Ribosomally encoded antibacterial proteins and peptides from Pseudomonas

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Abstract

Members of the Pseudomonas genus produce diverse secondary metabolites affecting other bacteria, fungi or predating nematodes and protozoa but are also equipped with the capacity to secrete different types of ribosomally encoded toxic peptides and proteins, ranging from small microcins to large tailocins. Studies with the human pathogen Pseudomonas aeruginosa have revealed that effector proteins of type VI secretion systems are part of the antibacterial armamentarium deployed by pseudomonads. A novel class of antibacterial proteins with structural similarity to plant lectins was discovered by studying antagonism among plant-associated Pseudomonas strains. A genomic perspective on pseudomonad bacteriocinogeny shows that the modular architecture of S pyocins of P. aeruginosa is retained in a large diversified group of bacteriocins, most of which target DNA or RNA. Similar modularity is present in as yet poorly characterized Rhs (recombination hot spot) proteins and CDI (contact-dependent inhibition) proteins. Well-delimited domains for receptor recognition or cytotoxicity enable the design of chimeric toxins with novel functionalities, which has been applied successfully for S and R pyocins. Little is known regarding how these antibacterials are released and ultimately reach their targets. Other remaining issues concern the identification of environmental triggers activating these systems and assessment of their ecological impact in niches populated by pseudomonads.

Scope of the review

Pseudomonas strains are able to indwell very diverse niches, ranging from terrestrial and aquatic environments to tissues of eukaryotic hosts. Population of such environments involves a struggle for living space and organic nutrients with a plethora of other microorganisms. Pseudomonads display a highly versatile metabolism and several secondary metabolites affecting other bacteria and fungi have been identified, such as 2,4-diacetylphloroglucinol, phenazines, pyrrolnitrin, pyoluteorin, and lipopeptides (Gross & Loper, 2009). While such antibiotics mainly affect phylogenetically distant rivals, only few secondary metabolites are toxic to fellow pseudomonads that are attracted to common niches (Li et al., 2011). The ribosomal machinery, on the other hand, enables biosynthesis of very diverse bacterial peptides and proteins, collectively designated bacteriocins, that are only deleterious to members of a certain bacterial species or a subset of phylogenetically close relatives of the producer that itself carries an immunity protein-based system preventing self-intoxication. The study of such protein antibiotics has regained attention as a possible way to minimize collateral damage to nontarget microbiota and as a potential source of novel molecular targets to alleviate problems with multiresistance to available antibiotics.

Among Gram-negative bacteria, the colicins produced by enterobacteria are by far the best studied group of such narrow-spectrum antagonistic proteins, and a wealth of information is available on the molecular mechanisms involved in the different stages of their killing action (reviewed by Cascales et al., 2007). Several bacteriocins of pseudomonads share basic characteristics with colicins and insights from colicin biology have been instrumental to identify novel so-called pyocins with similar cytotoxicities. Studies on interactions among Gram-negative bacterial relatives have disclosed in recent years that certain features of colicins and pyocins, such as the modular
nature of toxin/immunity pairs, are equally retained in substrates of Type V and Type VI systems that mediate antagonism (Braun & Patzer, 2013). In 2002, the review by Michel-Briand and Baysses was essentially confined to colicin-like and phage-like pyocins of Pseudomonas aeruginosa, as the only pseudomonad bacteriocins sufficiently characterized at that time. Here, we review the current knowledge of these systems and describe novel types of bacteriocins that have been identified in the last decade. This served as a basis to provide an overview of the bacteriocinogenic potential of the Pseudomonas genus by scrutiny of available (draft) genome sequences.

**S-type pyocins**

Soluble or S-type pyocins are protease- and heat-sensitive, chromosome-encoded bacteriocins from *P. aeruginosa* that are able to kill cells from the same species. These antibacterials are secreted as binary protein complexes consisting of a large protein that harbors the killing function and a smaller immunity protein that remains tightly bound to the cytotoxic domain of the former. The physical association of the toxin with its cognate immunity protein, reflected in the clustering of their structural genes, ensures that the producer strain is not harmed before the bacteriocin is released (Michel-Briand & Baysses, 2002).

To date, several S-type pyocins have been described and characterized: pyocins S1 (Ito et al., 1970), S2 (Ohkawa et al., 1973), AP41 (Holloway et al., 1973; Sano & Kageyama, 1981), S3 (Duport et al., 1995), S4 (Elfarash et al., 2012) and S5 (Ling et al., 2010). Pyocin Sa (Govan, 1986) turned out to be identical to pyocin S2 (Denayer et al., 2007). A bacteriocin nearly identical to pyocin S1 but equipped with a different type of killing and immunity function was designated pyocin S6 (Dingemans et al., 2013). Whereas all these proteins share identical parts or display significant local sequence homology, this is not the case for pyocin PaEM, which is produced without a known immunity partner (Barreteau et al., 2009).

Although the study of S-type pyocins has mainly focused on their occurrence and action in the human opportunistic pathogen *P. aeruginosa*, genes encoding structurally related proteins are found in other *Pseudomonas* species as well, but functional characterization of the latter is lacking (Parret & De Mot, 2002).

**Domain architecture of S-type pyocins**

To kill a target cell, a S-type pyocin would first bind to a specific receptor located on the outer membrane of the bacterial cells and it would then be further translocated to exert its inhibitory function. The modular organization design of the distinct domains correlates well with these multiple steps of mode of action (Michel-Briand & Baysses, 2002). In most S-type bacteriocins, the amino-terminal domain of the large protein bears the receptor-binding function and its carboxy-terminal part engenders the lethal effect (Sano et al., 1993b; Parret & De Mot, 2002). In pyocins with a cytoplasmic target, they are connected by a domain that mediates translocation (corresponding to Pfam domain PF06958; Pyocin_S). An additional polypeptide segment of unknown function can be positioned between the receptor-binding and translocation domains, but this part is dispensable for killing, as observed for pyocins S2 and AP41 (Sano et al., 1993a). The modular composition of S-type pyocins is also underlined by the fact that functional bacteriocins can be constructed by joining domains from different pyocins. Examples include combined domains of pyocins S1 and AP41 (Sano et al., 1993a) and a pyocin S5/S2 chimer (Elfarash et al., 2014). In addition, active pyocin/colicin hybrids with domains from pyocin S3 and colicin E3 (Gupta et al., 2013; see Potential applications for S-type pyocins) and with domains from pyocins S1 or S2 and colicins E2 or E3 have been engineered (Kageyama et al., 1996). Pyocin S5 and PaEM that do not require translocation to the cytoplasm for killing, exhibit a different domain architecture with the translocation domain preceding the receptor-binding domain (Barreteau et al., 2009; Elfarash et al., 2014). Pyocin size varies significantly, ranging from 289 amino acids for PaEM to 777 amino acids for AP41 (Table 1). A schematic representation of the gene and domain organization of characterized and selected predicted S-type pyocins in *Pseudomonas* spp. is shown in Fig. 1.

**Biological properties and structure of S-type pyocins**

Different S-pyocin killing domains have been described (Table 1). Pyocin S1, S2, S3, and AP41 display DNase activity (Seo & Galloway, 1990; Sano, 1993; Sano et al., 1993b; Duport et al., 1995), while pyocin S4 harbors a tRNase (Elfarash et al., 2012) and pyocin S6 a rRNase (Fig. 1; Dingemans et al., 2013). Pyocin DNase domains typically bear a conserved HNH-endonuclease motif, as observed in pyocins S1, S2, and AP41 (Parret & De Mot, 2002). This motif constitutes the core of the catalytic site of the endonuclease and can chelate a single metal ion, required for hydrolysis of the dsDNA strand. These HNH-nucleases have also been detected in colicins (Papadakos et al., 2012). Pyocin S3 on the contrary does not contain this HNH-motif and its lethal domain lacks sequence homology with the corresponding domains of other DNase pyocins (Parret & De Mot, 2002). Enzymatic
activity has not been detected for pyocin S5; instead, this pyocin is known to kill a target bacterium via pore formation, resulting in membrane damage and leakage of intracellular compounds (Fig. 1; Ling et al., 2010).

A pyocin with yet a different cytotoxic activity was identified in P. aeruginosa strains JJ692 and DET08 encoded within their exoU-carrying genomic islands. This enzyme, PaeM, displays homology with colicin M, a lipid II-degrading bacteriocin from Escherichia coli. It does not exert its enzymatic activity in the cytoplasm; instead, it is active in the periplasm where it blocks peptidoglycan synthesis (Fig. 1; Barreteau et al., 2009). Unlike the lytic activity of colicin M on sensitive E. coli cells, PaeM only exhibits a bacteriostatic effect on its target cells (Barreteau et al., 2009). For the plant pathogen Pseudomonas syringae pv. tomato DC3000 and the wheat rhizosphere isolate Pseudomonas fluorescens Q8r1–96, recombinant homologs (PsyM and PfM, respectively) were shown to be functional toxins as well, however, displaying lower in vitro phosphodiesterase activity. Of fourteen P. aeruginosa strains tested, only two strains were susceptible to PaeM and one of these indicators also was inhibited by PfM. No other target strain was identified among 40 strains representing the three species, pointing to a quite narrow activity spectrum for this type of pseudomonad bacteriocin, as compared to S-type pyocins. In a subsequent independent study, activity of the DC3000 recombinant enzyme, there denoted syringacin M, was shown against two P. syringae strains belonging to the pathovars syringae (LMG 5084) and lachrymans (LMG 5456), while other Pseudomonas species were not affected. The same narrow activity spectrum was exhibited by a close homolog purified from mitomycin-induced culture supernatant of P. syringae pv. syringae LMG 1247 (Grinter et al., 2012b).

Currently, structures of only two pyocins have been solved: PaeM from P. aeruginosa and syringacin M from P. syringae (Fig. 2). These proteins share structural similarities with colicin M. Their crystal structures consist of a short disordered amino-terminal translocation domain, followed by a central globular a-barrel fold, characteristic for these bacteriocins (Zeth et al., 2008) but adopting a modified active site architecture. A Mg2+ ion was identified in the active site of PaeM in line with the dependence of colicin M activity on this cation (Barreteau et al., 2012). However, in crystallized syringacin M, this site was occupied by Ca2+ that supports catalytic activity similarly to Mg2+ (Grinter et al., 2012b). Barreteau and coworkers (Barreteau et al., 2012) showed that in vitro catalytic activity of the isolated cytotoxic domain was enhanced, suggesting that interdomain interactions dampen the enzymatic activity which is supposed to be fully released upon cellular entry and interaction with its substrate. Although the syringacin M receptor-binding domains lacks discernible sequence homology to the equivalent colicin M region, they adopt a very similar fold, presumably as a result of diversifying selection (Grinter et al., 2012b) rather than recombination (Zeth et al., 2008).

Table 1. Characteristics of Pseudomonas aeruginosa pyocins

<table>
<thead>
<tr>
<th>Pyocin</th>
<th>Strain</th>
<th>Mode of action</th>
<th>Toxin</th>
<th>Amino acids</th>
<th>Domain(s)*</th>
<th>Immunity protein</th>
<th>Amino acids</th>
<th>Domain†</th>
<th>Receptor</th>
</tr>
</thead>
<tbody>
<tr>
<td>AP41</td>
<td>PA41-2</td>
<td>DNase (HNH)</td>
<td>777</td>
<td>PF06958; PF12639</td>
<td></td>
<td></td>
<td>90</td>
<td>PF01320</td>
<td>?</td>
</tr>
<tr>
<td>M1</td>
<td>J1692</td>
<td>Lipid II degradation</td>
<td>289</td>
<td>PF14859</td>
<td></td>
<td></td>
<td>–</td>
<td>–</td>
<td>?</td>
</tr>
<tr>
<td>S1</td>
<td>NIH-H</td>
<td>DNase (HNH)</td>
<td>618</td>
<td>PF06958; PF12639</td>
<td>87</td>
<td>PF01320</td>
<td>?†</td>
<td>FpvAI</td>
<td></td>
</tr>
<tr>
<td>S2</td>
<td>PA01</td>
<td>DNase (HNH)</td>
<td>689</td>
<td>PF03515; PF06958; PF12639</td>
<td>87</td>
<td>PF01320</td>
<td>FpvAII</td>
<td></td>
<td></td>
</tr>
<tr>
<td>S3</td>
<td>P12</td>
<td>DNase</td>
<td>766</td>
<td>PF06958</td>
<td></td>
<td></td>
<td>153</td>
<td>–</td>
<td>FpvAll</td>
</tr>
<tr>
<td>S4</td>
<td>PA01</td>
<td>rRNase</td>
<td>612</td>
<td>PF06958; PF12106</td>
<td>112</td>
<td>PF11480</td>
<td>FpvAI</td>
<td></td>
<td></td>
</tr>
<tr>
<td>S5</td>
<td>PA01</td>
<td>Pore-forming</td>
<td>498</td>
<td>PF01024</td>
<td>108</td>
<td>PF03526</td>
<td>FptA</td>
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<tr>
<td>S6</td>
<td>CT-PA39</td>
<td>rRNase</td>
<td>571</td>
<td>PF06958; PF09000</td>
<td>77</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>?</td>
</tr>
<tr>
<td>M4</td>
<td>BL01</td>
<td>Lipid II degradation</td>
<td>342</td>
<td>PF14859</td>
<td></td>
<td></td>
<td>–</td>
<td>–</td>
<td>?</td>
</tr>
<tr>
<td>S7</td>
<td>BWHP3A018</td>
<td>rRNase</td>
<td>642</td>
<td>PF06958; PF09000</td>
<td>77</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>?</td>
</tr>
<tr>
<td>S8</td>
<td>VRFP07</td>
<td>DNase (HNH)</td>
<td>772</td>
<td>PF06958; PF12639</td>
<td>85</td>
<td>PF01320</td>
<td>?†</td>
<td>FpvAI</td>
<td></td>
</tr>
<tr>
<td>S9</td>
<td>BL04</td>
<td>DNase (HNH)</td>
<td>421</td>
<td>PF06958; PF12639</td>
<td>84</td>
<td>PF01320</td>
<td>?†</td>
<td>FpvAI</td>
<td></td>
</tr>
<tr>
<td>S10</td>
<td>PABL056</td>
<td>DNase</td>
<td>517</td>
<td>PF06958; PF09000</td>
<td>157</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>?</td>
</tr>
<tr>
<td>S11</td>
<td>LESB58</td>
<td>rRNase</td>
<td>662</td>
<td>PF06958; PF11429</td>
<td>90</td>
<td>PF09204</td>
<td></td>
<td></td>
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</tr>
<tr>
<td>S12</td>
<td>PA7</td>
<td>rRNase</td>
<td>740</td>
<td>PF06958; PF11429</td>
<td>90</td>
<td>PF09204</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Proteins with demonstrated bacteriocin activity and representatives of predicted novel pyocin types are shown in bold and italic font, respectively.

*Pfam domains are ordered from amino- to carboxy-terminus: PF01320, Colicin_Pyocin; PF03526, ImmE1; PF09204, Colicin_immun; PF11480, ImmE5.†

‡Pfam domains: PF01320, Colicin_Pyocin; PF03526, ImmE1; PF09204, Colicin_immun; PF11480, ImmE5.

The receptor of pyocin S1 in unknown, but is FpvA independent (Denayer et al., 2007).

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Fig. 1. Gene organization of pseudomonad bacteriocins. Arrows illustrate representative coding regions and are grouped according to known or predicted toxic activity. The DNA regions encoding the respective bacteriotoxic domains are highlighted in color as specified in the inset box. The coding region(s) of the respective immunity protein(s) located downstream of the toxin gene, if present, are shown in a fainter shade of the same color. The Pfam accession numbers of killing and immunity domains are specified in Table 1. The Pyocin_S domain is shown in gray. The additionally detected toxin/immunity domains in putative bacteriocins are marked as Pore-2 (PF01024/PF03857) and trRNase-2 (PF11429/PF09204). Additional colors indicate conservation of an amino-terminal domain between different bacteriotoxic proteins and noncolored parts denote a lack of significant similarity. Genomic DNA regions with clustered bacteriocin genes and multiple bacteriocin operons within a single strain are differentiated with labels (a) through (d). Names of functionally characterized bacteriocins are highlighted with red font. Proposed names for new types of pyocins with a single toxic domain (blue) or hybrid forms with two toxic domains (green) are also shown in color. The crossed region represents a pseudogene. The scale bar represents a DNA region of 500 bp. Abbreviations used for species names: Paer, Pseudomonas aeruginosa; Pchl, Pseudomonas chlororaphis; Pent, Pseudomonas entomophila; Pflu, Pseudomonas fluorescens; Pman, Pseudomonas mandelii; Pple, Pseudomonas plecoglossicida; Ppro, Pseudomonas protegens; Pput, Pseudomonas putida; Psyr, Pseudomonas syringae; Ptol, Pseudomonas tolida. Other abbreviations: PyoS, pyocin S; Rhs, protein with Rhs domain; cdIBAI, CDI system operon; mcbABCD, B-type microcin operon. An overview of representative tailocin gene clusters is presented in Fig. 6.
et al., 2008). Taking into account that these colicin M-like proteins form a distinct group of pyocins as compared to other modular S-type bacteriocins, we propose pyocin M to refer to this *Pseudomonas* protein family.

**Extracellular release of S pyocin/immunity protein complexes**

S-type pyocins are released as bacteriocin/immunity protein complexes at equimolar ratio. The size of the immunity proteins of S-type pyocins ranges from 77 to 153 amino acids, much smaller than the cognate killer proteins (Table 1). Their coexpression is crucial as they transiently inhibit the lethal function of the pyocin (Sano & Kageyama, 1981; Seo & Galloway, 1990; Sano et al., 1993b; Duport et al., 1995; Rasouliha et al., 2013). Immunity proteins from S1, S2 and AP41 share homology as they shield homologous HNH nuclease domains. Pyocin S3 is associated with a different type of immunity protein, in line with its classification as a different type of DNase toxin (Parret & De Mot, 2002). Protection is provided by interaction of the amino-terminal end of the immunity protein and the carboxy-terminal cytotoxic part of the killer protein (Sano et al., 1993b; Kageyama et al., 1996). Bacteriocin-producing cells may need to neutralize pyocin produced by other clonemates. It was found that this so-called soaking effect causes a reduced fitness of the pyocin producer strain (Inglis et al., 2013).

To ensure a swift ‘trapping’ of a corresponding killing domain, immunity genes of nuclease-type of bacteriocins are located immediately downstream of the pyocin genes and transcribed as an operon (Fig. 1). Their Shine–Dalgarno boxes are located within the lethal part of the pyocin gene (Sano et al., 1993b). Interestingly, the presence of ‘orphan’ immunity genes, encoding proteins that complement a matching S-type pyocin toxicity domain but that are not preceded by toxin genes, confers protection to sensitive strains. This way, invading pyocins may be captured, impeding their action in target cells (Denayer et al., 2007; Elfarash et al., 2012; Rasouliha et al., 2013; Elfarash et al., 2014). Notably, the immunity gene of the pore-forming pyocin S5 is transcribed in the opposite direction of the toxin gene (Fig. 1; Stover et al., 2000).

