Research Article   **Open Access**

A Novel Cecropin A-derived Peptide as Specific Inhibitor of Appressoria in *Magnaporthe oryzae*

Aarón Rebollar and Belén López-García*

Department of Molecular Genetic, Centre for Research in Agricultural Genomics (CRAG), Campus UAB, Barcelona, Spain

Abstract

Magnaporthe oryzae causes crop losses around the world and is considered one of the most harmful pathogens in rice. The search for new types of antifungal compounds focuses on specificity in order to avoid toxicity to non-target species. In this work, we characterized the activity of the natural antimicrobial peptide Cecropin A and its derived peptide MgAPI16 as inhibitors of appressorium formation in *M. oryzae*. These peptides were able to control the development of blast disease in rice plants. Several lines of evidence indicated the different mode of action of both peptides. The addition of inducers of appressorium formation interfered with the inhibitory effect of MgAPI16 but not with Cecropin A. Moreover, antimicrobial activity assays showed a weak or no toxicity of MgAPI16 against bacteria and fungi suggesting high specificity in inhibiting appressorium formation. By fluorescence confocal microscopy, we observed a preferential binding of MgAPI16 to germinal tubes and appressoria causing the formation of aberrant non-functional appressorium structures. Based on our results, MgAPI16 is proposed as a potential target-orientated peptide that specifically blocks appressorium formation and control rice blast disease, being a promising compound with potential application in plant protection.

Introduction

Rice (*Oryza sativa*) is an important crop in the world and staple food for many countries. One of the major limitations to rice production is the blast disease caused by the fungus *Magnaporthe oryzae* [1]. Different strategies are required for rice blast management, such as cultural strategies for prevention, resistant varieties, biological control, and chemical fungicides [2]. But even with the integration of these techniques rice blast disease is still difficult to control, largely because *M. oryzae* presents a high pathogenic variability and a large number of fungal races [3-5]. Nowadays, the use of some chemical fungicides is being restricted due the long-terms repercussions in environment and human health. Legislation on the use of fungicides is becoming more restricted; many chemical fungicides are being reviewed for safety and efficacy and some of them may be deregistered as dangerous to humans or the environment (U.S. Environmental Protection Agency, The Center for Health and Wellness, European Food Safety Authority websites).

An obligatory feature of novel low risk fungicides is pathogen specificity, which will avoid unspecific toxicity and prevent undesirable effects on the environment. More pathogen-specific fungicides could be identified by the screening for molecules which specifically block infection-related processes such as appressorium formation, an essential developmental stage in the pre-penetration phase of some phytopathogenic fungi. Appressorium development in *M. oryzae* is a complex morphogenetic process regulated by multiple external signals (surface hydrophobicity, hardness, cutin monomers, and leaf waxes), and different transduction pathways (Pmk1 and Mps1 MAPK and cAMP-dependent signaling pathways) [1,6,7]. In previous studies, we have identified small synthetic peptides able to control rice blast disease by blocking appressorium formation in *M. oryzae* [8,9]. The proposed mode of action for one of these peptides, PAF104, is affecting the Pmk1 pathway by repression of the gene expression of *MoMSB2*, which encodes a surface sensing protein, and the mitogen-activated protein/extracellular signal-regulated kinase kinase kinase *MST11* [8]. Our previous results further support the hypothesis that peptides blocking a specific target have lower unspecific toxicity and suggest that the application of target-oriented antifungal compounds might be an environmentally sustainable strategy for plant protection.

One promising alternative to the classic chemical fungicides are antimicrobial peptides (AMPs), peptides broadly distributed in nature as innate defense molecules in all organisms [10-12]. The first family of antibacterial peptides clearly related to a bacteria-induced immunity in animals was cecropins in insects [13]. Cecropin A (CecA) is a linear and cationic peptide isolated from the hemolymph of *Hyalophora cecropia* which has antimicrobial activity against numerous pathogenic bacteria and fungi [13-16]. Moreover, several reports have shown that the transgenic expression of genes encoding CecA enhance resistance to plant pathogens [17,18].

The fact that CecA display cytotoxic activity against a wide range of microorganisms demonstrates its lack of specificity. An approach to identify more pathogen-specific peptides is the modification of known AMP sequences by residue substitution and/or reduction of size [19-22]. This rational design allows us to obtain new peptides with the favorable characteristics of the natural peptide but avoiding undesirable secondary effects.

In this work, we have identified a synthetic CecA-derived peptide called MgAPI16 that specifically blocks appressorium formation in *M.oryzae* and therefore has to potential for control of rice blast diseases. Moreover, the effect of this peptide has been compared with the lead peptide CecA.

