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Biochemical and Biophysical Research Communications xxx (2007) xxx–xxx

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Antimicrobial properties of derivatives of the cationic tryptophan-rich hexapeptide PAF26

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Received 20 December 2006

Abstract

Short antimicrobial peptides represent an alternative to fight pathogen infections. PAF26 is a hexapeptide identified previously by a combinatorial approach against the fungus *Penicillium digitatum* and shows antimicrobial properties towards certain phytopathogenic fungi. In this work, PAF26 was used as lead compound and its properties were compared with two series of derivatives, obtained by either systematic alanine substitution or N-terminal amino acid addition. The alanine scan approach underlined the optimized sequence of PAF26 in terms of potency and permeation capability, and also the higher contribution of the cationic residues to these properties. The N-terminal addition of amino acids resulted in new heptapeptides with variations in their antimicrobial characteristics, and very low cytotoxicity to human red blood cells. Positive (Arg or Lys) and aromatic (Phe or Trp) residue addition increased broad spectrum activity of PAF26. Noteworthy, addition of selected residues had specific effects on the properties of derivatives of PAF26.

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Keywords: Tryptophan-rich cationic antimicrobial peptide; AMP; Antifungal peptide; Phytopathogenic fungi; *P. digitatum*; *B. cinerea*; *M. grisea*; *F. oxysporum*

Antimicrobial peptides (AMP) are important components of an evolutionarily ancient mechanism of immunity, found in a wide range of organisms [1]. AMP differ in length, sequence, and structure, but generally are amphipathic and a great number have positive charge and are referred as cationic antimicrobial peptides (CAMP). In many examples, these peptides are effective against microorganisms resistant to antibiotics or fungicides. In addition, AMP are unlikely to cause rapid emergence of resistance [2]. These facts and their short length, fast and efficient action against microbes, and low toxicity to mammalian cells have made them potential candidates as peptide drugs.

Rational design of AMP is an attractive approach to the improvement of antimicrobial properties. Agriculture

could also greatly benefit from this emerging research area, with the identification, design, and selection of peptides targeted to specific plant protection problems [3–6]. Soluble combinatorial libraries (SCL) represent an extensive source of molecular diversity for the *de novo* identification of lead AMP with new properties [7]. SCL have been used to identify novel peptides towards phytopathogenic fungi such as 66–10 hexapeptide (Ac-frlrfh-NH₂) [8] and its derivative heptapeptide 77–3 (Ac-frlrfhf-NH₂), which has activity against fungal strains of *Fusarium sambucinum* that are resistant to the fungicide thiabendazole (TBZ) [5]. In a previous work, we have used a synthetic D-hexapeptide library in a positional scanning format to identify AMP against selected phytopathogenic fungi that cause postharvest decay in fruits, such as *Penicillium digitatum* [6]. One of these peptides is PAF26 (Table 1), which showed strong activity against certain filamentous fungi and lower toxicity to *Escherichia coli* and *Saccharomyces cerevisiae* [6].

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Table 1
Amino acid sequences of peptides

Peptide	Sequence ^a
PAF26	Ac-rkkwfw-NH ₂
PAF34	Ac-rk w lfw-NH ₂
PAF26.r1a	Ac- a kkwfw-NH ₂
PAF26.k2a	Ac-r a kwfw-NH ₂
PAF26.k3a	Ac-rk a wfw-NH ₂
PAF26.w4a	Ac-rkk a wfw-NH ₂
PAF26.f5a	Ac-rkkw a w-NH ₂
PAF26.w6a	Ac-rkkw f a-NH ₂
PAF38	Ac-r r kkwfw-NH ₂
PAF39	Ac- k rkkwfw-NH ₂
PAF40	Ac- h rkkwfw-NH ₂
PAF41	Ac- f rkkwfw-NH ₂
PAF42	Ac- w rkkwfw-NH ₂
PAF43	Ac- y rkkwfw-NH ₂
PAF44	Ac- l rkkwfw-NH ₂
PAF45	Ac- t rkkwfw-NH ₂
PAF46	Ac- q rkkwfw-NH ₂
PAF47	Ac- a rkkwfw-NH ₂

^a The D-amino acids are shown in lower case. Residues distinct from PAF26 are in bold.

