The minor groove-binding agent ELB-21 forms multiple interstrand and intrastrand covalent cross-links with duplex DNA and displays potent bactericidal activity against methicillin-resistant Staphylococcus aureus

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Objectives: The antistaphylococcal pyrrolobenzodiazepine dimer ELB-21 forms multiple adducts with duplex DNA through covalent interactions with appropriately spaced guanine residues; it is now known to form interstrand and intrastrand adducts with oligonucleotide sequences of variable length. We determined the DNA sequence preferences of ELB-21 in relation to its capacity to exert a bactericidal effect by damaging DNA.

Methods: Formation of adducts by ELB-21 and 12- to 14-mer DNA duplexes was investigated using ion-pair reversed phase liquid chromatography and mass spectrometry. Drug-induced changes in gene expression were measured in prophage-free Staphylococcus aureus RN4220 by microarray analysis.

Results: ELB-21 preferentially formed intrastrand adducts with guanines separated by three nucleotide base pairs. Interstrand and intrastrand adducts were formed with duplexes both longer and shorter than the preferred target sequences. ELB-21 elicited rapid bactericidal effects against prophage-carrying and prophage-free S. aureus strains; cell lysis occurred following activation and release of resident prophages. Killing appeared to be due to irreparable damage to bacterial DNA and susceptibility to ELB-21 was governed by the capacity of staphylococci to repair DNA lesions through induction of the SOS DNA damage response mediated by the RecA-LexA pathway.

Conclusions: The data support the contention that ELB-21 arrests DNA replication, eliciting formation of ssDNA-RecA filaments that inactivate LexA, the SOS repressor, and phage repressors such as Cl, resulting in activation of the DNA damage response and de-repression of resident prophages. Above the MIC threshold, DNA repair is ineffective.

Keywords: antistaphylococcal activity, pyrrolobenzodiazepine dimer, DNA cross-linking, DNA adduct formation, MRSA

Introduction

ELB-21 (Figure 1) is a pyrrolo[2,1-c][1,4]benzodiazepine (PBD) dimer that shows potent in vitro bactericidal activity against a wide range of Gram-positive clinical isolates, including methicillin-resistant strains of Staphylococcus aureus (MRSA) and vancomycin-resistant enterococci (VRE).1 This symmetrical agent belongs to a class of molecules that binds in a sequence-selective manner the minor groove of the DNA helix and cross-links opposing DNA strands by forming covalent bonds with appropriately separated guanine residues.2-4 The five-carbon diether linking the PBD units (Figure 1) facilitates preferential interstrand binding to 5′-Pu-GATTC-Py and 5′-Pu-GAATC-Py base-pair sequences (Pu, purine; Py, pyrimidine; reactive guanines shown in bold). Recently DNA footprinting studies using substrates containing symmetrical hexanucleotide sequences enabled the identification of further high-affinity binding sites: 5′-GAATTC-3′, 5′-GTTAAC-3′ and 5′-GTAAC-3′, flanked by a Pu at the 5′ and a Py at the 3′ end.1 In addition, a number of intrastrand binding sites were identified that may also block DNA replication and contribute to the potent antistaphylococcal profile of ELB-21. These sequences, which were not predicted from initial molecular modelling studies,5 included short (5′-GA4-3′) and extended (5′-GTTAACC-3′) flanked targets.
These observations increased the number of potential DNA binding sites within the genome of the nosocomial MRSA isolate EMRSA-16 to around 40000. As the footprinting substrates were designed to investigate binding to the preferred interstrand sequences, the genomes of target Gram-positive bacteria could contain further as-yet-unidentified interstrand and intrastrand binding sites.