The mechanism behind self-immunity of pseudomonads producing colicin M-like bacteriocins is currently not known. In *E. coli*, this is ensured by a coexpressed immunity protein (Cmi) anchored in the cytoplasmic membrane facing the periplasm (Cascales et al., 2007). Genes encoding homologs of Cmi or the structurally related YebF protein (Gérard et al., 2011; Usón et al., 2012) are not found in *Pseudomonas* genomes.

After synthesis, the pyocin complexes are released from the producers, without the need of a (cleavable) signal sequence. Colicins take advantage of a lysis protein, encoded nearby the colicin gene, whereas S-type pyocins do not have these available (Michel-Briand & Baysse, 2002). It was suggested that S pyocins may take advantage of the lytic systems enabling the secretion of phage tail-like bacteriocins (see Genetic determinants of R-type pyocins; Nakayama et al., 2000). However, several S pyocin-encoding *Pseudomonas* strains lack phage tail-like bacteriocin clusters and their accompanied release cassettes (see In silico analysis of tailocins in other *Pseudomonas* species).

**S-type pyocin receptors and translocation**

The observation that several S-type pyocins kill target cells much more efficiently under iron-poor conditions led to the idea that these bacteriocins take advantage of iron-regulated receptors for cell entry (Ohkawa et al., 1980; Sano et al., 1993b; Duport et al., 1995; Elfarash et al., 2012, 2014). When iron is limiting, bacteria will express outer-membrane proteins that promote its uptake. One important strategy used by *P. aeruginosa* to
enhance iron uptake is the secretion of the siderophores pyoverdine and pyochelin, low-molecular-weight Fe\(^{3+}\)-chelating molecules. Three pyoverdine types can be distinguished, classified based on their oligopeptide side chains and each recognized by a specific outer-membrane receptor. After iron binding, siderophores are taken up by the iron-regulated outer-membrane proteins (IROMPs). Energy for this process and siderophore recycling is transduced by the cytoplasmic membrane protein TonB (Cornelis & Dingemans, 2013).

Mutagenesis experiments provided unequivocal evidence that several S-type pyocins indeed use IROMPs as a receptor (Table 1). Pyocin S2 and S4 take advantage of the type I ferrirpyoverdine receptor (FpvAI; Ohkawa et al., 1980; Smith et al., 1992; Denayer et al., 2007; Elfarash et al., 2012), whereas pyocin S3 uses the type II ferrirpyoverdine receptor (FpvAII; Bayse et al., 1999). The pore-forming pyocin S5 hijacks the FptA ferrirpyochelin receptor to inhibit sensitive strains (Elfarash et al., 2014). As the latter receptor is widespread among P. aeruginosa strains, the percentage of sensitive strains in a representative test panel is higher than usual. The receptors of pyocins S1 and S6 have not yet been identified, but sensitivity seems independent of the ferrirpyoverdine receptor produced (Denayer et al., 2007; Dingemans et al., 2013).

Following contact with these receptors, pyocins are translocated across the outer membrane. The exact mechanism remains unknown though the use of the ferrisiderophore receptors suggests that S-type pyocins are translocated in a similar way as the pyoverdines and pyochelin, energized by the TonB system (Cornelis & Dingemans, 2013). Several colicins are translocated via the TonB machinery as well, equally taking advantage of outer-membrane receptors for siderophores, such as linear catecholate transporter Cir, iron-enterobactin transporter FepA and ferrichrome-iron receptor FhuA (Jakes & Cramer, 2012).

Pyocin AP41 seems to enter cells via another receptor and uptake mechanism, although iron was found to play a major role as well. Different mutants tolerant to pyocin AP41 (tol phenotype) were isolated (Holloway et al., 1973), revealing involvement of a cluster of seven genes, organized in three operons (orf1-tolQRA, tolB and orfL-orf2) and regulated by iron availability and growth phase (Duan et al., 2000). The orf1 gene is nonessential, while mutants in tolQ and tolA could not be obtained, probably because gene inactivation would result in a lethal phenotype (Wei et al., 2009). Nevertheless, introduction of the tolQRA genes in a tol mutant is able to restore killing by AP41 (also called AR41), indicating that the Tol proteins are involved in pyocin uptake (Dennis et al., 1996). High iron concentration (FeCl\(_3\)) causes a reduced expression of the complete locus, due to the presence of a Fur-repressor (Lafontaine & Sokol, 1998; Duan et al., 2000). In contrast, RegA functions as a positive regulator under iron-restricted conditions (Duan et al., 2000). Study of the expression profile of orf1-tolQRA demonstrated that this operon contains one constitutive promoter in front of orf1, and one iron-regulated promoter located within orf1 (Wei et al., 2009). The oprL gene encodes a 18 kDa outer-membrane peptidoglycan-associated lipoprotein required for a normal cellular morphology and is located downstream of tolB. An oprL knockout mutant is viable but is very sensitive to osmotic pressure, underlining its role in cell envelope integrity (Lim et al., 1997). More recently, the growth phase-dependent regulation of the tol-oprL locus was found to be controlled by quorum sensing (QS), dependent on N-acyl homoserine lactone (AHL). When residing in a stationary phase, bacteria will not opt for a pronounced expression of these genes as they are required for growth and cell division, explaining the downregulation of the locus (Wei et al., 2009). Although the receptor of pyocin AP41 is not known, the proposed uptake route via the Tol machinery is in line with observations made for colicins. In Tol-energized uptake of several colicins, the primary outer-membrane receptors (such as the TonB-dependent vitamin B\(_12\) transporter BtuB) and the outer-membrane proteins actually translocating the bacteriocins (such as the porin OmpF) are not involved in siderophore-mediated iron uptake (Jakes & Cramer, 2012).

**Potential applications for S-type pyocins**

The S-type pyocins may be valuable tools in future therapeautic applications. This is illustrated by the potent activity of pyocin S2 against P. aeruginosa biofilms. Tested against different clinical isolates, this bacteriocin kills both mucoid and nonmucoid strains with similar efficiency when these are growing in a biofilm. Moreover, survival rates of biofilms treated with tobramycin or aztreonam at equal concentrations are considerably higher (> 100-fold).

In *vivo* pyocin S2 activity was validated in a *P. aeruginosa*-infected *Galleria mellonella* caterpillar model (Smith et al., 2012).

Via synthetic biology, engineered *E. coli* strains were developed, able to sense the presence of *P. aeruginosa* cells and subsequently killing them, both in planktonic and biofilm growth conditions. In a first approach, *E. coli* was equipped with a pyocin S5 gene, under the control of a lasR promoter (Saedid et al., 2011). The latter is activated after binding of a LasR/3-oxo-C\(_{12}\)-AHL complex. In the construct, constitutive expression of lasR gene was driven by a tetR promoter. Hence, production of 3-oxo-C\(_{12}\)-AHL, a native AHL from *P. aeruginosa*, can trigger biosynthesis of pyocin S5, concomitant with the accumulation of
colicin E7 lysis protein, put under control of the same P_{las} promoter. When reaching a threshold intracellular concentration of E7 lysis protein, E. coli cells will burst, causing the release of the pyocin into the environment and killing P. aeruginosa (Saeidi et al., 2011). In a similar system, E. coli sentinels were armed with a chimeric pyocin, constituted of the receptor and translocation domain of pyocin S3 and the killing and immunity domain of colicin E3, under the control of the P_{las} promoter (Gupta et al., 2013). The target detection module provides LasR, specifically interacting with the P. aeruginosa autoinducer. A P_{las}-regulated gfp gene was included for fluorescence-based monitoring of the binding of 3-oxo-C_{12}-AHL to the regulatory protein. To enable secretion rather than suicidal release of the chimeric toxin, the flagellar secretion tag FgM was introduced. On semi-solid medium, the E. coli producer, insensitive to its own engineered toxin, inhibited the growth of co-cultured P. aeruginosa. In principle, the modular design of these sensitive sense and destroy systems allows to virtually target any pathogen of interest, based on the availability of an appropriate bacteriocin gene and the recognition of the specific cellular receptors. Provided that an appropriate bacteriocin gene is known, the modular design of these sensitive sense and destroy systems allows to virtually target any pathogen of interest, based on the availability of an appropriate bacteriocin gene.

**In silico analysis reveals novel S-type pyocins in Pseudomonas genomes**

So far most of the work on S-type pyocins has been focused on P. aeruginosa, relying on the functional characterization of growth-inhibitory proteins detected in supernatants or in agar. In silico analysis previously suggested that these antibacterials may be far more widespread among pseudomonads (Parret & De Mot, 2002). In the past few years, decreasing costs of sequencing led to an exponential growth in available (draft) genome sequence data. In this section, we highlight the distribution and diversity of S-type pyocinogenic genes in P. aeruginosa and other pseudomonads. This analysis revealed the existence of several novel S-type pyocin genes in Pseudomonas genomes.

**HNH DNase pyocins**

DNA degradation by pyocin S1, S2, and AP41 is mediated by their carboxy-terminal nuclease domain (HNH family; Pfam domain PF12639, SMART domain SM00507). Pyocins S1 and S2 have virtually identical DNase domains (apart from a single conservative Val-Ile substitution), but they share only 60% amino acid sequence identity with the corresponding part of pyocin AP41. This is reflected in the homology of their immunity proteins: those of pyocin S1 and pyocin S2 differ by only one amino acid but they share only 44% identity with the one of pyocin AP41. Current genome sequence data suggest a prevalence of genes encoding orthologs of pyocin S1 (23 strains) or pyocin AP41 (17 strains) over those encoding pyocin S2 proteins (11 strains; Supporting information, Table S1). AP41 and S1 pyocinogeny are combined in seven strains, significantly more than the pyocin AP41-S2 combination (two strains), whereas no strain carries both pyocin S1 and S2 genes. Probably, the occurrence of pyocin AP41 on a transposable element (TnAP41) has promoted its acquisition by various P. aeruginosa strains (Sano & Kageyama, 1993).

**Pseudomonas aeruginosa** genome analyses uncovered two additional HNH subtypes present in a few strains only. In three pyocin S2-positive strains (BL09, BL13 and BL20) and strain VRFFA07, the pyocin AP41 aminoterminal domain is fused to a distinct DNase domain that shares only 63% amino acid sequence identity with pyocins S1, S2, and AP41 (44% for the associated immunity protein). For this third HNH-type protein, the designation pyocin S8 is proposed (Fig. 1, Table 1). A fourth divergent HNH subtype is found in strains BWHPSA026 (presence also combined with pyocin S2), BL04, HB15, and VRFP01. Its DNase domain bears more similarity to the previous type (60% amino acid identity vs. only 48% for pyocins S1, S2, and AP41), but it contains a different, much smaller aminoterminal domain (c. 200/350 residues less than in pyocins S1/ AP41). This fourth type HNH pyocin is designated pyocin S9 here (Fig. 1, Table 1). The difference from the other P. aeruginosa pyocin systems is again reflected in a divergent cognate immunity protein.

Overall, pyocin S9 of P. aeruginosa is actually more similar (c. 50% amino acid identity) to a number of putative bacteriocins encoded in the genomes of strains related to the P. fluorescens clade such as *Pseudomonas chlororaphis* subsp. *aureofaciens* 30–84 (Loper et al., 2012). These are part of a large group of c. 70 different putative bacteriocins that were retrieved through a search of pseudomonad genomic sequences for gene product pairs consisting of a protein with a HNH DNase-like carboxy-terminal domain and its apparent self-immunity-conferring partner. Phylogenetic analysis of a representative subset of these predicted bacteriocins visualizes the broad diversity collectively represented by these DNase domains composed of about 135 amino acids (Fig. 3). The distribution of most subclusters is not confined to particular species, as already noted for the functionally characterized and predicted bacteriocins occurring in *P. aeruginosa*. Even more sequence divergence is present among the corresponding immunity proteins that comprise on average about 85–90 amino acids (Fig. S1). Also, the amino-terminal domains of the killer proteins are
very diversified in sequence and length, ranging from c. 270 amino acids (for the majority of them) to 780 residues for *P. fluorescens* Q2–87, a wheat rhizosphere isolate with take-all biocontrol activity (Fig. 1; Loper et al., 2012). Remarkably, the latter protein harbors two Pyocin_S domains. In some strains (e.g. *Pseudomonas* sp. GM25, *Pseudomonas pseudoalcaligenes* KF707), the first, probably cognate immunity gene is followed by a second immunity gene that might protect against related DNase bacteriocins produced by rival pseudomonads. The capacity of a particular strain to encode multiple functionally related HNH-type pyocins seems not to be uncommon among pseudomonad species (Table S1). Most prominent in this respect is *P. fluorescens* Pf0-1 with four such systems, of which two are organized as a tandem of toxin/immunity gene pairs. The cluster of one of the other systems is expanded with an additional immunity gene. The *P. chlororaphis* subsp. *aurantiaca* PB-St2 genome is equipped with the potential to encode three DNase bacteriocins of this type. In addition to the three respective immunity genes, this strain contains an extra immunity gene at a fourth genomic location that lacks an appropriate DNase partner (Fig. 1).

A dual DNase-based bacteriocinogenic capacity is also found in *P. syringae* pv. *syringae* B728a (Figs 1 and 3). The predicted toxins are of similar sizes (c. 650 amino acids) but lack pronounced sequence similarity, which also applies to the respective immunity proteins. Relatives of one of these systems occur in other *P. syringae* strains (e.g. *P. syringae* pv. *actinidiae* M302091, *P. syringae* pv. *tomato* DC3000), while the second one has a much more restricted distribution in this phytopathogenic species. In general, strains originating from soil and plant
environments, including some strains with biocontrol capacities such as *P. fluorescens* Q2-87 and SS101, *Pseudomonas syringanthia* BG33R, and *P. chlororaphis* subsp. *aureofaciens* 30–84 (Loper et al., 2012), are well represented in the pseudomonad collection displaying this kind of bacteriocinogeny. This is also apparent from the frequent occurrence of this antagonistic property in several isolates that were sequenced as part of a microbiome study of the poplar rhizosphere and endosphere (Brown et al., 2012). Of 21 isolates, 11 strains (*Pseudomonas* sp. GM18, GM21, GM25, GM33, GM50, GM60, GM67, GM78, GM79, GM80 and GM102) are potentially able to produce one or two DNA-targeting bacteriocins of the HNH family.

**Non-HNH DNase pyocins**

The DNase domain of *P. aeruginosa* pyocin S3 lacks homology to the cytotoxic part of members of the HNH DNase pyocin family. Genome querying revealed gene pairs encoding putative bacteriocins of this type in at least 23 *P. aeruginosa* strains in addition to strain P12 (Table S1). Close orthologs are encoded by some strains such as the highly virulent *P. aeruginosa* UCBPP-PA14 (Lee et al., 2006), whereas also more diverged homologs occur, for instance in the melon rhizosphere isolate *P. aeruginosa* M18 (Wu et al., 2011a). A putative novel representative of this bacteriocin group, only showing significant homology within the carboxy-terminal nuclease domain, is apparently encoded by the blood stream isolate *P. aeruginosa* PABL056 (Ozer et al., 2012) and is designated pyocin S10 (Fig. 1, Table 1). Notably, these strains lack the capacity to also produce a HNH-type of bacteriocin, with few exceptions: genes encoding pyocin S3 and the newly identified pyocin S9 are both present in strains BL04 and HB15, whereas the combination of pyocins S3 and AP41 genes only is found in strain M9A1. Phylogenetic analysis of the pyocin S3-like cytotoxic domains derived from predicted bacteriocin genes present in a rather limited number of strains from other pseudomonad species, visualizes the extensive sequence diversity that evolved for this module (Fig. S2). Compared with the S3 prototype from *P. aeruginosa* P12, the level of amino acid identity ranges from 73% (*P. aeruginosa* M18) down to 38% (*Pseudomonas putida* GB-1). The amino-terminal domains of these putative bacteriocins also vary markedly in size (between c. 300 and 750 amino acids). The degree of sequence conservation between the cognate immunity proteins is much lower compared with the respective DNase domains (Fig. S3). For instance, the modules of *P. aeruginosa* strains P12 and M18 share only 40% amino acid sequence identity, and alignment of the strain P12 and *P. putida* GB-1 sequences reveals only borderline similarity (24% identity). Contrary to the observed preference of *P. aeruginosa* strains for deploying only one of both DNase-type bacteriocins, combined HNH/S3-type bacteriocinogenic potential is more frequent in other pseudomonad species. Among nine different S3-like systems identified outside the *P. aeruginosa* species, three were harbored by strains equally carrying genes for a member of the HNH family: *P. chlororaphis* subsp. *aureofaciens* 30–84 and *P. fluorescens* SS101, two wheat isolates with biological control potential for fungal diseases (Loper et al., 2012), and the river isolate *Pseudomonas* sp. M1, of interest for its capacity to degrade recalcitrant organic compounds (Soares-Castro & Santos, 2013). Moreover, a novel type of hybrid bacteriocin protomer in which the regular carboxy-terminal pyocin S3-like module is combined with a centrally located HNH domain, is found in four additional strains (discussed in section Putative novel pyocins with a tandem DNase architecture).

In most of these strains, the characteristic genetic organization for nuclease bacteriocins is conserved, with a toxin gene immediately followed at its 3′-end by the cognate immunity gene. As already pointed out for the HNH family, in some S3 pyocinogens, the putative self-immunity gene is part of an expanded immunity locus, composed of additional immunity genes of the same type in a tandem organization (Fig. 1). Notable examples of expanded pyocin S3-related clusters are found in *P. chlororaphis* subsp. *aureofaciens* 30–84 and *P. fluorescens* SS101. In strain 30–84 a cluster of three such immunity genes is present. Their sequence similarity hints to a common origin and/or duplication events (Fig. S3). Even four immunity homologs are clustered in *P. fluorescens* SS101, but the second gene appears to be inactive due to a frameshift in the coding region (Fig. 1). The sequence similarity among these SS101 immunity gene products is quite low. The similarity of the fourth gene to a self-immunity gene present in another plant-associated pseudomonad (*P. syringae* pv. *avellanae* ISPaVe037; O’Brien et al., 2012) suggests its acquisition by horizontal transfer rather than gene duplication (Fig. S3).