56 PAF26 is a tryptophan-rich CAMP with sequence simi-
57 larities to other AMP [9–13]. It shares some properties with
58 similar peptides, as absence of hemolytic activity [12,14].
59 PAF26 is active against strains resistant to fungicides and
60 performed better than TBZ in experimental fruit decay
61 tests [15]. Additionally, we have also demonstrated that
62 PAF26 belongs to the class of AMP endowed with cell-
63 penetrating properties [16,17], being capable to specifically
64 interact with and locate inside target fungal cells [14].
65 PAF26 and similar peptides synthesized with either D- or
66 L-enantiomers do not differ substantially in antimicrobial
67 potency [9,11,14], which makes biotechnological produc-
68 tion feasible.

69 In this work, we have used PAF26 as a lead in an opti-
70 mization strategy to design two sets of peptides with single
71 residue variations. The purpose was to analyze the effect of
72 such variations in the antimicrobial properties of the result-
73 ing peptides. First, alanine substitution analogues
74 addressed the influence of each residue on PAF26 antimi-
75 crobrial properties. Second, we designed and compared novel
76 heptapeptides obtained by addition of different N-
77 terminal residues to PAF26 in terms of (i) spectrum of
78 activity, (ii) specificity, (iii) microbicidal properties, and
79 (iv) cytolysis of human red blood cells.

80 Materials and methods

81 *Microorganisms.* We used microorganisms that included fungal isolates
82 of agricultural relevance (three distinct species of *Penicillium*, and *Alter-*
83 *naria* sp., *Fusarium oxysporum*, *Botrytis cinerea* and *Magnaporthe grisea*)
84 as well as fungal (*Aspergillus nidulans*), yeast (*S. cerevisiae*) and bacterial
85 (*E. coli* and *Bacillus subtilis*) model strains (see Supplemental Table 4).
86 Fungi were cultured on potato dextrose agar (PDA) (Difco-BD Diag-
87 nostics, Sparks, MD) plates at 24 °C with the exception of *M. grisea*,
88 which was maintained on rice flour medium. Conidia were collected and
89 adjusted to the appropriate concentration. *S. cerevisiae* was grown in YPD

(1% yeast extract, 1.5% peptone, 2% dextrose) at 30 °C and bacteria were
90 grown in Luria-Bertani (LB) medium at 37 °C.

91
92 *Peptides.* Peptides used in this work (Table 1 and Supplemental Table
93 3) were purchased at >90% purity (GenScript Corporation, Piscataway,
94 NJ). Peptides were acetylated at the N-terminus (Ac) and amidated at the
95 C-terminus (NH₂). Stocks were prepared at 1 mM in 5 mM 3-(N-mor-
96 pholino)-propanesulfonic acid, pH 7, buffer and stored at –20 °C. Peptide
97 concentrations were determined by absorbance at 280 nm.

98
99 *Growth inhibition assays.* The antimicrobial activities of the peptides
100 were determined using a microtiter plate assay [6,18]. Growth was quan-
101 tified as optical density (OD) at 492 nm. Potato dextrose broth (PDB)
102 (Difco-BD Diagnostics) diluted one twentieth (5% PDB) was used as
103 growth medium for fungi, and YPD diluted one tenth (10% YPD) for
104 yeast, in both cases containing 0.003% (w/v) chloramphenicol. In anti-
105 bacterial assays, the medium was LB diluted one tenth (10% LB). Three
106 replicates were prepared for each treatment.