Materials and Methods

Microbial strains

M. oryzae isolates PR9 and FR13 (kindly provided by Dr. Tharreau, CIRAD, Montpellier, France) were grown on complete medium at 25°C under 16h/8h (light/dark) photoperiod for 11-13 days as previously described [9]. A fungal strain of *Fusarium proliferatum* isolated from rice was cultured in potato dextrose agar (PDA) plates at 25°C for 7 days. The laboratory strain of *Escherichia coli* (DH5α) was grown in Luria-Bertani (LB) medium at 37°C to exponential phase.

Synthetic peptides

Peptides (Table 1) were purchased at >90% purity (GenScript, New Jersey USA). Peptide MgAPI16 was also synthesized labeled with tetramethyl-rhodamine at the N terminus (TMR-MgAPI16) by the same company. Peptide solutions were prepared in sterile milliQ-water at the appropriate concentration.

Appressorium formation assay

Development of *M. oryzae* appressoria was monitored by microscopic examination as previously described [8]. Briefly, 8 μl-drops of a conidial suspension adjust to 5×10^5 conidia/mL and 2 μl of 5x peptide solutions (or sterile water as control) were placed on a hydrophobic surface. Pictures of 5 random fields of every drop were taken with an Olympus Stereoscope microscope SZX16 after 6h and 24h of incubation and the percentage of appressorium formation was determined by microscopic examination for at least 100 conidia per replicate. The data were shown as the relative percentage of appressorium formed after peptide treatment compared to the appressoria formed in control samples without peptide. At least three independent experiments were carried out.

To evaluate the effect of appressorium development inducers on the inhibitory activity of the peptides, 2.4 mM cAMP (Sigma-Aldrich, Missouri USA) or 10 μM 1,16-hexadecanediol (Sigma-Aldrich, Missouri USA) were added in determined assays. For that, we used cell-treated polystyrene plates as hydrophilic surface.

Growth inhibition assay

In vitro antifungal activity of the peptides was determined using a microtiter plate assay as previously described [9]. Fungus at 2.5×10^4 conidia/ml was grown in a 96-well plate in a final volume of 100 μl of 50% PDB with 10 μl of a 10x peptide solutions (or sterile milliQ-water as a control for fungal growth). The plate was incubated at 28°C, and fungal growth was determined by measuring optical density (OD) at 492 nm in a SpectraMax M13 (Molecular Devices, California USA) microplate reader. For bacteria, 10^5 cells/ml were grown in 20% LB medium for 6h at 37°C and bacterial growth was determined by measuring OD at 590 nm. In each antimicrobial experiment, the mean and standard deviation (SD) of three replicates were calculated for each treatment and were repeated at least three times.

In vivo plant infection assays

For these experiments, the commercial *japonica* rice cultivar Senia was used. Three week-old plants were sprayed with 1 ml of 10^5 conidia/ml suspension of *M. oryzae* PR9 with 0.5% Tween20 (Sigma-Aldrich, Missouri USA) and 20 μM final concentration of the appropriate peptide (or sterile milliQ-water for the control).

Plants were kept in high-humidity conditions in a plastic bag for 24h. Then they were removed from the bag and maintained to a normal atmosphere and maintained at 28°C with 80% humidity and 16h/8h (light/dark) photoperiod. Pictures were taken 7 days post-infection with a Nikon camera D7000 and lesion areas were quantified by image analysis software Assess v.2.0.

Interaction peptide-fungi assay

To characterize the interaction of the peptide MgAPI16 with fungal cells, a *M. oryzae* Guy11 isolate that constitutively produces GFP protein was used (*gfp-M. oryzae*; kindly provided by Dr. Sesma). Fungus at 10^5 conidia/ml was treated with 10 μM of labeled peptide (TMR-MgAPI16) in a polystyrene hydrophobic plate and incubated at 28°C in dark conditions. The appressorium formation stages were visualized at different times using an Olympus FV1000 confocal laser scanning microscope (Tokyo, Japan), using excitation at 488 nm and emission at 505 to 530 nm for visualization of *gfp-M. oryzae* and excitation at 543 nm and emission at 575 nm for TMR-MgAPI16.

Results

In vitro inhibition of appresorium formation in *Magnaporthe oryzae* by CecA and its derived peptide MgAPI16

Firstly, the effect of the antimicrobial peptide CecA on *M. oryzae* appressorium formation *in vitro* was evaluated. Incubation of the strain PR9 with the peptide in a hydrophobic surface for 6h revealed that there was a concentration-dependent inhibition of appressorium formation (Figure 1A). Control conditions allowed a percentage of appressorium formation of 85.5% ± 6.8 (mean ± SD), but appressorium formation decreased significantly with 10 μM of CecA (36.4% ± 3.8). Moreover, appressorium formation at high concentration of the peptide (i.e. 30 μM) was almost one tenth of the control values (7.9% ± 0.2).