Some pseudomonads that lack an identifiable pyocin S3-type nuclease gene, do carry a S3-type immunity gene (Fig. S3). Such chromosomal orphan is present in the biocontrol strain *Pseudomonas protegens* Pf-5 isolated from soil (Loper et al., 2012), while distinct but mutually related plasmid-borne genes are found in another biocontrol strain originating from pear phyllosphere (on plasmid pA506 of *P. fluorescens* A506; Stockwell et al., 2013) and in a cave isolate (plasmid pMP-R124 of *P. fluorescens* R124; Barton et al., 2013). Highly conserved orthologs of a related orphan gene designated *bip*, encoding a putative bacteriocin–immunity protein and residing on plasmid pPsV48B of the phytopathogen *Pseudomonas savastanoi*...
NCPPB 3335 (Bardaji et al., 2011), are located on plasmid pPSR1 of \textit{P. syringae} pv. \textit{syringae} A2 (Sundin et al., 2004) and also occur in the genome of several other pathovars [pv. \textit{glycinea} B076 (Qi et al., 2011); pv. \textit{maculicola} ES4326 (Schreiber et al., 2012); pv. \textit{theae} ICMP 3923]. In these plasmids, all members of the \textit{pT23A} family, the bacteriocin/immunity gene is part of a small cargo region located between two backbone regions (replication/stable maintenance and \textit{MOB}_{\textit{Pyo}}-type conjugative transfer). This strategic positioning suggests that such bacteriocin/immunity genes can spread by conjugal plasmid transfer and could fulfill an ecological role in competition among pseudomonads or, potentially, other pyocin S3-related DNase bacteriocin producers occupying similar environments. Production of one such bacteriocin, carocin S1, by the soft rot-causing \textit{\gamma}-proteobacterial phytopathogen \textit{Pectobacterium carotovorum} was reported (Chuang et al., 2007).

**Putative novel pyocins with a tandem DNase architecture**

Six predicted S1-type pyocins (\textit{Pseudomonas mandelii} 36MFcv1.1, \textit{Pseudomonas} spp. 45MFCol3.1, GM33, GM50, GM79, and GM102) and another putative S3-type pyocins (\textit{P. fluorescens} NCIMB 11674, \textit{Pseudomonas plecoglossicida} NB2011, \textit{P. putida} GB-1, and CSV86) have an unusual domain composition. Between the ‘regular’ carboxy-terminal and amino-terminal regions, they contain a similar extra segment of \textit{c}. 250 amino acids, consisting of a pyocin-diagnostic domain (Pyocin\textsubscript{S}; PF06958) followed by a pyocin S1-like cytotoxic domain (Colicin-DNase; PF12639; Fig. 1). Hence, these putative bacteriocins display a tandem DNase architecture. The extra internal nuclease domains constitute a phylogenetic cluster that is related to – but distinct from – the HNH DNase domains as present in the pyocin S1–S2–AP41 family (Fig. 3). These hybrid pyocins are tentatively designated pyocin H1 (with S1–S1 organization) and pyocin H2 (with S1–S3 organization).

These 10 atypical pyocin-like genes encode proteins range in length from 632 amino acids (strain NB2011) to 872 amino acids (strain CSV86) and are found in four different genomic contexts but, remarkably, their cognate immunity gene is consistently followed by a gene encoding a putative immunity-like protein with a peculiar domain configuration. The latter is composed of a carboxy-terminal Pyocin\textsubscript{S} domain (however not connected to any cytotoxic domain) and an amino-terminal domain quite similar to pyocin S1-type immunity protein, connected by a sequence of around 265 amino acids (Fig. 1). The different genomic locations are somehow reflected in the sequence similarity of these architecturally similar proteins. Five of them show orthology (> 80% amino acid identity for rhizosphere isolates 36MFcv1.1, 45MFCol3.1, GM50, GM79, and GM102), but their homology to the other proteins is moderate to low (from c. 50% for strains GM33 and NCIMB 11764 to < 30% for strains CSV86, GB-1, and NB2011). Notably, this strain set encompasses not only several rhizosphere isolates (including GM33) but also strains originating from quite diverse environments: the cyanide-utilizing river mud isolate \textit{P. fluorescens} NCIMB 11764 (Vilo et al., 2012), the manganese-oxidizing freshwater isolate \textit{P. putida} GB-1 (Wu et al., 2011b), the naphthalene degrader \textit{P. putida} CSV86 isolated from soil (Phale et al., 2013), and the fish pathogen \textit{P. plecoglossicida} NB2011 (Mao et al., 2013).

Despite the considerable divergence across these strains, which seems not to be dependent on the nature of the carboxy-terminal DNase domain already present (pyocin S1- or pyocin S3-like), the three-gene synteny is conserved. Furthermore, the quite similar cluster topology of the amino-terminal immunity domains vs. the upstream-encoded immunity proteins (Figs S1 and S3), strongly hints to a functional module in which accessory toxin/immunity pairs coevolved in separate strains. The unprecedented domain architecture of such chimeric immunity protein suggests that this may be required for self-protection against the expanded cytotoxic capacity engendered by the supplemental DNase activity. If so, such dual-activity toxin might be produced as a trimeric complex with both of its immunity promoters.

**tRNase pyocins**

**Pyocin S4-like tRNases**

In addition to \textit{P. aeruginosa} PAO1, the colicin E5-like pyocin S4 gene pair is found in about 24 currently available genomic sequences of this species, a number quite comparable to the occurrence of pyocin S3 family members. In both cases, only few of the immunity genes, although as highly conserved as the upstream toxin gene, are actually annotated. The pyocins S3 and S4 distribution profiles among \textit{P. aeruginosa} strains show however little overlap (Table S1). Strains showing this dual pyocinogenic capacity are UCBPP-PA14, BL16, and BWHPsa027. Conversely, nearly half of the pyocin S4-positive strains combine this feature with genes encoding either pyocin S2 (as found in strain PAO1) or pyocin S1, but no co-occurrence with pyocin AP41 is noted. Highly in contrast to the other S-type pyocin families, this tRNase toxin gene pair is rare among other pseudomonad species. Moreover, the single currently identifiable homologous system, found in \textit{P. fluorescens} NCIMB 11764, displays only moderate amino acid similarity for the
protein-mediated warfare among pseudomonads

Pyocins carrying Cold-like tRNase domains

Quite a number of *P. aeruginosa* strains carry a gene coding for a bacteriocin with a second type of rNase domain (Colicin_D; Pfam PF11429; Fig. S4). Their carboxy-terminal domain shows significant similarity to the cytotoxic domain of *E. coli* colicin D (Cascales et al., 2007), Klebsiella oxytoca klebicin D (Chavan et al., 2005), and *P. carotovorum* carocin S2 (Chan et al., 2011). Colicin D cleaves anticodon loops of at least three of the four tRNA\textsuperscript{Arg}, in contrast to the tRNase from colicin E5 (same type as present in pyocin S4) that prefers tRNA\textsuperscript{Asn}, tRNA\textsuperscript{Asp}, tRNA\textsuperscript{His}, and tRNA\textsuperscript{ Tyr} (Papadakos et al., 2012). The biological activity of this novel type of *P. aeruginosa* bacteriocin, currently found in about 35 strains, has not yet been investigated. In *P. aeruginosa*, this family harbors two different subtypes (pyocins S11 and S12, Table 1) that carry similar tRNase modules and immunity proteins (c. 65% and 54% amino acid identity, respectively) but differ in their amino-terminal domains (Fig. S5). For pyocin S11, it closely resembles the equivalent part of the HNH DNase pyocin S2, whereas pyocin S12 shares this domain with the non-HNH DNase pyocin S3 (Fig. 1). These similarities suggest that pyocins S11 and S12 recognize receptors on susceptible cells similar to those targeted by pyocins S2 and S3, respectively. The considerable sequence divergence of the cytotoxic domains, compared with colicin D and also between pyocins S11 and S12, suggests that their tRNA specificities may differ.

The S11-type is the most abundant, occurring in about 30 strains, including *P. aeruginosa* LESB58 (Liverpool Epidemic Strain B58; Winstanley et al., 2009). The multiresistant strain PA7 (Roy et al., 2010) and a few other isolates (BL01, BL21, S54485, X13273) encode the S12 type of pyocin. The misleading annotation of these proteins as pyocins S2 (strain LESB58) and S3 (strain PA7) reflects a common problem with reliable automatic annotation of such modular bacteriocins in which the cytotoxic moiety occupies only a small part of the toxin.

A number of strains display dual tRNase bacteriocinogeny mediated by pyocins S4 and S11 (strains 2192, BWHP SA009, BWHP SA028, SCV20265, WC55), but none of these isolates has the capacity to additionally produce a DNase pyocin (Table S1). Combination of colicin D-like rNase and pyocin AP41-mediated DNase activities is however found in at least two strains, either containing a LESB58 ortholog (strain BL07) or a PA7 ortholog (strain BL01). Remarkably, not only pyocin S4-type tRNase-mediated antagonistic potential is very rare in pseudomonad species other than *P. aeruginosa*. Also, the colicin D-type of tRNase is largely confined to this single species.

Pore-forming pyocins

Nearly 20 *P. aeruginosa* strains, including UCBPP-PA14, possess highly conserved orthologs of the pyocin S5 genes of strain PAO1, making it one of the smaller group of pyocins in this species. Most of the strains also contain a pyocin system based on DNA degradation (pyocins S1, S2, or S3) and/or tRNA degradation. For the latter category, pyocin S4 co-occurrence seems to be favored as it is combined with pyocin S5 in more than half of the strains, while pyocin S12 genes are absent in the identified S5 pyocinogens (Table S1). The inspection of pseudomonad genomes other than *P. aeruginosa* reveals additional bacteriocins with carboxy-terminal domains and cognate immunity proteins that display significant homology with the pore-forming domain and immunity protein of pyocin S5 (c. 30% and 30–35% amino acid identity, respectively; Fig. 1). This sequence conservation contrasts with the diversity of their amino-terminal domains which range in length from c. 190 residues (*P. fluorescens* 2–92) to c. 375 residues (*Pseudomonas* sp. GM60) and bear little sequence similarity among each other, apart from those encoded by *P. fluorescens* strains SBW25, A506, and – to a lesser extent – S12 (Fig. 1).

rNase pyocins

Until recently, a counterpart of the 16S rNase bacteriocins colicin E3 and cloacin DF13 was not characterized in a pseudomonad strain. A candidate gene cluster, identified in the epidemic cystic fibrosis clone CF-PA39, was shown to encode a new type of *P. aeruginosa* bacteriocin, designated pyocin S6 (Dingemans et al., 2013). Pyocin S6 is nearly identical to pyocin S1, except that its carboxy-terminal domain conferring DNase activity is replaced with a colicin E3-like module, likely to mediate killing by breakdown of ribosomal RNA (Fig. 1). The pyocin S6 operon is also present in an incorrectly annotated
genomic stretch of strain PA45 (Segata et al., 2013). Inspection of Pseudomonas genomes revealed yet another colicin E3-like gene pair, but in this case the rRNase domain is fused to an amino-terminal domain nearly identical to the equivalent part of pyocin S2. This additional pyocin system, designated here pyocin S7 (Table 1), is harbored by two other P. aeruginosa strains, JD312 (genes not annotated; Dettman et al., 2013) and BWHPSA018 (Fig. 1). The corresponding immunity proteins of pyocin S6 and pyocin S7 are identical.

Compared with the other pyocin families, the ribosomal RNA-targeting system appears to have by far the narrowest distribution among P. aeruginosa isolates. This is in stark contrast with the predicted abundance of this type of toxin family in other pseudomonads. Using the amino acid sequences of the colicin E3 catalytic domain and of the cognate immunity protein as queries, a large number of gene tandems (c. 60) potentially encoding several novel rRNase bacteriocin/immunity pairs emerged. Phylogenetic analysis of the cytotoxicity-mediating domain sequences (covering about 95 residues) of a representative subset highlights their pronounced and species-independent diversity, although two main branches can be distinguished (Fig. 4). This dichotomy is even more pronounced for the respective immunity proteins (Fig. S6). In the subset most related to the colicin E3 immunity protein, the diagnostic Pfam PF03513 domain is detected. This is not the case for the subset with somewhat shorter immunity proteins, including those of P. aeruginosa pyocins S6 and S7.

Some strains carry two rRNase bacteriocin operons at unlinked genomic locations. These pairs of cytotoxic domains and immunity proteins exhibit significant sequence relatedness for some strains (clustering in one main branch), but others exhibit only remote sequence similarity (present in different main branches). The pronounced phylogenetic dichotomy suggests that the latter systems may not share a common ancestor. The respective toxin pairs of a particular strain also carry rather divergent amino-terminal domains with amino acid identities ranging from c. 60% for P. chlororaphis O6 to only 35% for P. chlororaphis subsp. aureofaciens 30–84. The majority of the pyocin S6-related bacteriocins consist of about 400 amino acids, but the size varies between 642 amino acids for P. aeruginosa strains with the pyocin S2-type domain and only 280 amino acids for Pseudomonas sp. Ag1. Similar to the amino-terminal domain sharing between pyocins S6 and S1, and between pyocins S7 and S2, three P. chlororaphis strains encode a protein with a 90% identical amino-terminal domain (Fig. 1) but linked to a different cytotoxic domain. Pseudomonas chlororaphis O6 [Pchl O6 (b)] carries a rRNase domain, whereas P. chlororaphis subsp. aurantiaca PB-St2 and P. chlororaphis subsp. aureofaciens 30–84 bear a HNH domain [Pchl

Fig. 4. Phylogenetic analysis of the cytotoxic domains in representative pseudomonad bacteriocins of the novel pyocin S6 family. Based on alignment of the carboxy-terminal domains, a ML phylogenetic tree was constructed (rooted with the Escherichia coli colicin E3 rRNase domain; blue). Two predicted rRNase bacteriocins in a particular strain are discriminated by extensions (a) and (b). The Pseudomonas aeruginosa members (red and green) and a Rhs protein (pink) are highlighted. The two main groups of rRNase cytotoxic domains are indicated (groups 1 and 2). Abbreviations used for species names: Pmor, Pseudomonas moraviensis; Ppoa, Pseudomonas poae (others as in the legend of Figs 1 and 3). The scale bar represents 0.3 substitutions per site. Bootstrap values (percentage of 100 replicates) are shown at the branches.
PB-St2 (b)]. For the latter two proteins, the amino-terminal domains are better conserved than the DNase modules (only c. 60% id).

Also for S6-type pyocins, expanded immunity gene clusters have been assembled in some strains. For instance, Pseudomonas tolaasii 6264 and Pseudomonas sp. GM18 (cluster (a), Fig. 4) carry, just downstream of their self-immunity gene, respectively, one and two quite different immunity genes (Fig. 1). The quite low overall sequence conservation between the pyocin S6 immunity proteins, along with the deviating codon usage and their small size (75–95 amino acids), hampers their identification and genomic annotation. Manual inspection on the other hand is facilitated by the consistent tight opeon-like linkage with the cognate rRNase gene, similar to the other nucleic acid-degrading systems.

The rRNase-type bacteriocinogenic capacity seems to be common in populations of nonpathogenic pseudomonads isolated from soil and plant environments, including several biocontrol-active pseudomonads: P. fluorescens strains A506, F113, and SBW25, P. chlororaphis like linkage with the cognate rRNase gene, similar to the several biocontrol-active pseudomonads: P. fluorescens strains A506, F113, and SBW25, P. chlororaphis.

Screening of pseudomonad genomes using the pyocin M amino acid sequences from PaeM (pyocin M1), syringacin M (pyocin M2), and PiM (pyocin M3) as queries revealed several candidate lipid II-targeting bacteriocins (Fig. 1, Table S1). An identical ortholog of PaeM is found in a limited number of P. aeruginosa isolates (e.g. strains 6077, 39016, BL08, BL14, BL17, E2, JJ692, MH27, U2504), which reflects the distribution of the 80-kb genomic island carrying the corresponding gene (exa13) in addition to the virulence factor exoU (Kulasekara et al., 2006). In some other P. aeruginosa strains (e.g. BL01, BL03, BWHPS008, JD332), a distantly related colM-like gene was identified (encoding pyocin M4, Table 1), adjacent to the conserved arc operon for anaerobic arginine catabolism (Verhoogt et al., 1992). Genes encoding close syringacin M homologs have integrated at different locations in P. syringae pathovar genomes. Most of the proteins are composed of nearly identical killing domains (>95% amino acid identity; Fig. 5) and very similar translocation and receptor domains (>90% AA-identity). However, some of these strains (e.g. P. syringae pv. mors-prunorum M302280 and P. syringae pv. theae ICMP3923) carry genes coding for a second, only distantly related and less abundant colicin M-like protein, a variant of which is also found in P. syringae pv. aceris M302273 (Fig. S7).

Considerable diversification of this type of bacteriocinogenic potential is apparent among the few other strains identified, mostly nonpathogenic isolates from plants. Their enzymatic domains share <45% amino acid identity with syringacin M or PaeM (Fig. 5). The amino-terminal domains are of three different types showing no significant sequence similarities among them. They are either (distantly) related to PaeM (strains GM21, 6264, BG33R, and PB-St2 [b]) or to syringacin M (all P. syringae strains), with a third group consisting of putative M-type pyocins from P. fluorescens HK44 (Chauhan et al., 2011) and Pseudomonas sp. GM33, GM49, GM55, and NZ011 (Fig. S7). The amino-terminal region of
P. aeruginosa pyocin M4 represents a fourth type. However, such lack of discernable sequence similarity does not exclude a similar 3D architecture. In this bacteriocin family, a very similar killing domain can be combined with sequence-unrelated moieties, as exemplified by colicin M, syringacin M and pectocin M from Pectobacterium carotovorum (Fig. 5). For the latter protein, it will also be of interest to see how the amino-terminal domain, which shows striking similarity to plant [2Fe–2S] ferredoxins (Grinter et al., 2012a), is folded and integrated with the enzymatic domain.

The domain flexibility of these bacteriocins is further evident from a protein, encoded by the nematicidal strain P. syxanthan BG33R that displays an unprecedented domain combination. This putative colicin M-like bacteriocin is fused at its carboxy-terminus with an extra domain that bears similarity (c. 35% amino acid identity) to pore-forming modules as found in colicin N (Vetter et al., 1998). The presence of a downstream convergent immunity gene of the same category (GenBank Accession Number EIK72461) suggests that this may represent a toxin capable of interfering with both peptidoglycan assembly and cytoplasmic membrane integrity. This hybrid pyocin carrying two functionally unrelated inhibitory modules is designated pyocin H3 (Fig. 1).

In a number of strains, the M-type pyocins are encoded by cargo genes on prophages. This is the case for the related prophages that occupy the trpE–trpG intergenic regions in P. syringae pv. tomato DC3000 (pyocin M2) and P. syringae pv. syringae 642 (pyocin M2 ortholog), as well as the same prophage inserted between mutS and cinA in P. fluorescens Q8r1-96 (pyocin M3) and P. brassicaearum subsp. brassicaearum NF4421 (pyocin M3 ortholog). However, acquisition of the gene encoding a pyocin M3 homolog (65% amino acid identity) in another P. brassicaearum strain (DF41) apparently occurred independently of this type of mobile element.