107
108 The minimum inhibitory concentration (MIC) of a peptide for a given
109 microorganism was the lowest peptide concentration that showed no
110 growth at the end of the experiment. The IC₅₀ of a peptide was the con-
111 centration required to obtain 50% inhibition of growth, and the value in
112 each experiment was estimated by adjustment of the experimental data
113 (SigmaPlot v 8.02, SPSS Inc., Chicago, IL). Statistical analyses were
114 carried out with the software package StatGraphics Plus 4.0 (Manugistics
115 Inc., Rockville, MD).

116
117 *Membrane permeation assays.* Membrane permeation was determined
118 with the probe Sytox Green (SG) (Molecular Probes-Invitrogen Corp.,
119 Carlsbad, CA) and fluorometric measurement with a microplate reader
120 (Fluoroskan Ascent FL, Labsystems, Finland) at an excitation of 485 nm
121 and emission of 538 nm wavelengths [14]. Three replicates were prepared
122 for each treatment. The FC₅₀ of a peptide was defined as the concentration
123 inducing 50% of the maximum fluorescence emission, and the values were
124 calculated by adjustment of the experimental data as above.

125
126 *Fungicidal and bactericidal activity assays.* Assessment of peptide
127 microbicidal activity was conducted as follows. In the case of *P. digitatum*,
128 2.5 × 10⁴ conidia/ml were incubated with peptides in 5% PDB at 24 °C.
129 After 1 day of incubation, 50 µl samples were spread onto peptide-free
130 PDA plates to monitor colony forming units. *S. cerevisiae* and *E. coli*
131 (5.0 × 10⁵ CFU/ml) were incubated for 1 day with peptides in either 10%
132 YPD at 30 °C or 10% LB at 37 °C, respectively, and 2.5 µl drops of
133 samples were placed onto YPD or LB peptide-free plates. The lethal
134 concentration (LC) of a peptide was defined as the lowest peptide con-
135 centration at which no growth or <1% of CFU was recovered after peptide
136 treatment.

137
138 *Hemolytic activity assay.* The cytolytic activity of the peptides on
139 human red blood cells was determined as release of hemoglobin monitored
140 by absorbance at 415 nm [14]. Peptides were used at final concentrations
141 of 1, 10 or 100 µM. Zero percent hemolysis and 100% hemolysis controls
142 were determined in PBS and 0.1% Triton X-100, respectively.

139 Results and discussion

140 Antimicrobial properties of a series of alanine substitution 141 analogues of PAF26

142
143 We designed a set of six Ala substitution analogues of
144 the cationic tryptophan-rich hexapeptide PAF26
145 (PAF26.r1a to PAF26.w6a, Table 1 and Supplemental
146 Table 3). Distinct antimicrobial properties were determined
147 and the results are summarized as IC₅₀, MIC and LC
148 towards *P. digitatum* (Table 2). We observed lower activity
149 for all the analogues, although the decrease was higher in
150 the peptides with substitution of the positively charged res-
151 idues (PAF26.r1a, .k2a, and .k3a), which approximately

Table 2
Antimicrobial properties of PAF26 analogues towards *P. digitatum*

Peptide	IC ₅₀ (μM) ^{a,b}	MIC (μM)	LC (μM)	FC ₅₀ (μM) ^{a,b}
PAF26	2.2 ± 0.3 (a)	4	16	1.7 ± 0.2 (a)
PAF26.r1a	6.3 ± 1.1 (c)	16	>64	11.5 ± 1.1 (c)
PAF26.k2a	5.6 ± 1.5 (c)	16	64	7.7 ± 2.4 (b)
PAF26.k3a	6.6 ± 2.1 (c)	16	>64	7.9 ± 3.0 (bc)
PAF26.w4a	3.2 ± 0.7 (ab)	8	32	6.3 ± 1.4 (b)
PAF26.f5a	2.8 ± 0.6 (ab)	8	32	2.0 ± 0.4 (a)
PAF26.w6a	3.7 ± 0.5 (b)	16	32	5.7 ± 0.6 (b)

^a Mean values ± standard deviation, calculated from independent experiments.