For further characterization, we evaluated the inhibitory activity of CecA after 24h incubation, when mature appressorium is already formed. At this stage, in addition to melanized appressoria formed at the tip of germ tubes (AP), we observed that *M. oryzae* PR9 is able to develop appressorium-like structures at hyphal tips (ALS), as previously reported [9,23]. Both structures (AP and ALS) were quantified after 24h incubation with different concentrations of CecA (Figure 1B). Results showed that the number of mature AP decreased at increasing concentrations of peptide, in similar levels than when fungus was incubated in presence of CecA for 6h (Figure 1A). However, ALS frequency slightly increased at higher CecA concentrations, i.e., 33.8%, 31.2% and 36.9% of conidia were able to form ALS at 10 μM, 20 μM and 30 μM, respectively, while only the 22.8% of conidia formed ALS in control conditions.

In a further approach, three CecA-derived peptides were synthesized based on its primary structure (Table 1) and their effect on appressorium formation was compared with CecA (Figure 1C). Peptides #2 and #3 barely reduced *M. oryzae* appressorium formation, but 10 μM of peptide #1 performed equal or slightly better than the same concentration of CecA. This result supported the idea that appressorium inhibitory effect of CecA lies in the N-terminal site of the peptide. For further studies the peptide #1 was selected and renamed as MgAPI16.
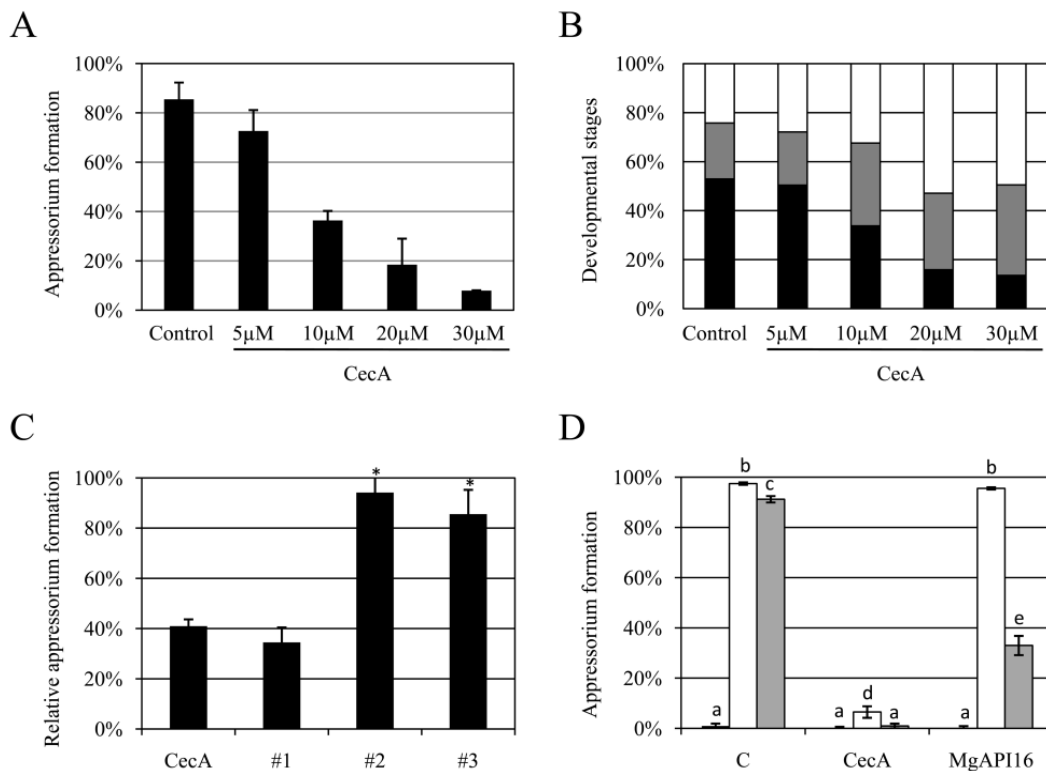
Peptide	Sequence
CecA	KWKLFKKIEKVGQNIRDGIIKAGPAVAVVGQATQIAK
#1 (MgAPI16)	KWKLFKKIEKVGQNIRDG
#2	QNIRDGIIKAGPA
#3	GPAVAVVGQATQIAK

Table 1: Amino acid sequences of the peptides used in this study.

Figure 1: Inhibitory activity of CecA and derived peptides on *Magnaporthe oryzae* PR9 appressorium formation. **(A)** Appressorium formation of fungi treated with increasing concentrations of CecA for 6h at 28°C. **(B)** Quantification of different fungal developmental stages after 24h incubation with increasing concentrations of CecA. The developmental stages are appressoria (black), appressorium-like structures (grey) and germinated spore (white). **(C)** Relative appressorium formation (referred to control condition) after 6h incubation with 20 μM of CecA and its derived peptides at 28°C. The absolute value of formed appressoria in control condition and corresponding to 100% was between 75-85% in all the experiments. Asterisks denote statistically significant difference p<0.01, ANOVA. **(D)** Effect of two appressoria inducers on the inhibitory activity of CecA and MgAPI16. Conidia of *M. oryzae* PR9 were incubated alone (black), or with 2.4 mM cAMP (white) or 10 μM 1,16-hexadecanediol (grey) and in the absence or presence of 20 μM of each peptide on a hydrophilic surface for 6h at 28°C.

