The potential of effector-target genes in breeding for plant innate immunity
Gawehns, F.K.K.; Cornelissen, B.J.C.; Takken, F.L.W.

Published in:
Microbial Biotechnology

DOI:
10.1111/1751-7915.12023

Citation for published version (APA):

General rights
It is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), other than for strictly personal, individual use, unless the work is under an open content license (like Creative Commons).

Disclaimer/Complaints regulations
If you believe that digital publication of certain material infringes any of your rights or (privacy) interests, please let the Library know, stating your reasons. In case of a legitimate complaint, the Library will make the material inaccessible and/or remove it from the website. Please Ask the Library: http://uba.uva.nl/en/contact, or a letter to: Library of the University of Amsterdam, Secretariat, Singel 425, 1012 WP Amsterdam, The Netherlands. You will be contacted as soon as possible.
The potential of effector-target genes in breeding for plant innate immunity

Fleur Gawehns1,2, Ben J. C. Cornelissen1 and Frank L. W. Takken1,2*

1Department of Molecular Plant Pathology, Swammerdam Institute for Life Sciences, University of Amsterdam, Science Park 904, 1098 XH Amsterdam, the Netherlands.
2Centre for Biosystems Genomics, Droevendaalsesteeg 1, 6708 PD, Wageningen, the Netherlands.

Summary

Increasing numbers of infectious crop diseases that are caused by fungi and oomycetes urge the need to develop alternative strategies for resistance breeding. As an alternative for the use of resistance (R) genes, the application of mutant susceptibility (S) genes has been proposed as a potentially more durable type of resistance. Identification of S genes is hampered by their recessive nature. Here we explore the use of pathogen-derived effectors as molecular probes to identify S genes. Effectors manipulate specific host processes thereby contributing to disease. Effector targets might therefore represent S genes. Indeed, the Pseudomonas syringae effector HopZ2 was found to target MLO2, an Arabidopsis thaliana homologue of the barley S gene Mlo. Unfortunately, most effector targets identified so far are not applicable as S genes due to detrimental effects they have on other traits. However, some effector targets such as Mlo are successfully used, and with the increase in numbers of effector targets being identified, the numbers of S genes that can be used in resistance breeding will rise as well.

Rearranged traits can be used in breeding for resistance against pathogenic fungi and oomycetes

Globalization is one of the most important modern comforts of human society. However, it also negatively affects our daily life in ways that, at first sight, are not clearly connected with it. Over the last decades a steady increase in virulence of plant-infecting fungi and oomycetes has been observed. This increased pathogen virulence causes dramatic losses in the yields of crops, such as rice or wheat, locally resulting in a complete loss of harvest (Fisher et al., 2012). This development, which seriously threatens our crops, relates to an increase of genetic exchange between formerly geographically separated fungi and oomycetes. The accelerated macro-evolutionary genesis of new genotypes is, among other factors, caused by worldwide trading and international travel (Fisher et al., 2012). Even if biosecurity would be enhanced worldwide to slow down the rapid increase in pathogenicity, it would still not abolish the persistent need for new control measures for plant diseases.

Fungal and oomycete plant diseases are generally controlled with the help of fungicides, soil management and resistance breeding (McDonald and McDermott, 1993; Lazarovits, 2001). Traditional resistance breeding is based on the introgression of dominant resistance genes (R genes) from wild species into elite varieties. Since R gene-mediated resistance is based on recognition of a single elicitor, the frequency of resistance breakdown is typically high. Therefore a continuous influx of novel resistance genes in breeding programmes is required. To break this boom-and-bust cycle, susceptibility genes (S genes) have been proposed as an alternative to R genes in resistance breeding (Gust et al., 2010). S genes encode plant proteins that are manipulated by pathogens in order to facilitate their proliferation thereby promoting disease development. Hence, removal or inactivation of an S gene will impair the pathogens’ ability to cause disease. This type of plant immunity has the potential to be more durable (Gust et al., 2010). Indeed, the mlo locus of barley, one of the best-described recessive resistances, has been introgressed already in the 1940s (Jorgensen, 1992). This gene still confers durable broad-spectrum resistance against powdery mildews since its widespread use in the 1980s (Ortiz et al., 2002). Mlo encodes a plasma-membrane protein involved in vesicle-associated processes, which is essential for the powdery mildew to cause infection (Collins et al., 2003; Schulze-Lefert, 2004; Panstruga, 2005). Notably, Mlo is conserved throughout