^b Values with the same letter do not differ at 95% confidence level (Fisher's LSD procedure).

150 fourfold higher MIC and LC, and higher significant differ-
151 ences in the IC₅₀.

152 We also used an assay based on the uptake of SG to
153 quantify the permeation of *P. digitatum* mycelium promot-
154 ed by the analogues. SG assays have been used to establish
155 a link between antimicrobial activity of AMP and cell per-
156 meation [5,19]. Previously, we demonstrated that incuba-
157 tion of fungal hyphae with PAF26 resulted in uptake and
158 increase in the fluorescence of SG [14].

159 We have quantified and compared the permeation capa-
160 bility of the Ala analogues with PAF26, by determining
161 permeation dose–response curves in conjunction with inhi-
162 bition curves (Fig. 1). Data allowed the calculation of FC₅₀
163 as an estimate of the permeation capability of peptides
164 (Table 2). In the case of PAF26 and the PAF26.f5a analog,
165 the permeation curve paralleled that of growth inhibition
166 (Fig. 1A and C), and both peptides had IC₅₀ and FC₅₀ val-
167 ues not significantly different (Table 2). Regarding the
168 other five analogs, a noticeable result was the slight but
169 consistently reproduced higher peptide concentrations
170 needed to achieve 50% permeation (FC₅₀) than 50% inhi-
171 bition (IC₅₀). This distinct effect could be visualized by plot-
172 ting the relative activities for the six analogs as compared
173 to PAF26 (Fig. 2). All the analogous except PAF26.f5a
174 had losses of permeation capability (white bars) higher
175 than losses of inhibition activity (black bars) (Fig. 2). Such
176 differences among peptides are exemplified in a representa-
177 tive experiment (Fig. 1). PAF26.f5a initiates permeation
178 and reaches maximum at concentrations similar to
179 PAF26, in a curve that mirrors the inhibition response,
180 while PAF26.r1a has a permeation curve shifted to higher
181 peptide concentrations as compared to growth inhibition.

182 This differential effect of each Ala substitution in either
183 the antimicrobial or the permeation properties dissociate to
184 some extent growth inhibition from permeation among the
185 different peptides, thus suggesting that PAF26 antimicrobi-
186 al action is not solely based on its ability to permeate target
187 cells. This has been previously proposed for other AMP
188 [1,2,9,16,17], and also explored in the case of PAF26, for
189 which it was shown microscopically that produces growth
190 alterations of mycelium in areas that are not permeabilized
191 [14]. Moreover, PAF26 is internalized by *P. digitatum*