Appressorium formation inducers bypass the inhibitory effect of MgAPI16

Some substances have been reported as *M. oryzae* appressorium formation inducers due their implication in one or more pathways involved on appressorium development, such as 1,16-hexadecanediol (a cutin monomer of the plants leaf cuticle) and cAMP (a regulator of appressorium morphogenesis) [1]. We evaluated the effect of these inducers on the inhibitory activity of CecA and MgAPI16 on a hydrophilic surface (Figure 1D). Hydrophobicity is one of most important signals sensed by the conidia to trigger appressorium formation. Our results showed that the fungus cannot form appressoria in hydrophilic conditions without the inducers. *M. oryzae* PR9 treated with CecA was unable to form appressoria even if it is supplemented with exogenous inducers. This result was consistent with the mode of action of CecA, i.e. forming channels in the membrane [24], killing the fungus and making it impossible to generate appressoria. However, *M. oryzae* PR9 treated with the peptide MgAPI16 was capable to develop appressorium when is supplemented with cAMP (93.5%) or 1,16-hexadecanediol (47.6%). Similar behavior was observed after treatment of another strain of *M. oryzae,* the FR13 strain, with MgAPI16 (data not shown). These results suggested a specific inhibitory effect of MgAPI16 on *M. oryzae* appressoria formation.
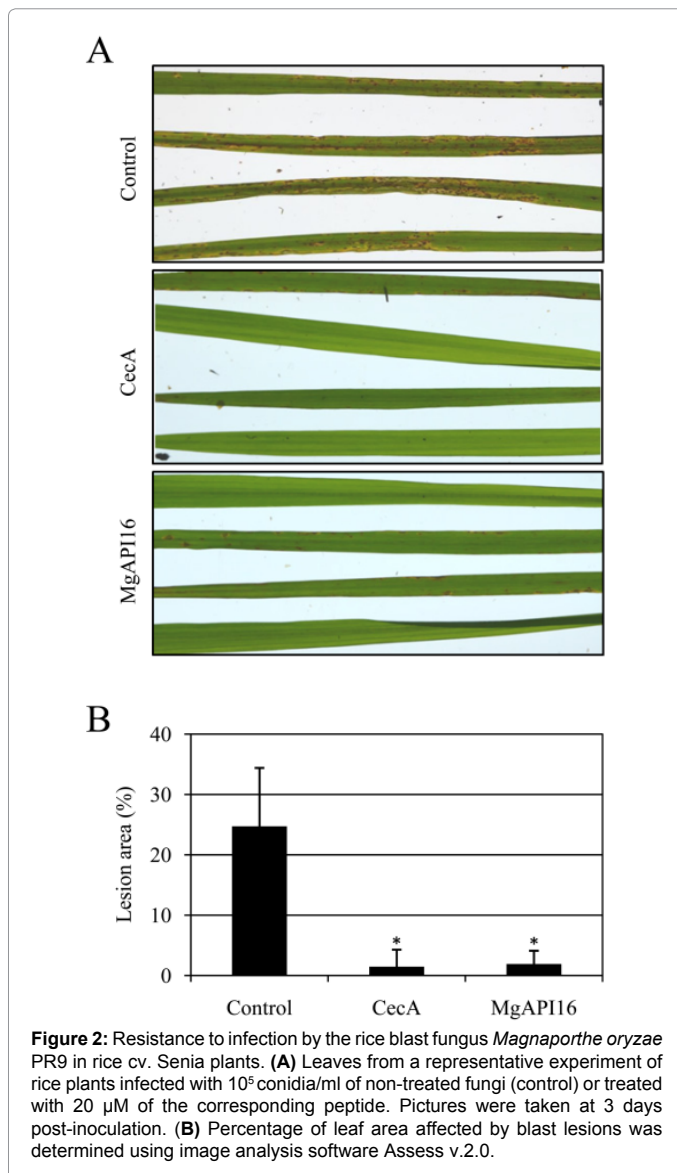
Application of CecA or MgAPI16 reduces the blast disease in rice plants.

An infection assay on *japonica* rice plants cv. Senia was developed to

evaluate if *M. oryzae* treated with CecA or MgAPI16 is still able to infect rice plants. Figure 2A shows representative leaves from the inoculated plants. Under the same experimental conditions, a clear reduction of the infection symptoms was observed when the fungus was treated with each peptide. Plant disease was also quantified by determining the percentage of the leaf area affected by blast lesions (Figure 2B). In control conditions, the fungus infected around 25% of the leaf surface (24.7% ± 9.6) (mean ± SD) at 7 days post-inoculation. However, CecA and MgAPI16 treatments significantly reduced the percentage of infected surface (1.4% ± 2.8 and 1.9% ± 2.2 respectively) in agreement with eyesight perception. This result was consistent with our previous data of reduction of appressorium formation by the peptides *in vitro*, which prevent to start the infection. Our data also showed that both peptides have similar efficacy inhibiting appressorium formation and controlling blast disease development.