© 2012 The Authors. Published by Society for Applied Microbiology and Blackwell Publishing Ltd. This is an open access article under the terms of the Creative Commons Attribution License, which permits use, distribution and reproduction in any medium, provided the original work is properly cited.
several plant species and recessive mlo-mediated powdery mildew resistance has also been identified in tomato and Arabidopsis thaliana (Consonni et al., 2006; Bai et al., 2008). Other examples of recessive resistance genes are eIF4E and eIF4G, conferring primarily resistance to potyviruses (Duprat et al., 2002; Ruffel et al., 2002) and xa5 and xa13, which are active against Xanthomonas oryzae in rice (Ogawa et al., 1987; Zhang et al., 1996; lyer and McCouch, 2004).

**Effectors from pathogens can be used as guides to identify S genes**

Most S genes currently used in agriculture have been identified in screens for recessive resistances in wild germplasms (Bai et al., 2005). As an alternative approach, mutagenized M2 populations have been screened for loss-of-susceptibility mutants towards the pathogen of interest. These screens are often done in genetically well-defined model species, such as A. thaliana – a brassicales representative – due to the relative ease of identifying and cloning of the affected gene. Such screens yielded, for instance, six DOWNY MILDEW RESISTANT (DMR) (Van Damme et al., 2005) and six POWDERY MILDEW RESISTANT (PMR) (Vogel and Somerville, 2000; Vogel et al., 2004) loci. A subset of these genes has been mapped and functionally analysed for their ability to function as negative regulators of the plant defence (Vogel et al., 2002; 2004; Consonni et al., 2006; van Damme et al., 2008). A functional screen has the advantage that mutations causing strong pleiotropic effects, or even lethality, will automatically be discarded. A drawback is that multi-copy S genes, or genes with a redundant function, are likely to be missed. Over the last 15 years about 30 S genes have been identified; unfortunately, only few of these genes have the potential to be used in commercial breeding programmes because they also affect other traits, such as yield or plant vigour (Pavan et al., 2010).

Because of the relative low success rate of genetic strategies to identify suitable S genes an alternative method is explored here. Since many S genes encode proteins manipulated by a pathogen, the pathogen might be used as a guide to identify S proteins. Pathogens manipulate their host via effector proteins that interfere with host processes. Therefore, identification of plant effector targets that are insensitive towards the activity of the effector could provide insensitivity towards the pathogen (Hogenhout et al., 2009). Hence, S genes and effector targets might represent the same genes (Pavan et al., 2010). Indeed, the virulence function of the Pseudomonas syringae effector HopZ was found to require A. thaliana MLO2 (Lewis et al., 2012), a functional orthologue of barley Mlo (Consonni et al., 2006). Interestingly, independent mlo2 knockouts were found to vary in their resistance levels to P. syringae. Whereas two independent T-DNA insertion lines became resistant (Lewis et al., 2012), a third insertion mutant and a point mutation mutant were not affected in their susceptibility towards this pathogen (Vogel and Somerville, 2000; Consonni et al., 2006). However, the latter mutants were resistant towards the powdery mildew Golovinomyces orontii. This difference shows that the type of mutation in the S gene can determine the outcome in resistance. This effect could also be used as an advantage with regard to pleiotropic effects as discussed later.

Besides identification of known S genes, also new candidates have been identified in effector-target screens. An example is the Xanthomonas campestris AvrBs3 effector that targets the promoter of the upa20 gene from pepper, thereby promoting disease development by altering the expression of a transcription factor (Kay et al., 2007; Zhou and Chai, 2008). This atypical example, where the effector target is not a protein but a promoter region, shows the versatility of S genes. Both the HopZ and AvrBs3 example show that effectors can be used as guides to identify known and novel S genes conferring disease resistance.