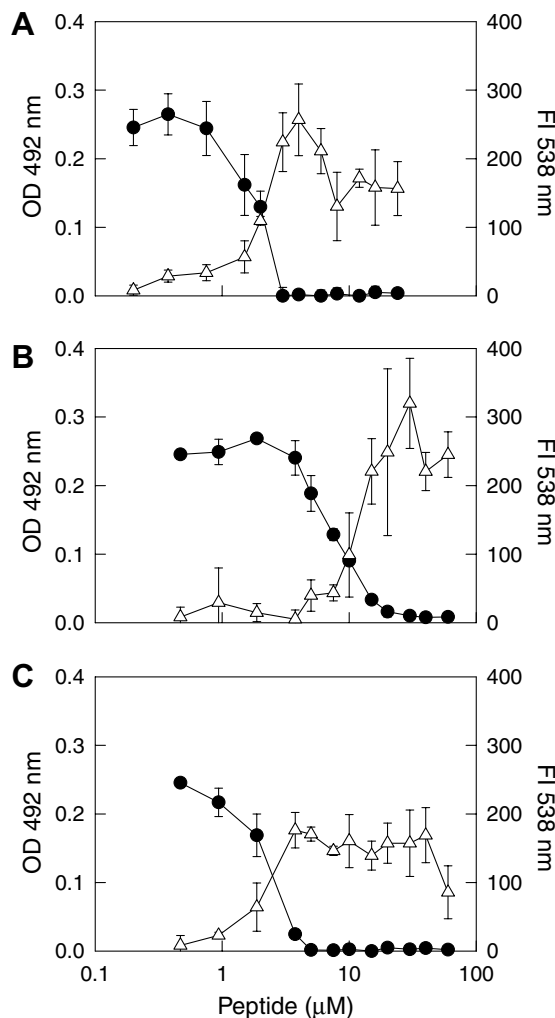


Fig. 1. Dose–response curves of inhibition (black circles) and permeation (white triangles) activity of peptides PAF26 (A), PAF26.r1a (B), and PAF26.f5a (C) on *P. digitatum*. Data shown are the mean values ± SD of either OD (492 nm) or (FI) (538 nm).

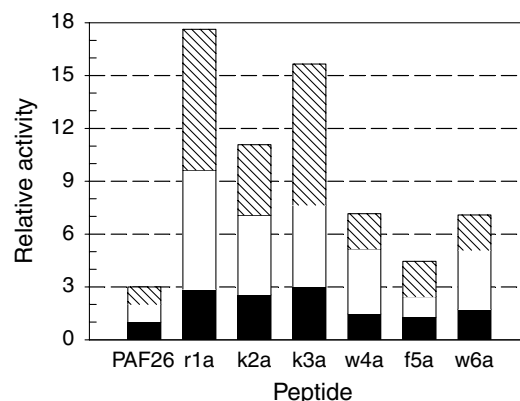


Fig. 2. Relative antimicrobial and permeation activity of the Ala substitution analogs as compared to the parental peptide PAF26. Bars represent the relative IC₅₀ as measure of growth inhibition (black bars), FC₅₀ as measure of permeation (white bars), and LC as measure of fungicidal activity to conidia (stripped bars). Relative values were calculated taking the corresponding parameter of PAF26 as reference.

192 hyphae at very low sub-inhibitory concentrations (i.e.,
193 300 nM) that have no detectable effect on growth, mor-
194 phology or permeation [14].

195 Therefore, our Ala scanning approach showed that all
196 the amino acid residues in PAF26 contribute to some
197 extent to its antifungal or permeation activities and that
198 none of them is dispensable for its properties towards *P.*
199 *digitatum*. However, differences among the analogs were
200 observed. PAF26 has an amphipathic arrangement with
201 three N-terminal cationic residues followed by three aro-
202 matic and hydrophobic residues at the C-terminus. Distinct
203 independent parameters (Table 2 and Fig. 2) indicated that
204 the antimicrobial potency and permeation properties were
205 more affected by substitutions of the cationic rather than
206 of the aromatic amino acids. The activity of CAMP,
207 including those rich in Trp as PAF26, is dependent on
208 the ionic environment [10,13,20], indicating that the initial
209 interaction with microbes is electrostatic. In fact, confocal
210 microscope observations have shown that indolicidin and
211 PAF26 primarily interact with surfaces of hyphae [13,14].
212 The results of the Ala scan approach confirm the impor-
213 tance of such electrostatic interaction for antimicrobial
214 activity and permeation.

215 Our data indicate that the two Trp residues follow in re-
216levance to the cationic ones (Table 2). It has been reported
217 that PAF26 interacts *in vitro* with membrane mimetics and
218 that substitution of Trp-4 for Pro decreases this interaction
219 and concomitantly also biological activity [21]. Finally,
220 Phe-5 was found to be the least significant residue since
221 its replacement produced a peptide with modest differences
222 as compared to PAF26 and in fact its dose response curves
223 were quite similar to that of PAF26 (Fig. 1).