**Tailocins: phage tail-like bacteriocins**

Phage tail-like bacteriocins represent a second class of antibacterial defence weapons, present in many proteobacterial genera. In Pseudomonas, two major classes of phage tail-like particles have been described, viz. R-type and F-type pyocins (Michel-Briand & Baysse, 2002). The more general term ‘tailocins’ has been proposed to mark the widespread occurrence of these antibacterials (Gill & Young, 2011).

**R-type pyocins**

R-type pyocins have mainly been studied in P. aeruginosa and display activity against other strains of this species. Multiple strains producing R pyocins have been described and they are classified according to their target spectrum. Currently, five subgroups have been characterized, named...
R1–R5 (Michel-Briand & Baysse, 2002; Leiman & Shneider, 2012). Some additional R-type pyocins, not assigned to one of these groups, include C9 (Higerd et al., 1967), pyocin 21 (Govan, 1974a), and 430c (Govan, 1974b).

Structure and mode of action of R-type pyocins

R-type pyocins closely resemble T-even bacteriophage tails and appear as rigid and non-flexuous particles. Electron microscopy study suggests that they are built from a double hollow cylinder, consisting of a rigid inner core and a contractible outer sheath, 1200 Å long and 150 Å in outer diameter. The surface of the extended sheath contains different sets of striations, originating from the helically structured six subunit-containing annuli. A baseplate is attached to the sheath and serves as a docking point for the six tail fibers functioning as an anchor for attachment to target cells (Ishii et al., 1965; Higerd et al., 1969; Takeda & Kageyama, 1975). The specific antigens defining target strain specificity are located at the distal portion of the fibers and categorize the pyocins in one of the five classes (R1–R5; Ohsumi et al., 1980; Kumazaki & Ishii, 1982).

Upon contact, the sheath contracts and the pyocin core is inserted into the cell envelope (Higerd et al., 1969; Govan, 1974a; Shinomiya et al., 1975; Uratani & Hoshino, 1984) and effects arrest of protein and nucleic acid synthesis (Kaziro & Tanaka, 1965; Ohsumi et al., 1980), ultimately resulting in cell death. This killing is very efficient as attachment of only a single particle may result in cell death (Kageyama et al., 1964).

Receptor of R-type pyocins

The receptor of R-pyocin tail fibers is mainly constituted of lipopolysaccharide. It was observed that upon addition of purified lipopolysaccharide, survival of cells to such pyocin was higher (Ikeda & Egami, 1969; Govan, 1974a, b; Meadow & Wells, 1978; Kumazaki et al., 1982). More specifically, the carbohydrate moieties of the lipopolysaccharide are part of the receptor sites. Using defined lipopolysaccharide mutants, a l-rhamnose residue and two distinct D-glucose residues in the lipopolysaccharide outer core were found to participate in the receptor site of pyocin R1, R2, and R5, respectively (Köhler et al., 2010). For pyocin R3, the absence of a terminal D-glucose residue in the lipopolysaccharide core confers resistance to R-pyocin killing (Kocincova & Lam, 2013).

Interestingly, R pyocins from P. aeruginosa also target strains of other bacterial genera, such as Campylobacter sp. (Blackwell et al., 1982), Haemophilus ducreyi (Campagnari et al., 1994), Haemophilus influenzae (Phillips et al., 1990), Neisseria gonorrhoeae (Morse et al., 1976; Blackwell et al., 1979), and Neisseria meningitidis (Blackwell & Law, 1981), suggesting that these bacteria share common lipopolysaccharide receptors with P. aeruginosa (Connelly & Allen, 1983; Filiatrault et al., 2001).

Genetic determinants of R-type pyocins

The genetic locus of pyocin R2 was taken into focus in P. aeruginosa PAO1 (Nakayama et al., 2000). Located between trpE and trpG, the pyocin R2 cluster is followed downstream by a pyocin F2 locus, separated from the latter by a lysis gene cassette (Fig. 6). The 16-ORF gene cluster (prf10–prf23, encoding PA0614–PA0627) displays similarities to phage P2, 186, and ΦCTX. Moreover, the gene order of the P2 homologs is quite conserved, with minimal rearrangements. This allows assignment of functions to these different ORFs as being involved in the assembly and the formation of the core and sheath, the tail fibers, and the baseplate. The R2 locus does not bear genes involved in head formation, replication and integration, despite its common ancestry with P2 phages, suggesting an independent evolution. Hence, R-type pyocins should be considered evolutionarily highly specialized phage tails, rather than defective phages (Nakayama et al., 2000). The common ancestry of R-type pyocins with bacteriophages is underlined by immunological cross-reactivity with bacteriophage PS17 (Shinomiya, 1984; Shinomiya & Ina, 1989).

Overall, the DNA sequences of the R-pyocin genomic regions are well conserved. The highest sequence divergence is noted for the tail fiber genes (Fig. 7). In R-pyocin-mediated killing, the tail fiber protein TfpH (Prf15/PA0620 in pyocin R2 of strain PAO1) is a major determinant for specific recognition of a target strain. Reflecting this diversifying role, the gene pair encoding TfpH and its cognate assembly chaperone (Prf16/PA0621 in pyocin R2 of strain PAO1) show the least conservation among pyocin R genes. At this point, five subtypes (R1 through R5) of Prf15 are known (Michel-Briand & Bayse, 2002; Williams et al., 2008). Although conferring different host ranges, the amino acid sequences of Prf15-R3 and Prf15-R4 are nearly identical to Prf15-R2 (strain PAO1), but Prf15-R1 (for instance of strain LESB58; Köhler et al., 2010) and Prf15-R5 (for instance of strain PABL056; Ozer et al., 2012) have quite different carboxy-terminal sequences. When considering these three main biochemical types for amino acid sequence-based comparison, a prevalence of the R2/R3/R4-types (26 strains) and R5-type (21 strains) compared with the less frequently occurring R1-type (12 strains) becomes apparent (Table S1). In P. aeruginosa PA7, a distinct putative tail fiber protein is
encoded that is much smaller (c. 400 amino acids) and lacks significant amino acid similarity apart from a conserved amino-terminal domain of unknown function (DUF3751; Pfam PF12571; Fig. 6). Currently, no orthologs of this additional type (designated here as R6) and the corresponding chaperone are known in other strains.

**R-type pyocin retargeting and potential applications**

Taking into account that R-type pyocins display very specific and potent bactericidal activities, these antibacterials may be considered for use as chemotherapeutic agents. Moreover, R and F pyocins are protease-resistant, which is not the case for S pyocins. The efficacy of R-type pyocins has been validated in *P. aeruginosa*-infected mice by intraperitoneal and intravenous administration (Merrikin & Terry, 1972; Haas et al., 1974; Scholl & Martin, 2008; Ritchie et al., 2011). The rather narrow antibacterial spectrum of R-type pyocins is a main disadvantage however and may compromise their clinical usefulness in the end.

As mentioned in section 'Genetic determinants of R-type pyocins', target strain specificity of R pyocins is mainly determined by the tail fibers, encoded by prf15. **Fig. 6.** Synteny of individual and fused R- and F-type pyocin gene clusters in pseudomonads. The gene organizations are compared with the R2/F2 genes of *Pseudomonas aeruginosa* PAO1. Homologous genes are represented in the same color, with color coding based on the functions assigned to the genes in strain PAO1. In addition, putative pyocin and cargo genes absent from the *P. aeruginosa* systems are highlighted in distinct colors. The upper box visualizes the extent of nucleotide sequence conservation (fully conserved, bright green; poorly conserved, red) among aligned dual RF clusters of the eight different combinations types discussed in the text. The more divergent combined RF cluster of strain *P. aeruginosa* PA7 is shown for comparison. In addition to genes discussed in the text (prf9, prf20), the tail fiber protein-encoding genes of strain PAO1 are numbered for the R pyocin (prf15) and F pyocin (prf38, prf41; Nakayama et al., 2000). As a representative for the highly similar gene clusters encoding R1- through R5-type pyocins, the genomic region of the mono-R strain LESB58 is shown. The genetic backbone of a F1-and F2-pyocinogenic strain is illustrated with the coding regions of strains M18 and BL02. Putative pyocin R-like gene organizations of type R-a are shown for *Pseudomonas fluorescens* strains F113, PI29Arp and SBW25, *Pseudomonas putida* W619, and *Pseudomonas* sp. TKP (not included similar clusters: *P. fluorescens* Q2–87; *Pseudomonas* spp. Ag1, GM60, and GM67). The R-b type of organization is illustrated for *P. fluorescens* A506, BBc6R8, and SS101 and for *Pseudomonas poae* RE*1-1-14 (not included similar clusters: *Pseudomonas* sp. CF150 (99% identity to the A506 sequence) and *Pseudomonas* sp. FH4). The pyocin genes are all located in the trpE–trpG intergenic regions of *P. aeruginosa* strains and between mutS and cinA of other pseudomonads, with the respective regulatory genes proximal to trpE or mutS. The scale bar represents a genomic region of 2 kb.
Interestingly, the exchange of prf15 of pyocin R2 with the corresponding tail fiber genes of other R-type pyocins results in functional bacteriocins with the target spectrum of the tail fiber ‘donor’ (Williams et al., 2008). Taking this idea further, the antibacterial spectrum of R2 can also be diversified by replacement with the tail fiber of a P. aeruginosa-specific bacteriophage, as demonstrated for PS17. Engineered pyocins targeting E. coli and Yersinia pestis strains were created by fusing the conserved R2 amino-terminal region-encoding portion of prf15 to the variable carboxy-terminal parts of the phage tail fiber genes. To ensure proper assembly and optimal activity of the engineered pyocins, coexpression of the cognate chaperone protein Prf16 is recommended (Williams et al., 2008). Several artificial pyocins carrying chimeric tail fiber genes were engineered. Targets include a number of food-borne pathogens, such as E. coli O157: H7 (Scholl et al., 2009; Ritchie et al., 2011) and E. coli O104:H4 (Scholl et al., 2012). Useful candidate bacteriophage tail spike proteins for introduction in the R-type pyocins may be selected after genome screening and identification of lysogenic bacteriophages in the corresponding bacterial genomes of interest (Scholl et al., 2012).

An additional advantage of these engineered, highly specific bacteriocin particles is that their potent activity does not induce Shiga toxin (Stx) production (Scholl et al., 2009). There is clinical evidence that antibiotic therapis of Stx-producing E. coli may lead to an enhanced risk of hemolytic-uremic syndrome (Wong et al., 2000). The potential usefulness of these engineered pyocins against E. coli O157:H7 has been demonstrated in a rabbit model of diarrheal disease by orogastric administration (Ritchie et al., 2011) and in the decontamination of beef surfaces (Scholl et al., 2009). This way, R-type pyocins may serve as an engineering platform for the production of different, highly specific antimicrobials targeting virtually any pathogen of interest without disrupting the normal host microbiota.

**F-type pyocins**

A second type of P. aeruginosa phage tail-like bacteriocins are the F pyocins. These particles do not exhibit the typical sheath-core structure of R pyocins. Several F-type pyocins have been reported: pyocin 28 (Takeya et al., 1967), 430f (Govan, 1974b), F1 and F2 (Kuroda & Kageyama, 1979) and F3 (Kuroda & Kageyama, 1981). Their production is often accompanied by a coexpressed R-type pyocin or bacteriophage (Govan, 1974b; Kuroda & Kageyama, 1979).

**F pyocin structure**

Electron microscopy study demonstrated that F-type pyocins appear as flexuous, noncontractile rods, with an estimated length of 106 nm and width of 10 nm.
Contrary to the pyocin length that may not be uniform, the width is fixed with regular striations demarcating the individual rings or annuli, 23 in total, constituted by a 19.5-kDa protein as main subunit protein. One end of the F-type pyocin is square, while the other tapers to a point from which a fiber complex originates, allowing the binding to a receptor cell. The latter structure is composed of several long and short filaments, with an estimated length of 43 nm (Takeya et al., 1969; Kuroda & Kageyama, 1979; Kuroda et al., 1979; Kuroda & Kageyama, 1981). These fibers are the main determinant of specificity and, consequently, are antigen specific (Kuroda & Kageyama, 1981; Kuroda & Kagiyma, 1983). Kinetic analysis of killing suggests that F pyocins act by a single-hit process, similar to R-type pyocins (Kuroda & Kageyama, 1979; Kuroda et al., 1979).

Genetic organization of F-type pyocins

The genetic determinants of pyocin F2 have also been studied in detail in P. aeruginosa PAO1 (Nakayama et al., 2000). Genetic analysis of this pyocin revealed a 16-ORF gene cluster (prf28–prf43, encoding PA0632–PA0648), downstream of a pyocin R2 gene cluster and separated from the latter by a lysis gene cassette (Fig. 6). Genetic similarities and synteny with λ phage suggest that several ORFs are involved in rod formation, guaranteeing overall integrity and proper length of the tail structure. Additional downstream-located genes are involved in the formation of the fiber-like filaments. They are organized as two similar three-gene cassettes, both of which are thought to be functional. Pseudomonas aeruginosa PML14 equally produces pyocin F2 and harbors a similar gene cluster with minimal changes but is not accompanied by a R-pyocin gene cluster (Nakayama et al., 2000; Michel-Briand & Baysse, 2002). The pyocin F1 cluster lacks such seemingly duplicated 3’-region (Nakayama et al., 2000) and this is the case as well for all other non-F2-type pyocin clusters identified in P. aeruginosa genomes (see Genomic backbones of pseudomonad tailocins). Despite the apparent common ancestry with phage λ, F-type pyocins should also be regarded as evolutionarily highly specialized phage tails, similar to R-type pyocins (Nakayama et al., 2000). Analogous to what is observed for R-type pyocins and related phages, anti-F sera may as well neutralize phages, such as KF1 (Kuroda & Kagiyma, 1983; Kuroda et al., 1983).

The highest sequence divergence among F-type pyocins is displayed by the tail fiber proteins (Fig. 6), as equally observed for the R-type pyocin fibers. The same trend is apparent for the two tail fibers within the F2 module of PAO1 [Prf38 (PA0643) and Prf41 (PA0646) (Nakayama et al., 2000)]. The amino acid sequence of the pyocin F3 tail fiber protein (strain PAF41, also producing pyocin AP41) is not known (Kuroda & Kageyama, 1983). To this extent, homologs of Prf15 (c. 700 amino acids) and of Prf38/Prf41 (ranging in length from c. 350 to 460 residues) are instrumental for sequence-based differentiation of R- and F-type pyocins, respectively.

Phylogenetic analysis of predicted tail fiber proteins encoded by the F-pyocin regions of P. aeruginosa strains indicates the existence of additional (sub)types (Fig. S8). These protomers share a conserved amino-terminal region of about 140 amino acids, but the remaining part (ranging in length from 210 to 340 residues) has diverged strongly. The PA14 protein is clearly related to the F2-type tail fiber protein Prf41 (89% amino acid identity) and the M18 protein is most similar to the F1-type protein Prf41 (66%). Two additional types represented by the more distant homologs of strain PA7 and strain DK2 cannot be particularly linked to one of the known F types. As the tail fiber proteins are major determinants of receptor-recognition specificity, this suggests that the PA7- and DK2-encoded pyocins adopt the general F-type tailocin architecture but likely bind to receptors different from those recognized on cells susceptible to either pyocins F1, F2, or F3. About half of the 61 F-type pyocin clusters inspected belong to the F2 type, followed in number by the DK2 type (12 orthologs). The F1 type appears much less abundant (six strains), comparable in frequency of occurrence to the M18 and PA14 proteins (Table S1).

Regulation of pyocin expression in P. aeruginosa

The expression of R-type, F-type, and S-type pyocins is regulated by a common mechanism in P. aeruginosa. Regulatory sequences called P-boxes, often presented in repeats, are located in noncoding upstream regions of the pyocin genes and clusters, and serve as a binding site for the PrtN activator (Matsui et al., 1993). These P-box elements share no similarity with the SOS boxes of the colicin genes from E. coli, and hence, the LexA repressor is not involved. Similar to colicins, however, pyocin production was found inducible upon DNA-damaging treatment by UV light or mitomycin C, and appeared dependent on recA (Sano & Kageyama, 1993; Sano et al., 1993b). Under stress conditions, an activated RecA will cleave the repressor protein PrtR. This will cause liberation of the promoter region of prtN, and hence, the expression of this gene. PrtN activator is able to bind the P-boxes which will ultimately initiate pyocin expression (Fig. 8). PrtR and PrtN are both small proteins encoded by genes located upstream of the R2/F2 locus in P. aeruginosa PAO1, in opposite direction (Fig. 6). PrtR shares
remarkable similarities with the cl repressor from phage Φ80 (Matsui et al., 1993). Together with ptrN, PrrR also inhibits expression of ptrB. The latter gene encodes a small protein that is involved in repression of exsA, a master activator of the type III secretion system. PtrB is not involved in pyocin expression, however (Wu & Jin, 2005). This P-box regulatory system has been detected in several P. aeruginosa pyocins, viz. S1, S2, AP41, R2, and F2 (Shinomiya et al., 1983; Sano & Kageyama, 1987; Matsui et al., 1993). Pyocin S5 expression on the contrary seems not to be subjected to this regulatory scheme as there are no P-box elements in its 5′ region (Parret & De Mot, 2000). Chang et al. (2005) found that H2O2-induced oxidative stress upregulates transcription of pyocin S5. In support of this, chromatin immunoprecipitation of the region upstream of the pyocin S5 immunity gene showed it to be bound by OxyR, a H2O2-responsive transactivator (Wei et al., 2012). Upon treatment with the antibiotic ciprofloxacin, the R2/F2 locus displays a strong upregulation (Brazas & Hancock, 2005), contrary to treatments with ceftazidime (Blazquez et al., 2011). These vesicles play a role as vehicles mediating interbacterial competition and may also contain murein hydrolases and antibacterial quinolones (Tashiro et al., 2012).

Genomic backbones of pseudomonad tailocins

**In silico analysis of tailocins in P. aeruginosa**

The trpE–trpGDC intergenic sequence represents a hot spot for integration of the R- and F-type of pyocins in P. aeruginosa (Nakayama et al., 2000). By PCR scanning, strains were identified in which the prototypical organization of P. aeruginosa, with an apparent fusion of R2-F2 type of pyocin genes, was conserved but also other configurations were proposed, in which either an R- or...
F-type or both types were absent. Current full and draft genomic sequence data disclose a more comprehensive picture of the particular gene organization in this region. Inspection of the fully sequenced trpE–trpG genomic regions of 91 P. aeruginosa strains showed a quite similar number of ‘mono-tailocin’ strains, pyocinogenic for either R (29) or F (31), as compared to ‘duo-tailocin’ strains, pyocinogenic for both R and F (30). A fourth type of trpE–trpG intergenic organization is found in the multidrug-resistant blood isolate VRFPA06, in which a 30.3-kb DNA sequence with several coding regions of unknown function is positioned between the end of a pyocin R2 cluster and the trpG gene (Murugan et al., 2014). The presence of a bacteriophage P4-like integrase gene flanking the R-pyocin lysis cassette genes suggests a mobile nature for this inserted DNA region (Kung et al., 2010).