**Identification of fungal and oomycete effector targets requires a tailor-made approach**

Far less effector targets have been identified for plant pathogenic fungi and oomycetes than for bacteria. The reason for this is because the former generally have more complex lifestyles, larger genomes and lower accessibility to genetic approaches, such as transformation and targeted gene knockout. Functional genomics enabled the rapid identification of up to hundreds of effector candidates from fungi and oomycetes (Hogenhout et al., 2009). Depending on the pathogen analysed most of those proteins suppress plant immunity, indicating a redundant function. However, suppression has mostly been studied in artificial and heterologous systems and the in vivo function of most effectors still has to be determined with gene knockouts in the pathogens (Bozkurt et al., 2012). Effectors that have a clear virulence function are prime candidates to identify potential S genes. Such key effectors can be selected with the help of effector detector screens, comparative genomics or in vivo studies (Alfano, 2009; see examples below). Most effector targets have been discovered using protein–protein interaction assays, but targets have also been predicted based on effector structure, their in vivo expression pattern or localization, or their biochemical activities (Alfano, 2009). Ideally, several of these effector characteristics are unveiled before the interaction study of choice is commenced. Also information about the pathogen lifestyle and the host immune system may play crucial roles in identifying the...
Table 1. Selection of plant effector targets and their method of identification.

<table>
<thead>
<tr>
<th>Effector</th>
<th>Pathogen</th>
<th>Host</th>
<th>Virulence target</th>
<th>Identified by</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Avr4</td>
<td>Cladosporium fulvum</td>
<td>Tomato</td>
<td>Chitin</td>
<td>Structure prediction and binding studies</td>
<td>van den Burg et al. (2004)</td>
</tr>
<tr>
<td>Ecp6</td>
<td>C. fulvum</td>
<td>Tomato</td>
<td>Chitin</td>
<td>Structure prediction and binding studies</td>
<td>de Jonge et al. (2010)</td>
</tr>
<tr>
<td>Pep1</td>
<td>Ustilago maydis</td>
<td>Corn</td>
<td>POX12</td>
<td>Transcriptomics, fluorescence complementation</td>
<td>Hemetsberger et al. (2012)</td>
</tr>
<tr>
<td>Avr2</td>
<td>C. fulvum</td>
<td>Tomato</td>
<td>Rcr3</td>
<td>Genetics 0026; co-IP (N. benthamiana, Pichia pastoris)</td>
<td>Dixon et al. (2000); Rooney et al. (2005)</td>
</tr>
<tr>
<td>Avrblb2</td>
<td>Phytophthora infestans</td>
<td>Potato</td>
<td>C14</td>
<td>Co-IP (N. benthamiana)</td>
<td>Bozkurt et al. (2011)</td>
</tr>
<tr>
<td>PopP2</td>
<td>Ralstonia solanacearum</td>
<td>Wide range</td>
<td>RD19</td>
<td>FLIM</td>
<td>Bernoux et al. (2008)</td>
</tr>
<tr>
<td>EPIC1/EPIC2</td>
<td>P. infestans</td>
<td>Potato</td>
<td>Rcr3</td>
<td>Co-IP (N. benthamiana, Escherichia coli)</td>
<td>Song et al. (2009)</td>
</tr>
<tr>
<td>Gr-VAP1</td>
<td>Globodera rostochiensis</td>
<td>Tomato</td>
<td>Rcr3</td>
<td>Yeast two-hybrid</td>
<td>Lozano-Torres et al. (2012)</td>
</tr>
<tr>
<td>Avr3a</td>
<td>P. infestans</td>
<td>Potato</td>
<td>CMPG1</td>
<td>Yeast two-hybrid</td>
<td>Bos et al. (2010)</td>
</tr>
</tbody>
</table>

Co-IP, co-immunoprecipitation; FLIM, fluorescence lifetime imaging.

genuine target from a list of candidates. Hence, there is no universal strategy to identify effector targets. The strategy chosen to identify effector targets depends on the identity and function of the effectors and the plant-pathosystem being studied.