Growth inhibitory activity profile of MgAPI16 and CecA

Indirectly, microscopic visualization of *M. oryzae* treated with peptides pointed to a lack of toxicity of MgAPI16 on fungal cells. In order to characterize a target-oriented peptide which specifically interferes with appressorium formation, the toxic effect of MgAPI16 was tested against two representative microorganisms and compared with the antimicrobial activity of CecA (Figure 3). The growth of *Eschericha coli* DH5α isolate was measured after incubation with different concentrations of each peptide (from 0.5 μM to 5 μM) at 37°C (Figure 3A). Results showed that bacterium is unable to grow at 2 μM and 5 μM of CecA; even the lesser tested concentration, i.e.

Figure 2: Resistance to infection by the rice blast fungus *Magnaporthe oryzae* PR9 in rice cv. Senia plants. **(A)** Leaves from a representative experiment of rice plants infected with 10⁵ conidia/ml of non-treated fungi (control) or treated with 20 µM of the corresponding peptide. Pictures were taken at 3 days post-inoculation. **(B)** Percentage of leaf area affected by blast lesions was determined using image analysis software Assess v.2.0.

followed by live-cell imaging using fluorescence confocal microscopy (Figure 4). At the first stages of the conidia development, the red signal from the peptide was located at the surface of the conidia with
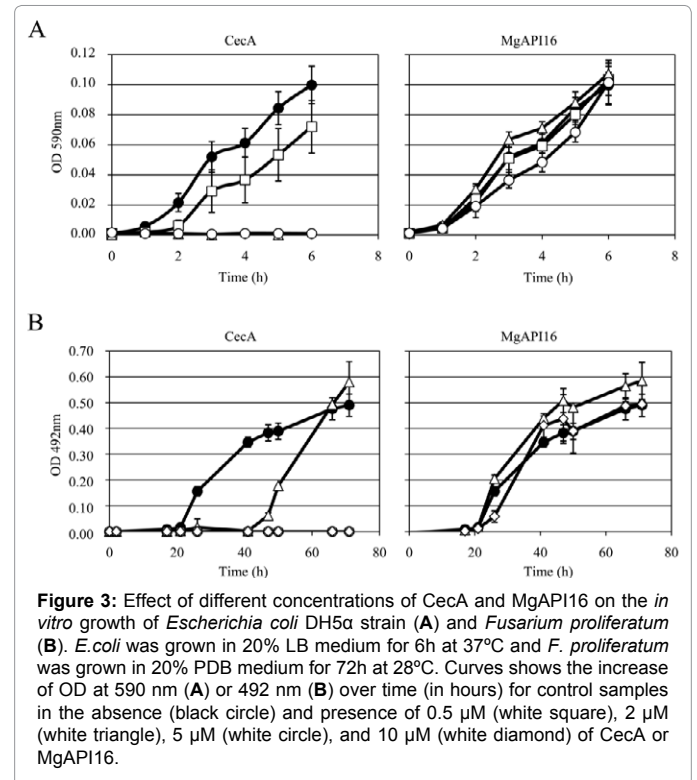

Figure 3: Effect of different concentrations of CecA and MgAPI16 on the *in vitro* growth of *Escherichia coli* DH5α strain **(A)** and *Fusarium proliferatum* **(B)**. *E.coli* was grown in 20% LB medium for 6h at 37ºC and *F. proliferatum* was grown in 20% PDB medium for 72h at 28ºC. Curves shows the increase of OD at 590 nm **(A)** or 492 nm **(B)** over time (in hours) for control samples in the absence (black circle) and presence of 0.5 µM (white square), 2 µM (white triangle), 5 µM (white circle), and 10 µM (white diamond) of CecA or MgAPI16.

0.5 µM, slightly reduced the viability of the bacterium. By contrast, MgAPI16 seemed harmless to the bacterium even at the highest tested concentration.

A similar experiment was performed in the eukaryotic organism *Fusarium proliferatum* (Figure 3B). In these assays, CecA inhibited the fungal growth with a minimum inhibitory concentration of 5 µM of peptide. Treatment with 2 µM CecA delayed fungal growth around 40h but at the end of the assay, i.e. 72h, fungal growth was no longer inhibited. On the other hand, no inhibitory activity was observed for the peptide MgAPI16 at the tested concentrations.