The different evolutionary relatedness of R- and F-type pyocins, to phage P2 and phage λ, respectively (Nakayama et al., 2000), suggests that the various types of co-integrated R/F clusters were assembled from separate pre-existing R- and F-type pyocins. In the various cluster combinations, production of both types of toxic particles by a particular strain relies on a shared conserved regulatory system to trigger expression and on a common lysis cassette for their release from producer cells (Fig. 6). Such dual R/F pyocin producers are not rare. The R2/F2 co-integrated pyocin region of strain PAO1, studied as a model system for both pyocin types, occurs in at least 10 other strains. In addition, alternative combinations of different R/F hybrid pairs exist, although occurring less frequently (Table S1). In the two strains encoding an F-PA7 ortholog, the genes are clustered with an R2 pyocin region (strain BL04) or with the PA7-specific R6 genes. Other variations on the theme of hybrid pyocin assemblages are the tandems R2/F-PA14 (strains PA14, BL17 and BWHPA028) and R2/F-M18 (strain BWHPA026) in R2-pyocinogenic isolates, and the paired clusters R1/F2 (strains BL18, BL25, MTB-1, and VRFPA07) and R1/F1 (strains PAK, CF5, and MA8.1) in R1-pyocinogenic strains. Apparently, also F1- and R5-types are compatible as such co-integrated clusters occupy the trpE–trpG intergenic regions of strains BL21, SS4485, and X13273.

In silico analysis of tailocins in other Pseudomonas species

Production of a phage-like bacteriocin from a pseudomonad species other than P. aeruginosa was reported only recently (Fischer et al., 2012). The activity of wheat rhizosphere isolate P. fluorescens SF4c, killing P. fluorescens CTR212, was attributed to a high-molecular mass bacteriocin whose production was upregulated by exposure of the producer to UV light or mitomycin C. An inactive mutant was obtained by disrupting a gene predicted to be involved in tail formation (equivalent of Prf20/PA0625 in P. aeruginosa PA01). By comparison with homologs present in some other P. fluorescens strains, this gene was presumed to reside in the intergenic region between mutS and cinA, a hotspot for the integration of prophages (Mavrodi et al., 2009; Loper et al., 2012). Sequence analysis of the mutS- and cinA-flanking regions revealed the presence of a prtR and lysis gene homolog, respectively, pointing to a potential R-type pyocin gene cluster. This genomic organization appears to be conserved in the genomic sequences of a number of other isolates, mostly originating from plant or soil environments: P. fluorescens strains A506, Q2-87, SS101, SBW25 (Loper et al., 2012), BBc6R8 (Deveau et al., 2014), F113 (Redondo-Nieto et al., 2013) and PZ29Arp (Marchi et al., 2013), P. poae RE1-1-14 (Müller et al., 2013), P. putida W619 (Wu et al., 2011b), and Pseudomonas spp. Ag1 (Alvarez et al., 2012), GM60, GM67 (Brown et al., 2012), TKP (Ohtsubo et al., 2014) and CF150 (McTee et al., 2013).

The overall synteny with the P. aeruginosa pyocin R clusters suggests that these genes compose the genetic backbone for production of R-type tailocins. However, a number of striking differences are apparent. Of the P. aeruginosa regulatory genes, only a prtR homolog is present and it is positioned in opposite orientation, convergent with the other pyocin genes. Although well conserved among these pseudomonads themselves, these PrtR proteins share < 40% amino acid identity with P. aeruginosa. Together with the absence of PrtN and PrtB, this divergence suggests that the regulatory mechanisms triggering expression deviate from P. aeruginosa (Wu & Jin, 2005).

A significant difference is also apparent in the respective lysis cassettes. The first two genes, encoding a holin (Prf9/PA0614) and a chitinase-like lytic enzyme (Prf24/PA0629; Pfam PF00182), are conserved but the additional genes are of different origin. The P. aeruginosa proteins Prf25 (PA0630) and Prf26 (PA0631) are homologous to the lambda P. aeruginosa phage D3 proteins OrfB2 and Orf33 (Kropinski, 2000; Canchaya et al., 2003). Their functions seem to be fulfilled by two small proteins encoded by a gene pair located in different reading frames within the same nucleotide stretch (Fig. 6). These proteins are homologous to the spanins required for lysis by phage λ, the integral cytoplasmic protein Rz (Pfam PF03245) and the outer-membrane lipoprotein Rz1 (Pfam PF06858; Summer et al., 2007; Berry et al., 2012). Due to this unusual gene organization, only few of the Rz1-encoding genes within these R-pyocin clusters are annotated (likewise for strain SF4c). Remarkably, these spanin genes are absent from the lysis cassette of P. fluorescens A506 and Pseudomonas sp. CF150. Like the overall clusters, also the
Rz and Rz1 sequences have diverged considerably among the different strains. For instance, amino acid sequence identity among the seven P. fluorescens strains ranges from 53% to 73% for Rz and from 61% to 83% for Rz1.

Another sequence stretch lacking synteny with P. aeruginosa corresponds to the region between the PAO1 genes encoding Prf18 (PA0623; tail tube protein) and Prf20 (PA0625; tail length determinant). Instead, significant homology (35% amino acid identity) is found with a protein encoded by a similarly positioned gene (orf30) of temperate Vibrio phage VP882 (Lan et al., 2009). Also, the tail fiber region of this plasmid-like prophage (in particular tail fiber protein Orf21 with 60% amino acid identity) shares homology with three tail protein genes in a subset of these strains (P. fluorescens strains A506, BBc6R8, FH4, SS101, and P. poae RE*1-1-14). However, all the other strains carry the corresponding phage P2-related genes, like all P. aeruginosa strains (Fig. 6).

The alignment also indicates that additional tailocin-associated cargo genes have been acquired by some of these strains. The P. fluorescens SS101 region upstream of the cinA-proximal lysis genes is loaded with a homolog of the P. aeruginosa gene encoding AmpDh3, a peptidoglycan peptidase involved in cell wall remodeling (Lee et al., 2013). Genes located between mutS and prrR encode a putative toxin of the Zeta family (inhibiting peptidoglycan synthesis; Mutschler & Meinhart, 2011) and of the YafO family (inhibiting protein synthesis; Zhang et al., 2009) in P. fluorescens strains BBc6R8 and SS101, respectively. The mutS–prrR intergenic sequences are the most variable parts of these clusters and expanded considerably in P. fluorescens SS101 (by 5.1 kb) and P. fluorescens A506 (by 6.7 kb). In the latter strain, this stretch codes for putative metabolic enzymes (a carboxylase, 2-hydroxyacid dehydrogenase, and methyltransferase).

**Type VI secretion systems**

One more complex competition-mediating machinery is the type VI secretion system (T6SS), of which multiple variants with differentiated functions may coexist in a particular strain. Originally identified in Vibrio cholerae (Pukatzki et al., 2006), this system was later found to be widespread among Gram-negative bacteria, including pseudomonads. Remarkably, the T6SS not only aims at bacteria but also at eukaryotic cells. Targeted microorganisms may be from the same or a different genus. Growth inhibition by the T6SS requires cell-to-cell contact and is mediated by a syringe-like apparatus that allows the transfer of toxic effector molecules. Contrary to the contact-dependent inhibition (CDI) system (see Contact-dependent inhibition), these toxins are not covalently coupled to their ‘carriers’. Similarly to S-type pyocins and CDI effectors, the inhibitory molecules of the T6SS require immunity proteins to prevent self-inhibition (Bönnemann et al., 2010; Silverman et al., 2012; Ho et al., 2014; Russell et al., 2014).

Type VI secretion (T6S) has been linked to a variety of processes, including conjugation, biofilm formation, virulence, quorum-sensing regulation and persistence in chronic infections, but these topics are not within the scope of this review.

**Structural features**

From a structural point of view, T6SSs share many similarities with phage-type infection systems. The T6SS consists of an inverted phage-derived syringe-like apparatus embedded in a cell envelope-spanning membrane-associated assembly. The core of the T6S machinery consists of a minimal set of 13 proteins that are required to obtain a functional architecture, most of them predicted to have a cytoplasmic localization (Filloux et al., 2008; Pukatzki et al., 2009; Bönnemann et al., 2010; Cascales & Cambillau, 2012; Silverman et al., 2012; Coulthurst, 2013; Ho et al., 2014; Russell et al., 2014).

To date, the global T6SS ultrastructure has not been determined, although several individual T6SS components have been characterized. T6SS landmarks include an AAA+ Clp-like ATPase (ClpB/ClpV), an IcmF (intracellular multiplication protein F) homolog, and a regulatory FHA (forkhead-associated) domain protein. The phage tail-like structure consists of Hcp (hemolysin-coregulated protein), VgrG (valine/glycine repeat protein G), TssB (type six secretion B) and TssC (Cascales & Cambillau, 2012; Silverman et al., 2012; Ho et al., 2014). The first two proteins are secreted by the T6S machinery and share structural homology with tail tube protein gp19 and tail spike proteins gp5/gp27 from bacteriophage T4, respectively (Kanamaru, 2009; Leiman et al., 2009). Hcp1 adopts a hexameric-ring structure and is the major constituent of the tube (Mougous et al., 2006), while VgrG appears as a trimer at the needle tip, allowing membrane breaching and puncturing of the bacterial envelope (Pukatzki et al., 2007; Hachani et al., 2011). Proteins from the PAAR repeat superfamily are present at the VgrG spike forming a sharp conical extension and are involved in attachment of effector domains for translocation into target cells (Shneider et al., 2013). Notably, an amino-terminal PAAR domain is present in the predicted DNase pyocin S10 (Table 1). Hcp and VgrG require a functional T6S apparatus for their release into the extracellular medium, to form the nanosyringe. TssB and TssC (HsbI/ HscI) form a Hcp tube-surrounding dynamic sheath that is able to undergo repeated cycles of extension and contraction, meanwhile remaining attached to the inner
membrane (Basler et al., 2012; Lossi et al., 2013; Zoued et al., 2013). Energy necessary to drive the secretion of Hcp is thought to be provided by the aforementioned ClpV that disassembles the contracted T6SS sheath structure (Basler & Mekalanos, 2012). Several other components participating in the process have been identified but their exact contribution in the syringe dynamics often remains unclear. TssE (or HsiF) is a gp25-like component (Lossi et al., 2011), while Tagl interacts with TssB, possibly by modulating its incorporation into the T6SS (Lossi et al., 2012).

The inhibitory effect caused by the T6SS originates from its ability to deliver deleterious effector molecules into the cytoplasm or periplasm of target cells (Hood et al., 2010; Russell et al., 2013). Recently, it was revealed that Hcp bears a key role in this process, as the central pore of the Hcp ring is able to temporarily bind the effectors. Consequently, Hcp not only acts as a structural tail tube protein, but also functions as a chaperone exporting the T6SS toxins (Silverman et al., 2013). Furthermore, the observation that several effectors may not be Hcp stabilized but be VgrG associated instead, hints to a second pathway for T6S effector export (Whitney et al., 2014).

**Multiplicity of T6SSs in pseudomonads**

The genome of *P. aeruginosa* PAO1 encodes three T6SS loci, termed Hcp secretion island I (HSI-I), HSI-II and HSI-III, each set up by 15 loci, termed Hcp secretion island I (HSI-I), HSI-II and overlapping sets of effector molecules (Bleves et al., 2010). These results support the previous observation that several *P. syringae* strains carry T6SS core genes (Shrivastava & Mande, 2008). Two distinct T6SS genomic islands were found in genome sequence drafts of several *Pseudomonas cannabina* pv. *alisalensis* strains, one orthologous to the T6SS-II cluster of strain DC3000, while the other is more closely related to T6SS-I from *P. aeruginosa* PAO1. The absence of orthologs of Tse effector genes in these strains hints to significant differences in the biological function of these systems (Sarris et al., 2013). Two T6SS islands were equally found in *Pseudomonas mendocina*, homologous to HSI-I and HSI-II from PAO1, while *Pseudomonas entomophila* carries one HSI-II-like locus (Sarris & Scoulica, 2011). Genome mining of several *P. fluorescens* genomes indicated that these strains carry one to three T6SS clusters, encompassing four types in total, three of these being similar to the *P. aeruginosa* loci (Loper et al., 2012). Model strain *P. protegens* Pf-5 equally carries a cluster similar to HSI-I (Hassan et al., 2010; Loper et al., 2012). In a broader genomic survey, comparison of 34 pseudomonad genomes indicated that virtually all *Pseudomonas* strains carry at least one T6SS locus. Clusters can be classified in five main phylogenetic groups based on comparison of 11 core genes. Specific sets of additional genes associated with vgrG genes, may play a role in secretion or could be new T6S effectors (Barret et al., 2011).

Functionality of a *P. syringae* T6SS has been demonstrated for strain DC3000, where Hcp2 is involved in competition of its producer with enterobacteria and yeasts. On the contrary, Hcp2 does not contribute to virulence or colonization of tomato or *Arabidopsis* plants (Haapalainen et al., 2012). Biocontrol strain *P. fluorescens* Pf29Arp, that is closely related to the *P. brassicaeavum*-like subgroup, carries four T6SS clusters. In the presence of necrotized wheat roots, infected with the pathogenic fungus *Gaeumannomyces graminis* var. *tritici*, expression of two clpV genes is significantly upregulated, but not for the other two clpV genes, although these are expressed as well. It is unclear however whether the upregulation of two T6SS clusters is linked with the biocontrol function of Pf29Arp (Marchi et al., 2013). *Pseudomonas fluorescens* MFE01 carries at least two hcp genes. Mutation of hcp2 results in reduced or abolished antagonism against a number of pseudomonads (Decoin et al., 2014).

**Toxic effectors and immunity proteins of T6SSs**

T6S-targeted bacterial cells are killed by inhibitory effectors, transferred via the tail-like apparatus and subsequently interfering with essential processes. As mentioned before, these proteins are guided to the T6S apparatus upon binding to the Hcp chaperone. To prevent self-inhibition of the
producer, immunity proteins are available that may form complexes with their cognate partners. Genes encoding such inhibitor proteins are typically located immediately downstream of the effector protein genes and are required for producing dedicated E-I (effector/immunity) pairs (Russell et al., 2014).

Secretome analysis of the H1-T6SS of \textit{P. aeruginosa} PA01 revealed three substrates that are secreted under tight posttranslational control, Tse1-2-3 (Hood et al., 2010). Recently, it was found that three more effectors are associated with H1-T6SS, hence called Tse4, Tse5, and Tse6 (Whitney et al., 2014). Tse1 and Tse3 (Fig. 9) are targeted to the periplasm, both acting as peptidoglycan-hydrolyzing enzymes (Russell et al., 2011). Their mechanism of action is quite different, however. Tse1 belongs to the superfamily of NlpC/P60 endopeptidases and cleaves the γ-D-glutamyl-L-meso-diaminopimelic acid of peptidoglycan in target cells (Russell et al., 2011; Benz et al., 2012; Chou et al., 2012; Ding et al., 2012; Zhang et al., 2012b). In addition to Tse1, three other amidase effector groups, able to cleave within the peptide stem of peptidoglycan and its cross-links, have been identified via a heuristic approach. The preferred cleavage sites of these Type VI amidase effector (Tae) proteins vary, however, suggesting that effector production may depend on the peptidoglycan structure of the targeted organisms (Russell et al., 2012). Next to Tae1 (or Tse1), two additional Tae structures have been solved. Tae3 in complex with Tai3 (Type VI amidase immunity, Fig. 9) from \textit{Ralstonia pickettii} 12D occurs as a heterohexamer, composed of two Tae3 proteins and two Tai3 heterodimers (Dong et al., 2013), while Tae4/Tai4 from \textit{Salmonella} Typhimurium LT2 and \textit{Enterobacter cloacae} ATCC13047 (Fig. 9) occur as a heterotetramer of two Tae4 molecules and a Tai4 dimer (Benz et al., 2013; Zhang et al., 2013). Tse3 that anchors to the target membrane in a calcium-dependent way (Lu et al., 2014), adopts a goose-type lysozyme-like structure and acts as a muramidase that cleaves the β-1,4 bond between \textit{N}-acetylmuramic acid (MurNAc) and \textit{N}-acetylglucosamine (GlcNAc) in peptidoglycan (Li et al., 2013b; Lu et al., 2013; Wang et al., 2013). In \textit{P. protegens} Pf-5, a peptidoglycan glycoside hydrolase effector not orthologous to Tse3 was identified via an informatics search and characterized. This effector protein is involved in inhibition of \textit{P. putida} KT2440 (Whitney et al., 2013). Immunity to the Tse1 and Tse3 effectors is provided by Tsi1 (Type VI secretion immunity 1) and Tsi3, respectively, present in the periplasm of the producer (Russell et al., 2011; Benz et al., 2012; Ding et al., 2012; Shang et al., 2012). Tse2, protected by a Tsi2 dimer, causes quiescence, but not death, in recipient cells by an unknown mechanism, possibly by exerting nuclease activity. As Tsi2 acts as a cytoplasmic neutralizer, Tse2 is thought to exert its function in the cytoplasm of the target cells (Hood et al., 2010; Li et al., 2012; Zou et al., 2012). Tsi1-3 are not exported and reside in the periplasm of the producer, while Tsi2 is complexed with Tse2 and dissociates prior to or during the secretion process (Hood et al., 2010; Russell et al., 2011; Li et al., 2012). Less is known about effectors Tse4, Tse5, and Tse6, protected by Tsi4-5-6, respectively, mainly due to a lack of homology with previously characterized proteins (Whitney et al., 2014). Tse4 is Hcp stabilized, similar to Tse1, Tse2, and Tse3, and acts in the periplasm via an unknown mechanism. Homologs of this effector/immunity pair are also encoded in the genomes of several other pseudomonads, such as \textit{P. brassicaeearum} NFM421, \textit{P. fluorescens} F113, and \textit{P. protegens} Pf-5, but their functionality remains to be demonstrated. Tse5 and Tse6 are PAAR repeat-containing proteins interacting with a cognate VgrG, but not with Hcp, for host export. Tse5 exerts its toxic function in the periplasm, in contrast to Tse6 that acts as a potent

![Fig. 9](https://academic.oup.com/femsre/article-abstract/38/4/523/754873/384623756873)
cytoplasmic toxin. Inhibitory domains of Tse5 and Tse6 are located at their carboxy-terminal termini, in the latter case carrying a putative Toxin 61 domain. The presence of Rhs/YD-repeats in Tse5 suggests that its secretion proceeds via the T6S pathway (see Rhs elements as mediators of intercellular competition).