Functional insights in fungal and oomycete effector targets identify S genes

So far, only a handful of fungal and oomycete effector targets have been identified (Table 1). They include both plant- and pathogen-derived molecules. For example, the *Cladosporium fulvum* effectors Avr4 and Ecp6 bind fungus-derived chitin oligomers thereby protecting it from plant chitinases and preventing chitin-triggered immunity (van den Burg et al., 2004, van den Burg et al., 2006, de Jonge et al., 2010). Among the effector plant targets there are several proteins with a positive regulatory function on the plant immune system, and these can therefore not be used as S genes. One such example is the haem-dependent peroxidase POX12 from corn that is targeted by the apoplastic effector Pep1 from *Ustilago maydis* (Hemetsberger et al., 2012). Transcriptomics and microscopical studies of the Pep1 knockout indicated a role of the effector in the apoplast (Doehlemann et al., 2009). Later Hemetsberger and colleagues (2012) showed via a biochemical approach that Pep1 is inhibiting POX12. Haem-dependent peroxidases are typically involved in the production of reactive oxygen species (ROS), an essential component of the early plant defence response, and their suppression enables the fungus to establish a biotrophic interaction with the host.

Various apoplastic effectors of different oomycetes and fungi target different papain-like cysteine proteases (PLCPs) (Kaschani et al., 2010). Some of these effectors, like Avr2 from *C. fulvum*, inhibit protease activity of specific PLCPs (Kruger et al., 2002; Rooney et al., 2005). Others prevent their secretion to the apoplast by retaining the PLCP in the cytoplasm, as has been shown for the *Phytophthora infestans* effector Avrblb2 (Bozkurt et al., 2011) and the *Ralstonia solanacearum* effector PopP2 (Bernoux et al., 2008). The Avrblb2 plant target was identified by *in planta* co-immunoprecipitation (Co-IP) from *Nicotiana benthamiana* leaves followed by mass spectrometric analysis. Five specific interacting plant proteins were found and among them was the C14 protease belonging to the class of PLCPs. The functional role of Avrblb2 was unravelled by microscopy studies showing inhibition of C14 secretion (Bozkurt et al., 2011).

In the apoplast of tomato the *C. fulvum* effector Avr2 targets Rcr3, which is also an PLCP (Kruger et al., 2002; Rooney et al., 2005). Rooney and colleagues (2005) confirmed their interaction using activity-based protease profiling and co-immunoprecipitation assays. Interestingly, Rcr3 also serves as a target for effectors from other pathogens. For example, both the *P. infestans* cystatin-like effectors EPIC1 and EPIC2B (Song et al., 2009) and the *Globodera rostochiensis* effector Gr-VAP1 (Lozano-Torres et al., 2012) exert their virulence function via Rcr3. These examples show that at least some PLCPs have the potential to be used as S gene.

Another interesting effector target was identified upon screening Y2H cDNA libraries made from *P. infestans* infected potato plants with the Avr3a effector. This effector specifically suppresses *P. infestans* INF1 triggered cell death (ICD) (Bos et al., 2006). Avr3a interacts in yeast and *in planta* with CMPG1, an E3 Ubiquitin (Ub) ligase (Bos et al., 2010). The ubiquitin proteasome pathway fulfills crucial functions in plant defence and several E3 Ub ligases have been found to play both positive and negative roles in immunity (Devoto et al., 2003). CMPG1 is required for defence response triggered by several R
genes, the basal immune system and for ICD (Gilroy et al., 2011). Although CMPG1 has a positive regulatory function in tobacco and tomato, a mutation of the rice CMPG1 homologue Spl11 confers resistance towards Magnaporthe grisea and X. oryzae revealing its potential use as an S gene (Yin et al., 2000). In line with this observation, a reduction in sporulation of P. infestans was observed in CMPG1 silenced N. benthamiana plants (Bos et al., 2010). It will be interesting to test whether a CMPG1 knockout in potato exhibits increased resistance against P. infestans. Besides CPMG1 also the A. thaliana E3 Ub ligases Pub21, 22 and 23 were found to be negative regulators of immunity, and pub21/pub22/pub23 mutants show spontaneous cell death and increased resistance against biotrophic pathogens (Trujillo et al., 2008). These findings make E3 Ub ligases interesting candidates to act as potential S genes.