224 Distinct activity profiles of heptapeptides derived from 225 PAF26 by amino acid addition

226 Improvement in PAF26 antimicrobial potency and/or
227 specificity could be achieved by means of replacement
228 for, or addition of, specific amino acids. We have explored
229 such scenario by addition of selected N-terminal residues
230 and screening of the resulting set of heptapeptides. Similar
231 approaches have been used to improve other lead AMP
232 [5,9]. Amino acids highly represented in AMP databases
233 [22] were chosen: the positively charged residues Arg,
234 Lys, and His, the aromatic residues Trp, Phe, and Tyr,
235 the aliphatic residues Leu and Ala, and hydrophilic resi-
236 dues Thr and Gln (Table 1). The ten different resulting hep-
237 tapeptides had 3–4 positive net charges at neutral pH and
238 distinct hydrophobic indexes that indicate a hydrophilic
239 character (Supplemental Table 3).

240 An evaluation of antimicrobial potency and specificity
241 was carried out against a panel of selected microorganisms
242 that include fungi of agronomic relevance as well as the
243 model filamentous fungus *A. nidulans*, the yeast *S. cerevisi-*
244 *ae*, the Gram-negative bacteria *E. coli* and the Gram-posi-
245 tive *B. subtilis*, in order to assay overall activity, specificity,
246 and bioactivity against reluctant fungi. The parameters

IC₅₀ and MIC were calculated (Supplemental Table 4). 247
The previously described hexapeptide PAF34, which differ 248
from PAF26 in two amino acid residues (Table 1), was 249
introduced as a control of antimicrobial peptide with lower 250
specificity than PAF26 [6]. 251

252 Distinct inhibitory profiles of the heptapeptides were
253 found (Supplemental Table 4). Considering the microor-
254 ganisms, *P. digitatum* was the most sensitive to AMP based
255 on the PAF26 lead, as expected given that this peptide was
256 found in a combinatorial screen against this fungus. On the
257 other hand, the least sensitive microorganisms were the
258 phytopathogenic fungus *M. grisea*, the yeast *S. cerevisiae*
259 and the bacteria *E. coli*. The non-filamentous microorgan-
260 ism that has the susceptibility pattern more similar to the
261 filamentous fungi was the Gram-positive bacterium *B.*
262 *subtilis*.

263 Taking into account the different peptides, the generally
264 most active ones were PAF38 (Arg) and PAF39 (Lys), a
265 result in agreement with the above demonstrated impor-
266 tance of cationic N-terminal residues in the activity of
267 PAF26. However, our study found no clear correlation
268 between the antimicrobial potency/specificity and the
269 molecular weight, net charge, or hydrophilicity character
270 of the peptides (Supplemental Table 4), suggesting that
271 more complex interactions between the amino acid residues
272 determine the antimicrobial properties. In other AMP, it
273 has been shown that appropriate position/clustering of resi-
274 dues are determinant for activity and selectivity [12].

275 The higher activity against the economically important
276 *M. grisea* of PAF41 (Phe) and PAF42 (Trp), but not of
277 PAF38 and PAF39 was remarkable. In the case of *B. cine-*
278 *rea* and *F. oxysporum* a modest twofold increase in the
279 MIC was found in PAF40 (His) and PAF38, respectively,
280 as compared to PAF26.

281 In most of the peptides, the increase in antifungal activi-
282 ty correlates with an even higher increase in activity
283 against the bacteria and yeast (Supplemental Table 4). In
284 fact, the addition of cationic (PAF38, PAF39) or aromatic
285 hydrophobic (PAF41, PAF42) residues showed a higher
286 increase in antibacterial than in antifungal properties.

287 There were peptides that showed an improvement in the
288 IC₅₀ but a deleterious effect on the MIC, for instance in the
289 case of PAF45 (Thr), PAF46 (Gln) or PAF47 (Ala) against
290 *P. digitatum*, emphasizing the existence of differently
291 shaped dose–response curves and the need for considering
292 different parameters when characterizing antimicrobials
293 [23].