Preferential binding of MgAPI16 to fungal hyphae and appressorium structure

Considering previous data from this study regarding the lack of toxicity of MgAPI16 to other microorganisms, this peptide was selected for further studies. In an attempt to know MgAPI16 mode of action, *gfp*-expressing *M. oryzae* conidia were incubated on a hydrophobic surface with MgAPI16 labeled with tetramethylrhodamine (TMR-MgAPI16). The location of TMR-MgAPI16 in *gfp-M. oryzae* was
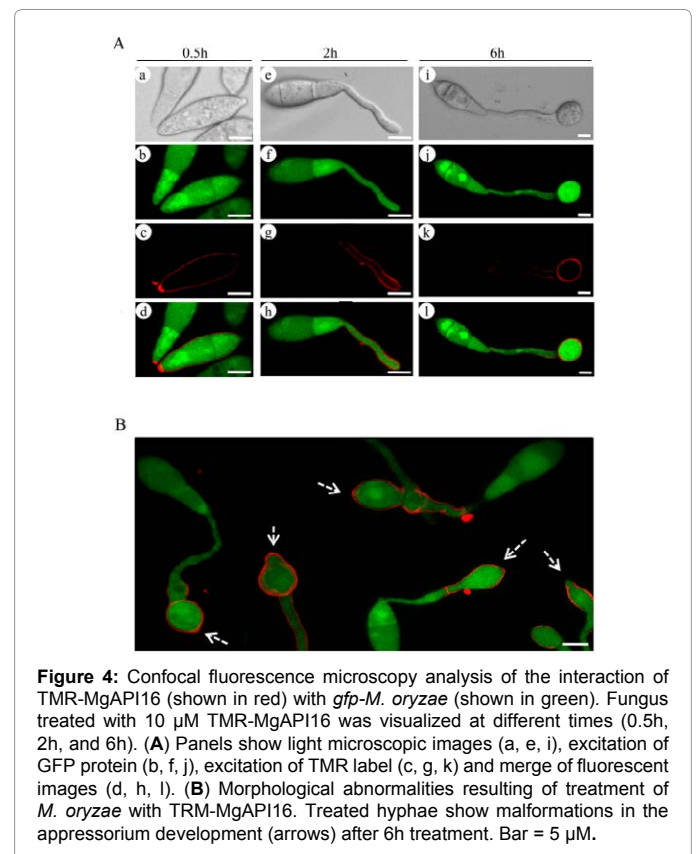

Figure 4: Confocal fluorescence microscopy analysis of the interaction of TMR-MgAPI16 (shown in red) with *gfp-M. oryzae* (shown in green). Fungus treated with 10 µM TMR-MgAPI16 was visualized at different times (0.5h, 2h, and 6h). **(A)** Panels show light microscopic images (a, e, i), excitation of GFP protein (b, f, j), excitation of TMR label (c, g, k) and merge of fluorescent images (d, h, l). **(B)** Morphological abnormalities resulting of treatment of *M. oryzae* with TRM-MgAPI16. Treated hyphae show malformations in the appressorium development (arrows) after 6h treatment. Bar = 5 µM.

a high preference for conidia tips (Figure 4A, panels a-d). At later developmental stages, when spores were completely germinated and the hyphae were growing up, the peptide was located surrounding the emerging germ tubes and hyphae (Figure 4A, panels e-h). These results indicated a preferential binding of the peptide where performed its inhibitory effect on appressorium formation. After 6h of incubation, although appressoria number was severely reduced, TMR-MgAPI16 preferentially bound at the surface of formed appressoria (Figure 4A, panels i-l). By confocal microscopy, we also observed that most of appressoria did not present the classic dome-shape structure after 6h treatment with MgAPI16; treated appressoria presented aberrant physical structure (tips or clearly shape deficiencies, Figure 4B).

Discussion

Nowadays, we are within a new legal and ecological framework in which the traditional fungicides do not meet all the imposed requirements. One problem refers to their toxicity to other species of the ecosystem. Current chemical fungicides are focused to kill fungal microorganisms, and frequently they present broad-spectrum activity showing toxicity to other organisms. The application of target-oriented antifungal compounds may be an environmentally sustainable strategy to control phytopathogenic diseases. Even more interesting could be the idea of a very specific compound that only affects the infective stage of the pathogen. During *M. oryzae* infective phase, conidia sense the hydrophobicity and the cutin composition of the rice leaf, triggering the formation of appressorium, a specialized structure for the cleavage of the leaf cuticle allowing the mesophyll invasion. However, if the conditions for infection are not suitable, conidia will germinate and become fungal hyphae. Therefore, blocking exclusively appressorium formation could prevent rice infection without causing a toxic undesirable effect on surrounding organisms.

Initially, we characterized appressorium inhibitory activity of a well-known antimicrobial peptide Cecropin A (CecA). The peptide inhibited the formation of appressoria (AP) while apparently promoting the formation of appressorium-like structures (ALS). In a previous work, we have demonstrated a similar behavior for other short peptides [9], suggesting that a possible secondary effect of the inhibition of AP structures would be the formation of ALS, a less efficient structure to penetrate into the plant [23]. Our data support the idea that the formation of both developmental structures involves different molecular mechanisms [23].