**Pleiotropic effects limit the application of S genes in resistance breeding**

When an effector target represents a potential S gene, its applicability for breeding has to be determined. Pleiotropic effects, such as dwarfism or spontaneous necrotic lesions, are a common problem for the application of S genes in breeding (Pavan et al., 2010). Furthermore, a gene that confers susceptibility to one pathogen might mediate resistance to another (Jarosch et al., 1999).

As discussed above, in a specific context CMPG1 might be considered an S gene. However, since CMPG1 is also necessary for basal immunity (Gilroy et al., 2011), application of cmpg1 in potato resistance breeding does not seem obvious, because the plants are likely to become (hyper)sensitive to other pathogens. This trade-off between increased resistance to one, but increased susceptibility to another pathogen is one of the major drawbacks for the application of S genes in recessive breeding. It also applies for barley mlo resistance: while mlo confers resistance against biotrophic powdery mildew it enhances susceptibility towards necrotrophic fungi such as the rice blast fungus M. grisea and Bipolaris sorokiana (Jarosch et al., 1999; Kumar et al., 2001). Therefore, the use of mlo is not recommended in areas where rice and barley are grown in close proximity (Jarosch et al., 1999).

Also among P. syringae effector targets, the majority of S genes cannot be used because of their pleiotropic effects. MPK4 is a negative regulator of the salicylic acid (SA) response, which is required for resistance to many biotrophic pathogens. Therefore, loss of MPK4 function in A. thaliana leads to increased resistance against P. syringae and the oomycete Peronospora parasitica due to an accumulation of SA, but also to dwarfism and spontaneous lesions (Petersen et al., 2000). Similar symptoms have been reported in soybean after silencing of one of the two MPK4 homologues (Zhang et al., 2009). Surprisingly, silencing of MPK4 in tomato did not lead to a phenotype (Chen et al., 2009). Nevertheless, MPK4 function also affects the response to ethylene, hence leading to increased susceptibility towards the necrotrophic fungus Alternaria brassicola (Brodersen et al., 2006). This result makes the application of mpk4 in recessive resistance breeding unlikely.

Another example concerns RIN4, an effector target and important component of basal immunity in A. thaliana. A rin4 mutant exhibits increased resistance to P. parasitica and P. syringae, indicating a function for this gene as a negative regulator of basal resistance (Mackey et al., 2002). Silencing rin4 in tomato enhanced resistance against P. syringae carrying avrPto, but surprisingly growth of P. syringae lacking avrPto was unaffected (Luo et al., 2009). Hence, the ability of rin4 to mediate P. syringae resistance is race-specific restricting its potential use as S gene.

Some effector targets are monitored by R proteins, which complicate their use in breeding. Besides a negative regulatory role in basal immunity, Rin4 has a positive regulatory function in the presence of the R gene Rps2. A knock-down of Rin4 triggers activation of the RPM1 gene in A. thaliana (Mackey et al., 2002). Likewise, a Rcr3 mutant shows an autoimmune phenotype due to erroneous activation of the Cf-2 protein (Kruger et al., 2002). Next to the pleiotropic effects described above, some S genes negatively affect abiotic stress tolerance. For example, silencing of OsMAPK5 leads to enhanced resistance to M. griseae and Burkholderia glumae, but at the same time reduces plant tolerance to cold, drought and salt (Xiong and Yang, 2003).

In summary, on a case-to-case basis, taking into account the genetic background of the plant and pleiotropic effects resulting from the mutation in the S gene, it has to be analysed whether an effector target has the potential to be used as an S gene in plant breeding.

**Conclusions**

Compared with R genes, S genes provide a potentially more durable type of plant immunity. The retrieval of Mlo as an effector target shows the potential use of effector proteins in the identification of S genes. Also other effector targets, such as RIN4, MPK4 and CMPG1, fit the criteria of being an S protein as their knockouts confer enhanced resistance to specific bacteria, fungi and oomycetes. However, their direct application in crops is hampered by the pleiotropic effects often observed in the knockouts. Possibly, specific mutations in an effector target could reduce the pleiotropic effects while maintaining its ability to confer resistance as exemplified by mlo2. Identification
of more effector targets will increase the number of S genes that can be used in resistance breeding.

Conflict of interest

None declared.

References


