Additional supporting information may be found in the online version of the article at the publisher’s website.