As substrates of P. aeruginosa PAO1 H2-T6SS, a superfamily of phospholipase effectors was identified. These enzymes probably target phospholipids that are accessible from the periplasm, as associated genes coding for immunity partners are predicted periplasmic proteins. Antibacterial activity of the lipase effector PldA (or Tle5, Type VI lipase effector) is effectuated by the degradation of phosphatidyethanolamine, the major phospholipid in bacterial membranes. Immunity to Tle5 is granted by Thi5 (Russell et al., 2013). In addition, the H2-T6SS is also required for bacterial internalization into epithelial cells and plays a role in worm virulence (Sana et al., 2012). In contrast to H1-T6SS and H2-T6SS, no role in interbacterial competition could yet be attributed to H3-T6SS, a system that also contributes to virulence in a worm model (Sana et al., 2013). In P. aeruginosa PA14, H2-T6SS and H3-T6SS can compensate for one another in mouse virulence (Lesic et al., 2009).

Regulation of T6SSs in Pseudomonas

Transcriptional regulation

In P. aeruginosa PAO1, the three T6SS loci are regulated in a different way. The latter is in line with their distinct evolutionary origins and the different roles these systems may fulfill. Cluster-dependent regulation also suggests that these systems act in completely different contexts (Bingle et al., 2008). Transcription of T6SSs depends on a myriad of factors, including environmental, QS and other bacteria-derived signals (Silverman et al., 2012). These topics will be briefly summarized, but the reader is referred to more specialized reviews for HSI regulation (Miyata et al., 2013).

QS was found to play a major role in HSI gene cluster regulation. It represses HSI-I, but activates the co-regulated HSI-II and HSI-III (Lesic et al., 2009; Sana et al., 2012; Sana et al., 2013). The RpoN S22 factor causes different effects on the T6SS operons. RpoN activates the expression of one of the H3-T6SS operons (left), but represses the other (right) and H2-T6SS (Sana et al., 2013), this negative regulation being rather atypical for T6SSs (Bernard et al., 2011). In addition, the Sfa3 enhancer-binding protein of H3-T6SS has no effect on RpoN-mediated transcription, while the repression of H2-T6SS by RpoN is Sfa2-dependent (Sana et al., 2013). Next to this, HSI-I is regulated by two-component systems and small RNAs (sRNAs) (Goodman et al., 2004; Mougous et al., 2006). Mutation of the subB gene causes an upregulation of GacA and the downstream sRNAs, RsmY, and RsmZ, which triggers T6S in P. aeruginosa PAK (Li et al., 2013a). Similarly, GacA was found to upregulate expression of different T6SSs in the rhizobacterium P. aeruginosa M18 (Wei et al., 2013). Mutation of the sensor RetS causes Hcp1 expression in PAK via enhanced c-di-GMP signaling (Moscoso et al., 2011). RetS forms a heterodimer with GacS, hereby preventing the autophosphorylation of the latter. Consequently, phosphotransfer-dependent activation of GacA cannot occur (Brencic et al., 2009). Next to RetS, sRNA production via GacA is also controlled by HptB via a complex regulatory cascade. Interestingly, HptB only regulates rsmY expression (Bordi et al., 2010). Furthermore, HSI-II is also regulated by iron. In its promoter region, two putative Fur boxes are present, causing negative regulation by iron (Sana et al., 2012). Interestingly, the H1-T6SS is assembled in response to foreign T6SS-mediated attack from hostile bacteria (Basler et al., 2013). This counterattack measure is also adopted upon gene transfer from Type IV secretion systems (Ho et al., 2013).

A number of other conditions have been associated with altered T6SS levels, though they are often the result of indirect effects. Subinhibitory concentrations of kanamycin induce the expression of H1-T6SS in P. aeruginosa PAK. This is only observed when a functional Gac/Rsm pathway is present (Jones et al., 2013). In the host-adapted, alginate-overproducing P. aeruginosa 2192, the presence of human respiratory mucus triggers expression of the HSI-I gene cluster (Cattoir et al., 2013). In P. syringae B728a, but not in strain DC3000, expression of T6SS can be induced by an osmotic upshift (Freeman et al., 2013). In P. fluorescens Pf0-1, a soil-induced gene product predicted to be a component of a T6SS (Pf01_5595) was shown important in arid soil persistence, underlining the role of microbial interactions in natural environments (Varivarn et al., 2013).

Posttranslational regulation

At posttranslational level, H1-T6SS functioning is strictly modulated by the phosphorylation state of Fha1. This is controlled by the transmembrane serine-threonine Hanks-type kinase PpkA. When Fha1 is phosphorylated, Hcp1 secretion will be triggered. The PP2C-type phosphatase PppA antagonizes the phosphorylation of Fha1 (Mougous et al., 2006). PpkA contains autophosphorylation sites and its kinase activity is positively regulated by TagR (Hsu et al., 2009). In addition to this, three other PpkA/ PppA checkpoint regulators, TagT–TagS–TagQ, were
found, with TagTS forming an ATP-binding cassette (ABC) transporter complex. Study of their cellular localization suggests that these four proteins participate in a trans membrane signaling pathway (Casabona et al., 2013). TagF functions as a posttranslational repressor, acting independently from the threonine phosphorylation pathway (Silverman et al., 2011).

**Contact-dependent inhibition**

CDI represents another strategy of bacteria to protect themselves from rival bacteria. CDI⁺ bacteria own a variety of toxins that allow growth inhibition of neighboring competitors via direct cell-to-cell contact. Similar to S-type pyocins and effectors of T6SSs, producers need to temporarily inactivate inhibitory domains by forming CDI toxin/immunity protein pairs. CDI systems belong to the type V two-partner secretion systems (TPS; Aoki et al., 2008). CDI has been well studied in *E. coli* and *Burkholderia*, but the exact nature of this inhibitory system in *Pseudomonas* remains poorly understood.

Similar to T6SS-mediated antagonism, CDI is thought to play a role beyond bacterial competition. In the model strain *Burkholderia thailandensis* E264, CDI proteins were associated with autoaggregation and adherence to an abiotic surface (Anderson et al., 2012) and with biofilm formation (Garcia et al., 2013). Bacteria may use CDI in cooperative behaviors to build communities and to prevent non-self bacteria from entering a biofilm community (Garcia et al., 2013).

**Genetic organization of CDI systems**

CDI mediated by the CdiB/CdiA system was initially observed in *E. coli* isolate EC93. The antibacterial effect is caused by expression of the cdiBAI gene cluster, which is sufficient to confer the CDI⁺ inhibitor phenotype to *E. coli* K-12 cells (Aoki et al., 2005). CdiB and CdiA are members of the TpsB and TpsA families of TPS proteins, respectively. TpsB is an outer-membrane β-barrel protein that facilitates the export of TpsA across the outer membrane. The latter is a very large hemagglutinin-repeat protein that extends far from the cell surface (Mazar & Cotter, 2007). The growth-inhibitory effect of CdiA is caused by a toxin domain, located at its C-terminus, called CdiA-CT. Overall, CdiA homologs share large regions of sequence homology, but their carboxy-terminal regions (c. 300 AA) diverge abruptly after a common VENN peptide motif (PF04829), suggesting that many different toxins (CdiA-CTs) in CDI⁺ strains exist. These findings also imply that CDI⁺ bacteria exploit a common secretion mechanism (Aoki et al., 2010).

In *Burkholderia*, the CDI operon organization is different, constituted as bcpA1OB (*Burkholderia* CDI proteins A, I, O and B). The additional small protein BcPO was predicted to be a lipoprotein (Anderson et al., 2012). Sequence divergence of the *Burkholderia* cytotoxic domains is observed after a different conserved Nx(Q/E) LYN motif (Anderson et al., 2012; Nikolakakis et al., 2012).

**Receptor binding of CdiA proteins**

CdiA initially interacts with the BamA receptor of CDI-sensitive *E. coli* cells (Aoki et al., 2008). BamA is an essential, highly conserved protein participating in the β-barrel assembly machinery (BAM complex), required for the appropriate integration of proteins into the outer membrane (Webb et al., 2012). Replacement of bamA alleles with the *E. coli* MC4100 bamA, sensitizes other enterobacteria to the *E. coli* EC93 system CDIEC93. Vice versa, several heterologous bamA genes confer CDIEC93 resistance on *E. coli*. Sequence variation among enterobacterial BamA orthologs seems concentrated to three surface-exposed loops. Scrutiny of these stretches showed that the CdiAEC93-binding epitope is defined by the combination of two of these loops (loops 6 and 7). Though BamA sequence variation is quite high, only a limited number of loop sets seem to exist, suggesting that BamA⁶⁷ coli and CdiAEC93 fulfill a key role in self-nonself discrimination (Ruhe et al., 2013b). Using CdiA-specific antibodies it was found that CdiA from *E. coli* 536 is deposited onto the surface of target bacteria. The CdiA-CT is translocated into target cells, while the amino-terminal region stays at the surface, suggesting cleavage prior to translocation (Webb et al., 2013). One cleavage site is located at the amino-terminus, likely removing the signal peptide, while (at least) two other cleavage sites are situated within the carboxy-terminal portion of CdiA (Aoki et al., 2005). Furthermore, AcrB was identified as a potential CdiA downstream target (Aoki et al., 2008). Located in the inner membrane, this protein is part of a distinct multicomponent machine, exporting small molecules into the extracellular environment, hereby acting as a multidrug resistance pump (Nikaido & Pages, 2012). At this point it is still unclear however how the CdiA effector would exploit AcrB to deliver its toxin domain (Aoki et al., 2008).

Interestingly, knocking out additional proteins of the Bam and Acr multi-component machines does not affect CDI. This suggests that inhibition resulting from interactions between (parts of) CdiA with BamA or AcrB originates from novel, import-related functions of the latter proteins (Aoki et al., 2008). Key interaction partners for binding of CdiAs in other genera than *E. coli* remain undisclosed at this moment.
Biological activity of CdiA-CTs

The toxicity function of a CdiA is located at its C-terminus, therefore termed CdiA-CT. This small domain is bound and inactivated by a cognate immunity protein, called CdiI, protecting the CDI+ cells from auto-inhibition. Sequence heterogeneity suggests a wide range of toxic activities being displayed by CdiA-CTs (Aoki et al., 2010; Nikolakakis et al., 2012). The carboxy-terminal domain of CdiA3937-2 from Dickeya dadantii 3937 shares 35% identity with the pyocin S3 nuclease domain and was confirmed to exert DNase activity. On the contrary, the toxic domain of E. coli 536 cleaves tRNA (Aoki et al., 2010). In Burkholderia pseudomallei ten different CDI sequence types were identified based on polymorphisms within the cdiA-CT/cdiI coding regions. Three of these were found to display trRNA activity, based on their similarities with the cytotoxic domain of colicin E5 (Nikolakakis et al., 2012). HecA (or CdiAEC16) from D. dadantii EC16 carries a carboxy-terminal domain that resembles the rRNA from colicin E3 (Walker et al., 2004). Crystal structures of the CdiA-CT/CdiI complexes of a Zn2+-dependent DNase from E. coli EC869 and the trRNA from B. pseudomallei 1026b were solved, showing that each immunity protein binds and inactivates its cognate toxin in a unique way (Morse et al., 2012). Bioinformatic analysis predicts that several CDI toxins are nucleases, adenosine deaminases, ADP-ribosyl cyclases or metallopeptidases. Despite low sequence homology for the relatively short CdiA-CT domains and similarities with the cytotoxic domain of colicin E5, these toxins can be recognized by a well-conserved tripartite motif, PF04829, along with a well-conserved tripartite organization assists in recognizing potential CDI gene clusters in pseudomonads (Table 2, Table S2). These genomic regions are often poorly annotated due to the low level or even lack – of discernable sequence homology for the relatively short CdiA-CT domains and the small-sized CdiI proteins (Poole et al., 2011).

Interestingly, certain CdiA-CT/CdiI pairs are found in diverse bacterial clades. This suggests that cdiA-CT/cdiI gene pairs can be horizontally exchanged between bacteria. The modular nature of CdiAs is underlined by the observation that chimeric CdiAs are functional (Aoki et al., 2010). Additional cdiA-CT/cdiI gene pairs are often located downstream of the main cdi cluster. These toxin/immunity proteins pairs are called orphan modules as they seem displaced from their full-length CdiAs. As such these orphans do not encode functional CdiAs, though they may provide a reservoir for CdiA-CT/CdiI variation. They often contain insertion sequence elements and transposon-related genes, pointing to horizontal gene transfer as well (Poole et al., 2011).

CdiI as a protector from auto-inhibition

The cdiI gene is tightly linked to cdiA and encodes a small immunity protein that protects CDI+ cells from auto-inhibition (Aoki et al., 2005). Structures of two different CdiA-CT/CdiI complexes indicate that the interaction between both partners causes an occlusion of the active site, though the way this is achieved may be somehow different (Morse et al., 2012). The presence of a functional CdiI is sufficient to protect the strain from auto-inhibition (Aoki et al., 2009). CdiI immunity proteins are specific for their cognate CdiA-CTs but may display a high level of variability. Therefore, proper immunity will only be provided if a suitable antitoxin partner is present. Consequently CDI concerns a network of toxin/immunity protein pairs, each having the potential to mediate inter-strain competition (Aoki et al., 2010; Nikolakakis et al., 2012).

In D. dadantii EC16, a CDI immunity protein called VirA has been associated with plant virulence (Rojas et al., 2004). This effect could be explained in D. dadantii 3937, where a virA mutant is outcompeted when grown together with the wild-type strain on chicory (Aoki et al., 2010). Such mutant is viable under laboratory conditions but on plants expression of the associated toxin gene is induced, resulting in cell death due to the lack of protection by the cognate immunity protein.

Putative CDI systems of pseudomonads

The presence of diagnostic structural motifs (hemagglutinin repeats; Pfam families PF05594 and PF13332), secretory signature motifs (hemagglutination activity domain, PF05860) and carboxy-terminal border region (VENN motif, PF04829), along with a well-conserved tripartite organization assists in recognizing potential CDI gene clusters in pseudomonads (Table 2, Table S2). These genomic regions are often poorly annotated due to the polymorphic nature of the CdiA and CdiI proteins and the low level – or even lack – of discernable sequence homology for the relatively short CdiA-CT domains and the small-sized CdiI proteins (Poole et al., 2011).

In addition to D. dadantii, some P. syringae strains, as well as a few other phytopathogenic bacteria, are equipped with a gene cluster for a putative CDI system with DNase activity related to pyocin S3: P. syringae pv. theae ICMP 3923 (partially sequenced CdiA of > 1383 amino acids), Xanthomonas axonopodis pv. citri 306 (CdiA of 4753 amino acids; da Silva et al., 2002), and Pantoaea ananatis LMG 5342 (CdiA of 3728 amino acids; De Maayer et al., 2012). Sequence comparison of the corresponding predicted activity domains of CdiA and of the CdiI proteins (all in the range of 140–145 amino acids) supports an evolutionary relationship with the DNase and immunity modules of S3-type pyocins (Figs S2 and S3). A close homolog of the ICMP 3923 CdiA protein is encoded by the P. syringae pv. syringae SM genome (full-length protein of 6173 amino acids; GenBank Accession Number EPF67127), but the pyocin S3-like carboxy-terminal sequence is replaced by a domain of unknown
function, illustrating the polymorphic nature of such toxins. In the unannotated region downstream of \textit{P. syringae} SM \textit{cdiA} not only the putative cognate immunity gene is present, but also an orphan \textit{cdiA}-CT/\textit{cdiI} module. This gene pair encodes a small CdiA-like protein (only 155 amino acids) and immunity protein nearly identical in sequence to the CdiA-CT/immunity protein pair of \textit{P. syringae} and \textit{P. brassicacearum}.

Another example of apparent recruitment of a CdiA-CT/immunity module from a bacteriocin family is found for a putative CDI system of \textit{P. fluorescens} FH5 (Rhodes et al., 2013; Fig. 1). Phylogenetic analysis of the CT domain assigns these CdiA/CdiI components (5688/90 amino acids) to the colicin D family, suggesting that this domain assigns these CdiA/CdiI components (5688/90 amino acids) and immunity protein nearly identical in sequence to the CdiA-CT/immunity protein pair of \textit{P. syringae} (Table 2). In addition to the pyocin-like modules targeting DNA or RNA already described, 11 different types of CdiA toxins were identified, each with a conserved Rhs system (\textit{P. syringae} USA011; see Rhs elements as mediators of intercellular competition), both of unknown cytotoxic type, while others are still associated with sequence remnants of a CDI system (\textit{P. syringae} \textit{pv. tomato} T1) or putative S-type pyocin (\textit{P. gingeri} NCPPB 3146).

The lack of functional data for CDI-like proteins of pseudomonads does not preclude that they may be of importance for interactions between \textit{Pseudomonas} strains and other bacteria. Bioinformatic analysis of polymorphic cytotoxins has revealed the existence of a multitude of toxin modules and immunity proteins, in particular systems that affect nucleic acids. Many of these belong to recently defined \textit{P. syringae} \textit{pv. tomato} T1) or putative S-type pyocin (\textit{P. gingeri} NCPPB 3146).

<table>
<thead>
<tr>
<th>CDI protein</th>
<th>Immunity protein*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Name</td>
<td>Size</td>
</tr>
<tr>
<td>Burkholderia-like deaminase</td>
<td>5207</td>
</tr>
<tr>
<td>Burkholderia-like tRNase</td>
<td>3213–3563</td>
</tr>
<tr>
<td>ColD-like tRNase</td>
<td>5688</td>
</tr>
<tr>
<td>Endo U nuclease</td>
<td>5627–5644</td>
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<tr>
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<td>2776</td>
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<td>HNHC-HHH nuclease</td>
<td>4058</td>
</tr>
<tr>
<td>HNHC-LHH nuclease</td>
<td>4310</td>
</tr>
<tr>
<td>MafB19 deaminase</td>
<td>3484–3871</td>
</tr>
<tr>
<td>Pyocin S2-like DNase</td>
<td>&gt;1383</td>
</tr>
</tbody>
</table>

GenBank Accession Numbers are provided in Table S2.

*Product of gene located immediately downstream of toxin gene.

†Based on domain present in CT module; –, not assigned.

‡Number of amino acids or size range of different proteins.