In this work, we also identified a novel CecA-derived peptide (MgAPI16) with similar appressoria inhibitory activity than CecA but without antimicrobial activity against the microorganisms tested. CecA is a lytic peptide whose channel-forming properties resides in its double α-helix structure linked by a flexible hinge region [24-26]. The non-antimicrobial peptide MgAPI16 corresponds with the first 18 amino acids of the N-terminal region of CecA, losing the ability to form the helix-hinge-helix structure. This fact supports that the typical structure of CecA is important for its high antimicrobial activity. Many CecA derived peptides have been designed in order to increase antimicrobial properties [19,20,25,27]. But, in our knowledge, this is the first report of a CecA-derived peptide targeted to block a specific pathogenic step, i.e. appressorium formation, but without antimicrobial activity.

Our results obtained for CecA and MgAPI16 after the addition of appressorium inducers clearly suggest their different mode of action. Appressorium inhibitory activity of CecA was due mainly to its lytic activity, being the fungus unable to form appressorium even after the addition of an inducer. However, the inhibitory activity of MgAPI16 was bypassed by the addition of cAMP that restored appressorium formation at the same level of the control sample. By contrast, *M. oryzae* partially overcame MgAPI16 inhibition effect after the addition of 1,16-hexadecanediol, suggesting that this peptide may affect the fungal ability to recognize external signal such as hydrophobicity and cutin monomers.

By fluorescence confocal microscopy, we observed that TMR-MgAPI16 preferentially binds to the germinal tubes and appressoria, whose cell wall presents different composition of polysaccharides; specifically, they are rich in α 1,3-glucan which is not observed in the conidia cell wall [28]. Whether the different composition of cell wall, or the presence of a specific receptor, would explain the preferential binding of MgAPI16 remains to be elucidated.

It has been reported the importance of the endosomal system and the autophagy in appressorium formation in *M. oryzae* [29-31]. During germination and appressorium development, small vacuoles in the apical cell of conidia move into the germ tube and nascent appressorium, as our confocal microscopic images shown. However, the appressoria formed after MgAPI16 incubation did not present the classic dome-shape structure (Figure 4B). The clear reduction of blast disease symptoms on rice plants after peptide treatment suggests that these aberrant appressoria are not able to perform the infection process.

Taking together, the results present in this report suggest that MgAPI16 specifically block appressorium formation and could be a promising compound with potential application for the control of rice blast disease. This is the first step to develop new kind of target-oriented antifungal compounds without toxicity to other organisms, such as beneficial microorganisms or host plants.

References

1. Wilson RA, Talbot NJ (2009) Under pressure: investigating the biology of plant infection by Magnaporthe oryzae. Nat Rev Microbiol 7: 185-195.

2. Wang X, Valent B (2009) Advances in Genetics, Genomics and Control of Rice Blast Disease. Springer Science and Business Media BV, New York.

3. Ebbole DJ (2007) Magnaporthe as a model for understanding host-pathogen interactions. Annu Rev Phytopathol 45: 437-456.

4. Park SY, Milgroom MG, Han SS, Kang S, Lee YH (2008) Genetic differentiation of Magnaporthe oryzae populations from scouting plots and commercial rice fields in Korea. Phytopathology 98: 436-442.

5. Maciel JL, Ceresini PC, Castroagudin VL, Zala M, Kema GH, et al. (2014) Population structure and pathotype diversity of the wheat blast pathogen Magnaporthe oryzae 25 years after its emergence in Brazil. Phytopathology 104: 95-107.

6. Hamel LP, Nicole MC, Duplessis S, Ellis BE (2012) Mitogen-activated protein kinase signaling in plant-interacting fungi: distinct messages from conserved messengers. Plant Cell 24: 1327-1351.

7. Lengeler KB, Davidson RC, D'souza C, Harashima T, Shen WC, et al. (2000) Signal transduction cascades regulating fungal development and virulence. Microbiol Mol Biol Rev 64: 746-785.

8. Rebollar A, López-García B (2013) PAF104, a synthetic peptide to control rice blast disease by blocking appressorium formation in Magnaporthe oryzae. Mol Plant Microbe Interact 26: 1407-1416.

9. Rebollar A, Marcos JF, López-García B (2014) Screening of a synthetic peptide combinatorial library to identify inhibitors of the appressorium formation in Magnaporthe oryzae. Biochem Biophys Res Commun 454: 1-6.

10. Brogden KA, Ackermann M, McCray PB Jr, Tack BF (2003) Antimicrobial peptides in animals and their role in host defences. Int J Antimicrob Agents 22: 465-478.