294 Microbicidal assays of heptapeptides derived from PAF26

295 The killing capacity of peptides to conidia of *P. digita-*
296 *tum*, or cells of *E. coli* and *S. cerevisiae* was evaluated
297 (Fig. 3). It has been previously shown that inhibitory and
298 fungicidal properties against *P. digitatum* are not linked
299 in selected AMP, as lactoferricin-derived peptides and
300 melittin [14,18]. This experiment confirmed the reverse
301 microbicidal properties of PAF26 and PAF34 (Fig. 3A).

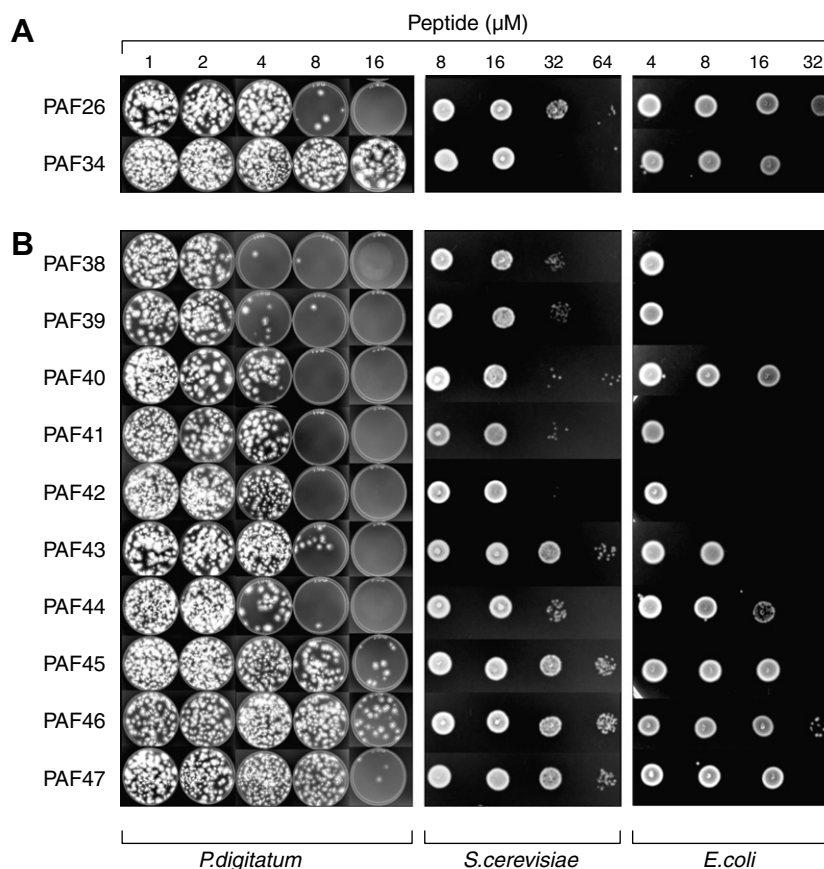


Fig. 3. Assessment of microbicidal activity of peptides against *P. digitatum* (left), *S. cerevisiae* (middle) and *E. coli* (right). Microorganism samples, either conidia (*P. digitatum*) or CFU (*S. cerevisiae* and *E. coli*), were treated with selected peptide concentrations (top) for 1 day, and spread (for the fungus) or applied as droplets (for the yeast and bacteria) onto peptide-free plates. Representative photographs are shown for (A) the previously described PAF26 and PAF34, and (B) for the novel heptapeptides described here (PAF38 to PAF47).

302 These two peptides have distinct activity profiles: PAF26 is
 303 more microbicidal than PAF34 to *P. digitatum*, while less
 304 to *S. cerevisiae* and *E. coli*.