§Pfam (PF) or SMART (SM); –, not defined.
Rhs elements as mediators of intercellular competition

Rearrangement hotspot (rhs) elements were initially identified in E. coli as genomic sites that promote recombination, based on their role in chromosome duplications (Lin et al., 1984). Later, these elements were detected in numerous other bacterial genera, including Pseudomonas. From a structural point of view, Rhs proteins share similarities with CdiA proteins, though the mechanism required for the secretion of the former seems to be different (Hayes et al., 2014). Similar to T6SSs, Rhs proteins have been associated with both bacterial/bacterial and bacterial/host interactions.

Structural features of Rhs proteins

Rhs proteins are large and typically comprise c. 1500 residues in Gram-negative bacteria. They are composed of a central repeat region constituted from tyrosine/aspartate (YD) repeat units (PF05593), unrelated to the hemagglutinin repeats from CdiA. This large domain is encoded by a GC-rich rhs region and is called the core. The number of YD repeats may vary, but overall this region displays a high degree of intra- and interspecies sequence conservation (Jackson et al., 2009). In front of the core, at the amino-terminus, a clade-specific domain is located. The carboxy-terminal domains of Rhs proteins are termed ‘tips’ and are separated from the core by a highly conserved 61-amino acid region. In Enterobacteriaceae, the latter is typified by a PXXXXDPXGL sequence at the end. The Rhs carboxy-terminal domains, referred to as Rhs-CTs, are encoded by GC-poor sequences and several of them share features with the toxin modules of CdiAs (Jackson et al., 2009). Comparative genomics indicated that the Rhs core domains and variable carboxy-terminal modules are evolutionarily decoupled, hinting that rhs diversity originates from recombination events (Jackson et al., 2009; Zhang et al., 2011). Interestingly, the toxin domain-encoding 3'-ends are also followed by small genes encoding self-immunity factors, called RhsI proteins, recognizing specifically their cognate toxin partners, similar to CdiA-CdiII and pyocin-type bacteriocin/immunity pairs (Poole et al., 2011; Koskiniemi et al., 2013). Furthermore, rhs loci are frequently followed by orphan modules, similar to the cdiA-CT/cdiI toxin/immunity gene pairs (see Biological activity of CdiA-CTs; Poole et al., 2011; Zhang et al., 2011). Generation of functional chimeric genes through recombination between such orphan rhs-CT and the main rhs can provide a competitive advantage, as was recently demonstrated in Salmonella Typhimurium LT2 populations subjected to experimental evolution in liquid culture and within a mouse host (Koskiniemi et al., 2014). Recent work indicates that Tsc5, a Rhs protein from P. aeruginosa PA01, requires the T6SS because it is dependent on ClpV/VgrG4 for its secretion (see Toxic effectors and immunity proteins of T6SSs in Pseudomonas; Whitney et al., 2014). Similar to this, RhsA and RhsB from D. dadantii 3937 have been associated with VgrGs for proper export (Koskiniemi et al., 2013).

Inhibitory activities of Rhs systems

The inhibitory function of Rhs proteins has been demonstrated in numerous studies, both in interbacterial and in bacterial/host interactions. Expression of the carboxy-terminal fragment of rhsA from E. coli initiates a toxic cellular effect. This effect could be impeded by the coexpression of a downstream gene (Vlazny & Hill, 1995), apparently functioning as an antitoxin module. Subsequently, Aggarwal and Lee demonstrated that the RhsA function interferes with transcription and translation, though the exact mechanism of its action remains unknown (Aggarwal & Lee, 2011). In P. savastanoi pv. savastanoi IITM317, a rhs-like genetic element was found to confer bacteriocin-like activity against multiple strains of the same pathovar. A highly homologous YD-repeat protein is also encoded by P. syringae pv. syringae B728a, though the respective Rhs-CTs share no discernable similarities. Analysis of the molecular size of the P. savastanoi inhibitor indicates that this Rhs protein is proteolytically cleaved (Sisto et al., 2010), reminiscent of the processing observed for CdiA proteins (see Receptor binding of CdiA proteins). Two Rhs proteins from D. dadantii 3937 and the distantly related cell wall-associated protein A (WapA) from Bacillus subtilis 168 carry polymorphic carboxy-terminal toxin domains that are accompanied by neutralizing immunity proteins (RhsI and WapI, respectively; Poole et al., 2011; Koskiniemi et al., 2013). These Rhs proteins are deployed to sustain growth inhibition of neighboring cells. The D. dadantii proteins harbor DNase domains, whereas WapA acts by tRNAse activity on tRNAArg. Interestingly, the secretion route of these proteins seems to be different. WapA appears to follow the general secretory pathway, directed by the presence of a cleavable Sec-secretion signal sequence, whereas the rhs genes from Dickeya are linked to hcp and vgrG genes, pointing toward T6SS-mediated translocation (see Structural features of Rhs proteins). As the T6S apparatus typically transports smaller effectors, cleavage of the Rhs protein may be required at some point (Koskiniemi et al., 2013).
In the enterohemorrhagic strain _E. coli_ O26:H7, it was found that intestinal colonization of calves is disturbed in a _rhsA_ insertion mutant (van Diemen et al., 2005). The presence of a _rhs_ gene in an endosymbiotic bacterium of aphids was associated with increased survival following attack by parasitic wasps (Degnan & Moran, 2008). XadM, a Rhs family protein identified in _Xanthomonas oryzae pv. oryzae_ BXO43, with several homologs in other _Xanthomonas_ and _Burkholderia_ strains, is required for attachment, biofilm formation and virulence to rice. Its carboxy-terminus displays similarity to a domain of unknown function (NLPC_P60) detected in several lipoproteins (Pradhan et al., 2012). The _rhsT_ gene located on the genomic island PAGI-9 of _P. aeruginosa_ PSE9 encodes a virulence protein that is delivered to eukaryotic cells and activates the inflammasome (Kung et al., 2012). The presence of two conserved histidines in the toxic domain of RhsT suggests that this protein acts as a RNase A-like nuclease (Zhang et al., 2013). Similar to _Dickeya_, a _rhs_ element accompanied by a _hcp_ and a _vgrG_ gene, was found in _P. aeruginosa_ PA14. There was no evidence, however, that this Rhs protein was an effector of the associated T6SS (Jones et al., 2014).

In the enterohemorrhagic strain _E. coli_ O26:H7, it was found that intestinal colonization of calves is disturbed in a _rhsA_ insertion mutant (van Diemen et al., 2005). The presence of a _rhs_ gene in an endosymbiotic bacterium of aphids was associated with increased survival following attack by parasitic wasps (Degnan & Moran, 2008). XadM, a Rhs family protein identified in _Xanthomonas oryzae pv. oryzae_ BXO43, with several homologs in other _Xanthomonas_ and _Burkholderia_ strains, is required for attachment, biofilm formation and virulence to rice. Its carboxy-terminus displays similarity to a domain of unknown function (NLPC_P60) detected in several lipoproteins (Pradhan et al., 2012). The _rhsT_ gene located on the genomic island PAGI-9 of _P. aeruginosa_ PSE9 encodes a virulence protein that is delivered to eukaryotic cells and activates the inflammasome (Kung et al., 2012). The presence of two conserved histidines in the toxic domain of RhsT suggests that this protein acts as a RNase A-like nuclease (Zhang et al., 2012a). These different studies underline the diverse role of Rhs proteins as secreted toxins but also add to the role of these systems in bacterial pathogenesis.

**Rhs polymorphic domains in pseudomonads**

Functional data on Rhs proteins from pseudomonads is still limited at this point. Consequently, their role in interbacterial competition processes is hard to predict. Similar to CdiA proteins, a multitude of cytotoxic domains appears to be encoded by these Rhs elements, primarily affecting nucleic acids (Zhang et al., 2011, 2012a). Scrutiny of pseudomonad genomes for gene clusters encoding Rhs systems with a known type of toxin and immunity domain (Pfam and SMART databases) indicates the presence of a large array of strain-specific toxin modules (Table 3). Although it cannot be excluded that some of the Rhs proteins (also) play a role in interaction of pseudomonads with a eukaryotic host (as demonstrated for the virulence factor RhsT of _P. aeruginosa_ PSE9; Kung et al., 2012), most likely their primary function lies in competition with other bacteria. In addition to the pyocin-like modules targeting DNA or RNA and putative nuclease-active CDI systems already described, 20 different types of Rhs proteins were identified, nearly all of them targeting nucleic acids (Table 3, Table S2). Many of these belong to recently defined DNase families of the HNH superfamily (Zhang et al., 2012a). Although the _rhs_ loci are often incompletely annotated, it is clear that much more Rhs proteins are encoded by pseudomonad genomes. However, their highly diverse carboxy-terminal domain and immunity partner protein often cannot be assigned to a particular protein family.

**Pseudomonas fluorescens** NCIMB 11764 carries a Rhs protein with a carboxy-terminal _Toxin_ 61 domain, the latter homologous to the _P. aeruginosa_ _Tse6-CT_ domain (Whitney et al., 2014). It appears that some of the toxin modules of Rhs proteins share a common ancestry with certain S-type pyocins. A HNH domain predicted to confer DNase activity is present in a Rhs protein of _P. syringae pv. syringae_ SM but its immunity partner lacks discernable homology with those of the HNH-type pyocins (Table 3). The RhsB protein of another phytopathogen, _D. adiantii_ 3937, is equipped with a similar carboxy-terminal module/immunity protein combination and mediates _T6SS_-dependent intercellular competition relying on its capacity to degrade target cell DNA (Koskineni et al., 2013). A Rhs protein bearing a pyocin _S6_ S7-related rRNase domain and cognate immunity protein was identified in _P. putida_ S16 (Yu et al., 2011). By one of the _rhs_ loci of _P. entomophila_ L48 (Vodovar et al., 2006), a colicin D-like Rhs protein/immunity pair (putative _tRNase_ activity) is encoded (Table 3; Fig. 1). The L48 Rhs cytotoxic domain is most similar to the CdiA-CT domain of _P. fluorescens_ FH5, but quite distant from the _rRNase_ modules of pyocins S11 and S12, suggesting a different ancestry for the enzymatic modules present in these pyocins, on the one hand, and those incorporated in the polymorphic toxins, on the other hand (Fig. S5). The colicin _D_ type of immunity gene was also detected in _P. syringae_ USA011, located in the polymorphic region downstream of the genes encoding a conserved Rhs system of unknown cytotoxic type. Apparently, acquiring and maintaining individual immunity genes may contribute to protection against toxins from competitors.

**Lectin-like bacteriocins**

The first lectin-like bacteriocin was identified in banana rhizosphere isolate _P. putida_ BW11M1 as a secreted heat- and protease-sensitive chromosome-encoded antibacterial protein, able to kill other plant-associated _Pseudomonas_ strains (Parret et al., 2003). Similar bacteriocins were characterized in _P. putida_ (Parret et al., 2005), _P. syringae_ (Ghequire et al., 2012b) and _P. aeruginosa_ (McCaughhey et al., 2014), though sequence homology proved to be low. Contrary to _S_ -type pyocins, lectin-like bacteriocins do not bear a known cytotoxic domain, nor do they require an immunity protein to prevent autoinhibition (Parret et al., 2003).
Table 3. Predicted Rhs toxins with known CT domains and corresponding immunity proteins in Pseudomonas genomes

<table>
<thead>
<tr>
<th>Name*</th>
<th>Size†</th>
<th>CT domain‡</th>
<th>Name*</th>
<th>Size†</th>
<th>Domain‡</th>
<th>Strains</th>
</tr>
</thead>
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<tr>
<td>ColD-like tRNase</td>
<td>1502</td>
<td>PF11429</td>
<td>Colicin immunity</td>
<td>96</td>
<td>PF9204</td>
<td>P. entomophila L48</td>
</tr>
<tr>
<td>ColE3-like 16S rRNase</td>
<td>417</td>
<td>PF09000</td>
<td>–</td>
<td>84</td>
<td>–</td>
<td>P. putida S16</td>
</tr>
<tr>
<td>DYW deaminase</td>
<td>410</td>
<td>–</td>
<td>Imm5</td>
<td>193</td>
<td>PF14423</td>
<td>P. syringae pv. glycinea B076, P. syringae pv. phaseolicola 1448a</td>
</tr>
<tr>
<td>HNH-AHH nuclease</td>
<td>1107–1400</td>
<td>PF14412</td>
<td>–</td>
<td>176–199</td>
<td>–</td>
<td>P. plecoglossicida NB2011, P. putida DOT-T1E, P. putida F1, P. putida ND6, P. syringae BRIP39023</td>
</tr>
<tr>
<td>HNHc nuclease</td>
<td>881</td>
<td>SM000507</td>
<td>–</td>
<td>158</td>
<td>–</td>
<td>P. syringae pv. syringae SM</td>
</tr>
<tr>
<td>HNH-EEHH nuclease</td>
<td>1569–1603</td>
<td>PF15657</td>
<td>Imm30</td>
<td>130–134</td>
<td>PF15549</td>
<td>P. fluorescens SBW25, P. fluorescens SS101, P. poae RE*1-1-14, P. syxantha BGR33, P. syringae ICMP 18806</td>
</tr>
<tr>
<td>HNH-GH-E nuclease</td>
<td>1399</td>
<td>PF14410</td>
<td>YjeC-like</td>
<td>108</td>
<td>PF09639</td>
<td>P. syringae BRIP34881</td>
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<td>HNH-GHH nuclease</td>
<td>1484</td>
<td>PF15636</td>
<td>SUKH-1</td>
<td>199</td>
<td>PF09346</td>
<td>Pseudomonas sp. TPK</td>
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<td>PF15635</td>
<td>–</td>
<td>188</td>
<td>–</td>
<td>P. putida S16, P. monteilii SB3078</td>
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<td>HNH-LHH nuclease</td>
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<td>PF14411</td>
<td>SUKH-6</td>
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<td>P. putida DOT-T1E, P. syringae BRIP34881</td>
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<td>HNH-SHH nuclease</td>
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<td>PF15652</td>
<td>SUKH-1</td>
<td>161–197</td>
<td>PF09346</td>
<td>P. putida KT2440, P. plecoglossicida NB2011</td>
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<tr>
<td>HNH-WHH nuclease</td>
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<td>PF14414</td>
<td>SUKH-1</td>
<td>136–157</td>
<td>PF09346</td>
<td>P. brassicaevarum subsp. brassicaevarum NFM421, P. fluorescens F113, P. fluorescens Q2-87, P. poae RE*1-1-14, P. putida W619</td>
</tr>
<tr>
<td>HYD1 ADP-ribosyltransferase</td>
<td>1534–1537</td>
<td>PF15633</td>
<td>–</td>
<td>97–212</td>
<td>–</td>
<td>P. poae RE*1-1-14, P. putida SPM58</td>
</tr>
<tr>
<td>NS endonuclease</td>
<td>1407–1599</td>
<td>PF13930</td>
<td>DUF1963</td>
<td>220–222</td>
<td>PF09234</td>
<td>P. chlororaphis subsp. aureofaciens 30–84, Pseudomonas sp. GM41</td>
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<td>–</td>
<td>NTF2 fold</td>
<td>97–150</td>
<td>PF15655</td>
<td>P. syringae BRIP34881, P. syringae pv. glycinea B076, P. syringae pv. syringae B64, Pseudomonas sp. GM55, Pseudomonas sp. VLB120</td>
<td></td>
</tr>
<tr>
<td>P.put2613-deaminase</td>
<td>866–1560</td>
<td>PF14427</td>
<td>Imm7</td>
<td>127–131</td>
<td>PF15588</td>
<td>P. entomophila L48, P. putida ND6</td>
</tr>
<tr>
<td>Toxin 61</td>
<td>1631</td>
<td>PF15538</td>
<td>–</td>
<td>90</td>
<td>–</td>
<td>P. fluorescens NCIMB 11764</td>
</tr>
<tr>
<td>URI nuclease</td>
<td>898–1562</td>
<td>PF15653</td>
<td>DUF2384</td>
<td>93–95</td>
<td>PF09722</td>
<td>P. fluorescens SBW25, P. mendeli 36MCv11.1</td>
</tr>
<tr>
<td>–</td>
<td>–</td>
<td>Imm25</td>
<td>135–144</td>
<td>PF15655</td>
<td>P. fluorescens B6c688, Pseudomonas sp. Ag1, Pseudomonas sp. VLB120</td>
<td></td>
</tr>
<tr>
<td>Ywql-like deaminase</td>
<td>1561</td>
<td>PF14431</td>
<td>–</td>
<td>120</td>
<td>–</td>
<td>Pseudomonas sp. GM80</td>
</tr>
</tbody>
</table>

GenBank Accession Numbers are provided in Table S2.
*Product of gene located immediately downstream of toxin gene.
†Based on domain present in CT module; –, not assigned.
‡Number of amino acids or size range of different proteins.
§PFam (PF) or SMART (SM); –, not defined.

Structure and domain organization of lectin-like bacteriocins

The first identified member of this novel family of antibacterial proteins was called LpA, abbreviation for lectin-like putidacin A and referring to its remarkable sequence homology with monocot mannose-binding lectins (MMBLs) from plants (Parret et al., 2003). In the latter organisms, these carbohydrate-binding proteins have been associated with a number of antimicrobial activities, such as antifungal, antiviral, or nematicidal action, though no antibacterial plant MMBL has been identified at this point (Ghequire et al., 2012a). The amino acid sequence of LpA suggests the presence of a tandem of such MMBL domains, followed by a short, highly variable carboxy-terminal extension that does not occur in plant MMBLs (Parret et al., 2003; Van Damme et al., 2008). Monocot mannose-binding lectin domains typically adopt
a β-prism fold, stabilized by a conserved tryptophan triad, and harbor three potential carbohydrate-binding pockets, each set up by a conserved QxDxNxxVxY sequence motif (with x, any amino acid). However, motif degeneracy suggests that several of these sites may be inactive in LlpAs (Ghequire et al., 2012a; McCaughey et al., 2014). The size of the MMBL domain is c. 12 kDa, resulting in a rather narrow molecular weight range of 28–32 kDa for LlpAs, contrary to S-type pyocins where considerable size variation is observed (Table 1).