11. López-García B, San Segundo B, Coca M (2012) Antimicrobial Peptides as a Promising Alternative for Plant Disease Protection, in: Rajasekaran K, Cary JW, Jaynes JM, Montesinos E, Small Wonders: Peptides for Disease Control. American Chemical Society, Washington, DC.

12. Zasloff M (2002) Antimicrobial peptides of multicellular organisms. Nature 415: 389-395.

13. Steiner H, Hultmark D, Engstrom A, Bennich H, Boman HG (1981) Sequence and specificity of two anti-bacterial proteins involved in insect immunity. Nature 292: 246-248.

14. DeLucca AJ, Bland JM, Jacks TJ, Grimm C, Cleveland TE, et al. (1997) Fungicidal activity of cecropin A. Antimicrob Agents Chemother 41: 481-483.

15. Giacometti A, Cirioni O, Kamysz W, D'Amato G, Silvestri C, et al. (2003) Comparative activities of cecropin A, melittin, and cecropin A-melittin peptide CA(1-7)M(2-9)NH2 against multidrug-resistant nosocomial isolates of Acinetobacter baumannii. Peptides 24: 1315-1318.

16. Lee E, Shin A, Kim Y (2015) Anti-inflammatory activities of cecropin A and its mechanism of action. Arch Insect Biochem Physiol 88: 31-44.

17. Coca M, Peñas G, Gómez J, Campo S, Bortolotti C, et al. (2006) Enhanced resistance to the rice blast fungus Magnaporthe grisea conferred by expression of a cecropin A gene in transgenic rice. Planta 223: 392-406.

18. Bundó M, Montesinos L, Izquierdo E, Campo S, Mieulet D, et al. (2014) Production of cecropin A antimicrobial peptide in rice seed endosperm. BMC Plant Biol 14: 102.

19. Ferre R, Badosa E, Feliu L, Planas M, Montesinos E, et al. (2006) Inhibition of plant-pathogenic bacteria by short synthetic cecropin A-melittin hybrid peptides. Appl Environ Microbiol 72: 3302-3308.

20. Cavallarin L, Andreu D, San Segundo B (1998) Cecropin A-derived peptides are potent inhibitors of fungal plant pathogens. Mol Plant Microbe Interact 11: 218-227.

21. López-García B, Ubhayasekera W, Gallo RL, Marcos JF (2007) Parallel evaluation of antimicrobial peptides derived from the synthetic PAF26 and the human LL37. Biochem Biophys Res Commun 356: 107-113.

22. Marcos JF, Gandía M, Harries E, Carmona L, Muñoz A (2012) Antifungal peptides: exploiting non-lytic mechanisms and cell penetration properties, in: Rajasekaran K, Cary JW, Jaynes JM, Montesinos E (Eds.), Small Wonders: Peptides for Disease Control. American Chemical Society, Washington, DC, pp. 337-357.

23. Kong LA, Li GT, Liu Y, Liu MG, Zhang SJ, et al. (2013) Differences between appressoria formed by germ tubes and appressorium-like structures developed by hyphal tips in Magnaporthe oryzae. Fung Gen Biol 56: 33-41.

24. Christensen B, Fink J, Merrifield RB, Mauzerall D (1988) Channel-forming properties of cecropins and related model compounds incorporated into planar lipid membranes. Proc Natl Acad Sci U S A 85: 5072-5076.

25. Fu HM, Bjorstad A, Dahlgren C, Bylund J (2004) A bactericidal cecropin-A peptide with a stabilized alpha-helical structure possess an increased killing capacity but no proinflammatory activity. Inflammation 28: 337-343.

26. Lee E, Jeong KW, Lee J, Shin A, Kim JK, et al. (2013) Structure-activity relationships of cecropin-like peptides and their interactions with phospholipid membrane. BMB Rep 46: 282-287.

27. Fox MA, Thwaite JE, Ulaeto DO, Atkins TP, Atkins HS (2012) Design and characterization of novel hybrid antimicrobial peptides based on cecropin A, LL-37 and magainin II. Peptides 33: 197-205.

28. Fujikawa T, Kuga Y, Yano S, Yoshimi A, Tachiki T, et al. (2009) Dynamics of cell wall components of Magnaporthe grisea during infectious structure development. Mol Microbiol 73: 553-570.

29. He M, Kershaw MJ, Soanes DM, Xia Y, Talbot NJ (2012) Infection-associated nuclear degeneration in the rice blast fungus Magnaporthe oryzae requires non-selective macro-autophagy. PLoS One 7: e33270.

30. Veneault-Fourrey C, Barooah M, Egan M, Wakley G, Talbot NJ (2006) Autophagic fungal cell death is necessary for infection by the rice blast fungus. Science 312: 580-583.

31. Weber RWS, Wakley GE, Thines E, Talbot NJ (2001) The vacuole as central element of the lytic system and sink for lipid droplets in maturing appressoria of Magnaporthe grisea. Protoplasma 216: 101-112.