305 Microbicidal data confirmed and extended the growth
 306 inhibition results described above. The cationic derivatives
 307 PAF38 and PAF39 showed a twofold improvement of fun-
 308 gicidal activity against *P. digitatum* but also killed *S. cere-*
 309 *visiae* and *E. coli* more efficiently (Fig. 3B).

310 PAF40 has activity against *P. digitatum* and *S. cerevisiae*
 311 similar to the sequence-related PAF38, PAF39, PAF41 and
 312 PAF42, but a fourfold reduction in killing capacity to *E. co-*
 313 *li* (Supplemental Table 4 and Fig. 3B). On the contrary,
 314 some of the peptides as PAF43 (Tyr) showed an increase
 315 in activity against bacteria while had activity against sever-
 316 al fungi similar to PAF26 (Supplemental Table 4 and
 317 Fig. 3B). In fact, PAF40 and PAF43 showed reversal
 318 microbicidal properties towards *S. cerevisiae* and *E. coli*
 319 (Fig. 3B).

320 Also noticeable was the loss of fungicidal activity
 321 against conidia of *P. digitatum* of some peptides as
 322 PAF46 (Fig. 3B). We have reported that peptides derived
 323 from the antimicrobial motif of bovine Lactoferricin [10],
 324 which shown sequence similarities with PAF26 and also
 325 contain a Gln residue, have IC₅₀ values very similar to

PAF26 but a much lower fungicidal activity to *P. digitatum* 326
 [18]. This finding will guide future experiments to test 327
 whether Gln residues negatively impact fungicidal proper- 328
 ties of CAMP while maintaining growth inhibition, and 329
 thus whether determinants of CAMP fungistatic and fun- 330
 gicidal properties differ. 331

332 Overall, our results indicate that some of the modifica- 332
 tions resulted in broader antimicrobial activity, and there- 333
 fore would be undesirable whenever filamentous fungi are 334
 the specific target of the antimicrobial approach. Also, data 335
 provide information to the development of novel peptides 336
 with broader activities. The detrimental loss of antifungal 337
 properties of some heptapeptides also demonstrates that 338
 the presence of the PAF26 sequence by itself does not guar- 339
 antee high inhibitory activity, confirming that a specific 340
 arrangement of a peptide sequence and interactions 341
 between residues are also important for the properties of 342
 AMP [12,24]. 343

Evaluation of hemolytic activity of heptapeptides derived 344
from PAF26 345

An evaluation of toxicity was performed by conducting 346
 hemolytic assays on human red blood cells at different 347

peptide concentrations (1, 10, and 100 μM). All except one of the PAF26-derived peptides described in this work exhibited no hemolysis even at 100 μM (i.e., below the detection limit, which in our assay is 0.3% of the hemolysis of the control). The only peptide showing marginal toxicity was PAF42 (Trp) that produced 0.6% hemolysis at 100 μM . The well-known toxic peptide Melittin (used as control) was 100% hemolytic at 100 μM and 38% at 10 μM . Data indicate that PAF heptapeptides are at least 1000 times less cytolytic to red blood cells than Melittin. It has been reported that PAF26 and Melittin are similarly active against *P. digitatum*, being Melittin more toxic to bacteria [6].

361 Conclusion

We have generated a series of peptides derived from PAF26, with different profiles of antimicrobial properties and negligible hemolysis. They are of interest in the development of novel AMP, adding to the catalog of compounds with potential application in agriculture and biomedicine. Selection of the most suitable peptide would depend on the importance for each particular use of potency and/or specificity.

370 Acknowledgments

Work was supported by Grants BIO2003-00927 and BIO2006-09523 from the Spanish Ministry of Education and Science (MEC). B.L.-G. acknowledges the post-doctoral program “Juan de la Cierva” of the Spanish MEC. We also acknowledge M. José Pascual for her excellent technical assistance.

377 Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at [doi:10.1016/j.bbrc.2006.12.173](https://doi.org/10.1016/j.bbrc.2006.12.173).

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