The crystal structure of the prototype LlpA from *P. putida* BW11M1 revealed a rigid, tightly interconnected, tandem MMBL structure sharing unequivocal similarities with plant MMBLs (Fig. 10; Parret et al., 2004; Ghequire et al., 2013a). More recently, the structure of pyocin L1, a distant LlpA homolog from *P. aeruginosa* C1433 sharing c. 27% amino acid identity, was elucidated, displaying a similar lectin architecture but apparently more closely related to dimeric plant lectins due to a different relative orientation of the MMBL modules (McCaughey et al., 2014). Loyal to their protein family, these LlpAs were found to act as genuine lectins though binding to mannose and oligomannosides is rather weak (Ghequire et al., 2013a; McCaughey et al., 2014), hinting to another preferred carbohydrate ligand. Recently it was found that these tandem MMBLs bind D-rhamnose with higher affinity (McCaughey et al., 2014). Consistent with this, binding to CPA, the *P. aeruginosa* common polysaccharide antigen that is predominantly composed of D-rhamnosyl residues (Lam et al., 2011), was demonstrated. Furthermore, lipopolysaccharide mutants in CPA biosynthesis genes were shown to be almost insensitive to pyocin L1. Further support for D-rhamnose-containing lipopolysaccharide acting as a receptor for these MMBL lectins stems from the capacity of *P. putida* LlpA to bind lipopolysaccharide of sensitive *P. syringae* cells (McCaughey et al., 2014). The ability to bind carbohydrates could only be attributed to the second, carboxy-terminal MMBL domain. The construction of *P. putida*–*P. protegens* chimeric LlpA forms revealed that the amino-terminal MMBL module hosts the target specificity function (Ghequire et al., 2013a).

**Occurrence of MMBL bacteriocins**

Originally identified in a *P. putida* rhizosphere isolate, whole-genome sequencing projects have revealed a number of putative LlpAs in other *Pseudomonas* strains. The occurrence of *llpA* sequences seems biased toward plant- and soil-associated isolates, and it is tempting to speculate about plant-to-bacterium transfer of the ancestral prokaryotic genes (Ghequire et al., 2012a; Loper et al., 2012). Next to LlpA from *P. putida* BW11M1, narrow-spectrum antibacterial activity was also assigned to two proteins in biocontrol strain *P. protegens* Pf-5, called LlpA1 and LlpA2 (Fig. 1), with near identical amino acid sequences and indistinguishable target spectrum (Parret et al., 2005). More recently, a *P. syringae* LlpA (Ghequire et al., 2012b) and a *P. aeruginosa*-specific LlpA (Fig. 1; McCaughey et al., 2014) were demonstrated to act as functional bacteriocins as well. One peculiar characteristic of these LlpAs is their overlapping activity spectrum: a strain

![Fig. 10. Ribbon structures of lectin-like bacteriocins *Pseudomonas putida* LlpA (a, PDB 4GC2) and *Pseudomonas aeruginosa* pyocin L1 (b, PDB 4LED). Oligomannoside (GlcNAcβ(1→2)Manα(1→3)(GlcNAcβ(1→2)Manα(1→6)Man) in complex with LlpA and D-rhamnose residues in complex with pyocin L1 are shown as spheres bound to the respective carboxy-terminal MMBL domains.](https://academic.oup.com/femsre/article-abstract/38/4/523/754873)
may be sensitive to more than one LlpA, even if sequence homology between the amino-terminal domains of the LlpAs involved is barely present. Tandem-MMBL bacteriocins were also retrieved in two Xanthomonas pathovars (Ghequire et al., 2012b) and in Burkholderia cenocepacia (Ghequire et al., 2013b), equally displaying genus-specific activity.

The sequence divergence among currently known LlpA proteins is visualized in Fig. S10. The most distant Pseudomonas sequences share only 27% amino acid sequence identity, mostly focused around the MMBL motifs and the MMBL-stabilizing tryptophan triads. No obvious correlation is apparent between the LlpA sequence-based phylogeny and taxonomic relatedness of the respective producers, suggesting LlpAs to act as highly diversified niche-specific molecular weapons. Considering the limited number of identified llpA genes, it appears that LlpA production is relatively rare among pseudomonads, compared to the abundance of pyocin-like bacteriocins. The llpA clusters from recently sequenced P. aeruginosa genomes extend the occurrence of these antimicrobials to a human pathogenic pseudomonad. At this point, it remains unclear how MMBL bacteriocins are released by their producer strains as Pseudomonas LlpAs are typically not preceded by a cleavable signal sequence. Exception to this are the proteins encoded by one of the P. aeruginosa clusters, apparently following a different Sec-dependent route (Fig. S10).

Phylogenetic analysis of individual MMBL modules unveiled a clustering of the amino-terminal MMBL domains, separate from clustered branches with carboxy-terminal domains (Ghequire et al., 2012a). The latter is consistent with the domain-function segregation demonstrated for P. putida–P. protegens LlpA chimeras (Ghequire et al., 2013a). Higher sequence conservation of the carboxy-terminal MMBL may be imposed by binding to a common lipopolysaccharide moiety. Conversely, the amino-terminal domains evolved rather independently to define diversified target spectra.

Genome mining of MMBL domains among pseudomonads also revealed a second type of putative lectin-like bacteriocin (Ghequire et al., 2012a), which we call LlpB (Fig. 1). Consisting of only a single MMBL domain, these LlpBs equally carry a poorly conserved carboxy-terminal extension. Initial assays with recombinantly produced LlpBs indicate that these proteins are functional bacteriocins as well (Ghequire, 2013).

**Lectin-like bacteriocins as a cargo in Pseudomonas prophages**

Similar to pyocin M2 and some of its homologs, a number of lectin-like bacteriocins are also encoded by cargo genes of putative prophages. In *P. syringae* pv. *syringae* 642, this is the case for both a pyocin M2 and a LlpA homolog, albeit in different prophages and unlinked genomic locations. A similar prophage carrying a llpA-like gene is present in the *Pseudomonas* sp. GM80 genome, whereas its counterpart in *P. fluorescens* A506 has taken up an llpB gene (Fig. 1). In *Pseudomonas* sp. GM80, a second distinct llpA gene is equally located on a prophage that has inserted in the mutS-cinA intergenic region and the latter configuration is also found in *P. chlororaphis* subsp. *aureofaciens* 30–84 for yet another llpA gene. Like strain GM80, *P. protegens* Pf-5 also displays a dual LlpA bacteriocinogeny (Parret et al., 2005). LlpA1 of this strain is encoded by a cargo gene on prophage-1, equally integrated between the mutS and cinA genes, whereas its llpA2 gene is located in the defective prophage-4 region (Mavrodi et al., 2009). The llpA2 gene is also present in *P. protegens* CHA0, a strain closely related to Pf-5 (Jousset et al., 2014), but only a short prophage-4 remnant remains, apparently due to a c. 10-kb deletion in the llpA2 upstream region. The llpA1 gene is lacking in this strain. Actually, its mutS–cinA hotspot has been targeted by the same type of llpA-carrying phage as present in *Pseudomonas* sp. GM80 and *P. chlororaphis* subsp. *aureofaciens* 30–84, however, without bringing an LlpA cargo. The high sequence similarity between LlpA1 and LlpA2 of *P. protegens* Pf-5, exhibiting indistinguishable activity spectra (Parret et al., 2005), suggests that LlpA1 may have been acquired more recently and is maintained to enable further divergence of the both bacteriocin genes toward a broader antagonistic spectrum.

**Regulation of LlpA synthesis**

At this point, only limited information is available on the regulation of llpA genes. Constitutive expression has been observed for the LlpAs of *P. putida* BW11M1 and *P. protegens* Pf-5 (Parret et al., 2003, 2005), and – similar to S-type pyocins – LlpA*BW11M1* production is enhanced upon exposure to UV light (Parret et al., 2003). For the *P. putida* bacteriocin, reduced production was detected upon recA and *spoT* inactivation, similar to S-type pyocins (see Regulation of pyocin expression in *P. aeruginosa*). Conversely, a recA mutant exhibited an overexpression phenotype (de los Santos et al., 2005).

**Thiazole-/oxazole-modified microcins**

**Microcin B-like bacteriocins of *P. syringae***

In contrast to their capacity to produce very diverse secondary metabolites (Gross & Loper, 2009), pseudomonads are not endowed with elaborate tools for post-translational
modification of ribosomally synthesized peptides (Arnison et al., 2013). Recently, the genetic capacity to produce B-type microcins was however demonstrated for strains of the *P. syringae* pathovars *glycinea* and *acescii* by genome exploration with genes of the *E. coli* microcin B17 (Ec-Mcb) operon mcABCDEF as queries (Metelev et al., 2013). The DNA glyrase inhibitor microcin B17 is derived from the ribosomally synthesized McbA precursor by extensive post-translational processing (reviewed by Duquesne et al., 2007; Severinov et al., 2007). The McbA leader peptide drives substrate binding by the McbBCD complex that converts selected serine and cysteine residues to azoles or thiazoles by consecutive McbCD-mediated ATP-dependent cyclodehydration (Dunbar et al., 2012) and McbB-catalyzed dehydrogenation. The unmodified leader peptide is proteolytically removed by conserved enzymes (TldD, TldE) prior to export by the dedicated ABC transporter McbEF. Both this transporter and McbG contribute to self-immunity of the microcin B-producing *E. coli* cells.

In two *P. syringae* strains, an equivalent mcABCDEF operon was identified, but production of a microcin-like compound was not detected, albeit active mcb transcription was demonstrated (Metelev et al., 2013). However, two biologically active glyrase-targeting microcins, Ps-McB1 (minor product) and Ps-McB2 (major product with the five McbA carboxy-terminal amino acids lacking), were produced by *E. coli* carrying the *P. syringae* mcba gene cluster. Two mcba-lacking *P. syringae* strains and *P. aeruginosa* PAO1 were found susceptible to both Ps-McBs. While these pseudomonads are not susceptible to Ec-Mcb, *P. syringae* microcin exhibits anti-*E. coli* activity. By using chimeric mcba genes, Metelev et al. (2013) identified a centrally located unmodified tri-glycine moiety as a key determinant for activity against the pseudomonads, apparently required for uptake by a specific, as yet unidentified transporter.

**Microcinogenic potential of pseudomonads**

Scrutiny of currently available genome sequences of pseudomonads indicates that several strains of different species are potential producers of microcin B-like bacteriocins, as inferred from the presence of an equivalent mcABCDEF cluster, however, consistently lacking mcbG (Fig. 1). The mcb clusters, which are often incompletely annotated, are not located in a particular genomic region of these strains. The azole-thiazole pattern in mature Ec-Mcb and Ps-McB peptides is essentially the same, but more diversity among putative B-type microcins from other *Pseudomonas* strains is potentially present in the deduced McbA amino acid sequences (Fig. 11). On both sides of the conserved central glycine triplet, the presence of potential modification sites allows for patterns different from those of *E. coli* and *P. syringae* microcins. The sequence divergence is also apparent for the respective leader sequences. This trend is reflected in the phylogenetic relationship among the cognate synthetase and transporter proteins, indicating that, unexpectedly, the *P. syringae* microcin assembly system is actually more similar to the *E. coli* machinery (including the presence of the McbG protein) in comparison to the putative Mcb proteins in other pseudomonads. No equivalent *mcba* gene cluster was found in one of the many available *P. aeruginosa* genome sequences. It appears that microcin production is relatively rare among pseudomonads compared with the abundance of pyocin-like bacteriocins.

**General discussion**

Current knowledge on pseudomonad bacteriocins is largely based on early study carried out with *P. aeruginosa* to characterize the antagonistic behavior observed among strains of this pathogenic species. When this aspect of pseudomonad sociomicrobiology was reviewed by
Michel–Briand and Baysse (Michel-Briand & Baysse, 2002), two main different types of DNA-degrading S-type pyocins and two main sorts of phage tail-like particles (R and F pyocins) had been identified. Subsequently, cytotoxic activities that were initially discovered in colicins from E. coli, targeting RNA or disrupting cell envelope integrity, were also assigned to S-type pyocins. However, insights in the biology of these pseudomonad, bacteriocins is lagging behind the colicin field, in particular with respect to structural characterization which is instrumental to elucidate how these proteins reach their target. Some recent additions to the armamentarium of pseudomonads are B-type microcins and lectin-like bacteriocins, the latter not (yet) known to be produced by enterobacteria.

Inspection of currently available pseudomonad genome sequences provides a glimpse inside the bacteriocin profiles of these bacteria and highlights the strain-specific nature of bacteriocinogeny. Even within the P. aeruginosa species, considered to be a phylogenetically well-defined entity, few strains display the same bacteriocinogenic profile. This is illustrated in Fig. 12 in which the known bacteriocins of the model strain P. aeruginosa PAO1 are compared with 52 different bacteriocin gene combinations predicted for individual strains. In P. aeruginosa, the systems acting on nucleic acids (DNA or RNA) predominate together with the widespread tailocins. The latter class of bacteriocins, evolutionary related to phages, is relatively rare among other Pseudomonas species and is confined to two subtypes of R-like pyocins. These predicted tailocin systems differ from their P. aeruginosa counterparts not only in the host specificity determinants and lysis cassettes used but also in the regulatory modules. Furthermore, these mobile units are integrated at a different but specific genomic location and seem apt to expansion with cargo genes. Certain bacteriocin genes are also loaded onto prophages, as noted for some members of the pyocin M and LlpA families. Such hitchhiking is reminiscent of prophage-carried eukaryote-targeting toxins such as Stx and Dtx (diphtheria toxin) that can assist in defense of their bacterial-host population against bacteria-predating amoebae (Arnold & Koudelka, 2014). The assembly and fine structure of pseudomonad tailocins is an unexplored field and application of a structural biology approach, as currently used to elucidate the intricacies of the T6S toxin delivery system – also sharing features with certain phages – is likely to provide new insights in the mode of action of this killing machinery.

Categorization of S-type pyocins based on their carboxy-terminal cytotoxic domains further highlights their dynamic modular architecture. It was already described in P. aeruginosa that the same receptor-recognition domain can be fused to a different HNH-type DNase domain present in pyocins S1 and S2. Genomic analysis shows that certain receptor-recognition domains are also polyvalently employable with toxin modules of a different nature (Fig. 1). Such domain sharing occurs between a HNH DNase and a rRNase in both P. aeruginosa and P. chlororaphis, and between a non-HNH DNase and a tRNase among P. aeruginosa strains. Combinations of a HNH DNase, a non-HNH DNase or a tRNase with a particular receptor-recognition domain are found in different P. aeruginosa strains. Proof-of-principle that this modularity can be exploited to engineer bacteriocins with novel target specificities or equipped with a different type of warhead has already been delivered. The functionality of certain pyocin–colicin chimeras shows that this mimicry of Nature’s recombinational strategy is not constrained by genus limits. A conceptually similar strategy can even be applied to tailocins by transposing insights from phage biology to these complex bacteriocins, enabling the construction of inter-generic tailocin hybrids with new functionalities by exchange of tail fiber genes.

Some novel features not associated with P. aeruginosa bacteriocins emerge from the genomic perspective on bacteriocinogeny broadened to other members of the Pseudomonas genus. This highlights the huge genetic diversity contributed by other pseudomonad species, being most prominent for strains originating from plant and soil environments (Fig. 13). Microcin-encoding gene clusters were not yet identified in P. aeruginosa but are present in several other species. Although nucleic acids are equally the preferred target in species other than P. aeruginosa, the widespread occurrence and broad diversity of predicted rRNase bacteriocin genes, encoding a novel type of cytotoxic activity only recently described for P. aeruginosa and present in only few of its strains, is striking. Certain strains dispose of an expanded offensive arsenal composed of multiple bacteriocins, in particular enzymes of the HNH DNase and rRNase types. On the other hand, strains tend to enlarge their defensive capacity against intruding toxins from competitors by expanded immunity loci or acquisition of orphan immunity genes. Of particular interest are three different types of hybrid genes that encode putative bacteriocins with two different cytotoxic modules integrated in a single polypeptide. Conceivably, such dual mode of action may enhance the efficacy of a bacteriocin-mediated strike, as tolerance of the attacked to two different cytotoxic agents is less likely.

Whereas little is known how various types of pyocins are secreted, studies with P. aeruginosa have contributed substantially to recognition of the important role played by T6S-translocated effector molecules in antagonistic interactions with rival bacteria. Though not yet well understood in pseudomonads, conceptually similar strategies, making use of T5S-translocated CDI-mediating substances and of
Rhs protein release, appear to be at hand for pseudomonads. The modular nature of pyocins is reflected in the general architecture of CdiA and Rhs proteins. Apparently, these three classes of toxins share certain types of cytotoxic modules, along with cognate self-protective immunity proteins. Whereas most predicted pyocin gene products can be assigned to a known group of pyocins or colicins, the equally carboxy-terminally located cytotoxic modules seem to have diversified to a much larger extent in CdiA proteins and Rhs proteins, warranting their classification as polymorphic toxins. With only few of such toxin modules being functionally characterized and many escaping sequence homology-based familial assignment, it is clear that a considerable part of the ribosomally encoded armory remains to be uncovered. Nevertheless, it seems that the use of the nucleic acid-targeting strategy, dominating S-type pyocin action, is also deployed frequently with these polymorphic toxins.

The functionality of many of the bacteriocin genes described in this review, including divergent members of known groups as well as representatives of novel groups, requires experimental validation. Often, expression of bacteriocin genes in a natural host cannot be provoked in laboratory conditions. Hence, identification of the environmental factors triggering production of bacteriocins is another imperative toward assessment of their ecological role in bacterial rivalry and of their impact on populations of related bacteria favoring similar niches.

**Fig. 12.** Bacteriocin profiles of *Pseudomonas aeruginosa* strains. The bacteriocin complement of strain PAO1 is compared to the predicted bacteriocin profiles of representative strains carrying genes or gene clusters for at least two different types of bacteriocins. The presence of a particular type of bacteriocin gene or gene cluster, classified by assigned/predicted toxic domain or mode of action, is indicated by colored dots.

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The stimuli that activate bacteriocin-mediated warfare may differ among particular niches, such as plant rhizospheres colonized by saprophytic bacteria or eukaryotic host tissues invaded by pathogenic, symbiotic, or endophytic bacteria.

Acknowledgements

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Protein-mediated warfare among pseudomonads


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**Supporting Information**

Additional Supporting Information may be found in the online version of this article:

**Fig. S1.** Phylogenetic analysis of HNH DNase pyocin immunity proteins.

**Fig. S2.** Phylogenetic analysis of the cytotoxic domains of non-HNH DNase pyocins.

**Fig. S3.** Phylogenetic analysis of non-HNH DNase pyocin immunity proteins.

**Fig. S4.** Phylogenetic analysis of cytotoxic domains of bacteriocins with a colicin D-like tRNase domain.

**Fig. S5.** Phylogenetic analysis of colicin D-like immunity proteins.

**Fig. S6.** Phylogenetic analysis of immunity proteins associated with pyocin S6-like rRNase bacteriocins.

**Fig. S7.** Sequence alignment of amino-terminal regions of lipid II-degrading M pyocins.

**Fig. S8.** Phylogenetic analysis of tail fiber proteins of F pyocins.

**Fig. S9.** Sequence alignment of CdiA-CT tRNase domains.

**Fig. S10.** Phylogenetic analysis of tandem-MMBL bacteriocins.

**Table S1.** Bacteriocin/pyocin genes present in genome sequences of pseudomonads.

**Table S2.** Genes encoding Rhs or CDI proteins present in genome sequences of pseudomonads.