At supra-inhibitory concentrations, ELB-21 elicited potent bactericidal activity against MRSA and VRE isolates, with a greater than 4 log reduction in viability over a 2 h period; DNA extracted from ELB-21-treated MRSA was cross-linked, as evidenced by substantial increases in DNA melting temperature and increased molecular weight of DNA adducts identified by Southern blot analysis. Exposure of EMRSA-16 to subinhibitory concentrations of ELB-21 resulted in up-regulation of more than 160 genes in both the logarithmic and stationary phases of bacterial growth and, surprisingly in view of the capacity of PBD dimers to prevent DNA strand separation and transcription initiation, twofold or greater down-regulation of only 16 genes. Almost half of the genes affected by ELB-21 were induced prophage genes associated with the resident S. aureus prophages ϕSa2 and ϕSa3. All sequenced S. aureus strains, with the exception of COL, carry ϕSa3; ϕSa2 is integrated into the EMRSA-16 genome. Genes associated with the staphylococcal pathogenicity island SaPI4 were also up-regulated, as were genes indicative of a DNA damage (SOS) response; 10 genes, including those encoding the LexA repressor, recombinase A, topoisomerase, and nucleotide excision repair proteins, were modulated by ELB-21. Transcriptional and proteomic analysis provided little evidence that ELB-21 selectively down-regulated genes involved in key cellular functions or bacterial pathogenicity. The SOS response in S. aureus has been characterized using non-selective DNA interactive agents such as mitomycin C (MMC), an anti-tumour antibiotic with substantial anti-staphylococcal activity. MMC; the PBD dimer preferentially forms DNA intrastrand complexes by virtue of covalent interactions with appropriately spaced guanine residues.

**Materials and methods**

**Bacterial strains, culture and antibacterial agents**

S. aureus EMRSA-16 is a MRSA isolate from the Royal Free Hospital (London, UK). S. aureus RN4220, a derivative of NCTC 8325 cured of all prophages, was the gift of Friedrich Götze (University of Tübingen, Germany). S. aureus RN981 and RN1030 are recA mutant derivatives derived from, respectively, RN450 and RN451; RN450 (8325-4) is a prophage-free derivative of NCTC 8325 and RN451 is RN450 but lysogenic for SaPI. RN450, RN451, RN981 and RN1030 were kindly provided by José Penadés (Instituto Valenciano de Investigaciones Agrarias, Segorbe, Spain). Bacteria were grown in Mueller-Hinton (MH) broth (Oxoid) or on MH agar plates at 37°C. The PBD dimer ELB-21 was obtained from Spirogen Ltd. (London, UK) and was synthesized as described. MMC was obtained from Sigma (Poole, UK). MICs were determined by the CLSI (formerly NCCLS) broth microplate assay as previously described. For MIC determination, agents were dissolved in DMSO prior to dilution in broth; at the concentrations used, the solvent had no effect on bacterial growth. For cross-linking studies, ELB-21 was maintained as a 3 mM stock solution in 50/50 v/v methanol/water at −20°C for no longer than 4 months. Working solutions of 200 mM were prepared by diluting stock solution with nuclease-free water; these were stored at −20°C for no more than 1 week. Lytic phage particles in bacterial cultures were enumerated using the soft agar overlay method and RN450 as indicator strain.

**Transmission electron microscopy**

Phages were fixed in 1.5% glutaraldehyde for at least 2 h at room temperature, treated with osmium tetroxide and embedded in epoxy resin. Sectioning and staining with uranyl acetate was followed by Reynolds’ lead citrate. Ultrathin sections were viewed and photographed using a Philips 201 transmission electron microscope.

**Microarray analysis**

Total bacterial RNA was purified from each sample, labelled and hybridized to the B4G@S SAv1.1.0 microarray as described previously. This array has been described elsewhere and contains PCR products representing all predicted open reading frames from the initial seven S. aureus genome sequencing projects. The array design is available in...
Table 1. Single-strand (ss) and double-strand (ds) oligonucleotides designed as substrates for RPLC-MS investigations of DNA:drug adduct formation

| Label | ssDNA Sequence | Average mass (Da) | Label | dsDNA Sequence | Average mass (Da) | ELB-21:dsDNA adduct mass (Da) |
|-------|----------------|------------------|-------|----------------|------------------|-------------------------------|
| Seq-1 | Seq-2 Seq-3 | 3956.5 | Seq-4 Seq-5 | 3906.5 | Seq-6 Seq-7 Seq-8 | 3683.4 | Seq-9 Seq-10 Seq-11 | 4211.8 | Duplex-1 Duplex-2 Duplex-3 | 7904.1 | 8516.8 | 7904.1 | 8516.8 | 7287.4 | 7900.1 | 7286.7 | 7899.5 | 8522.05 | 9106.66 | 8522.05 | 9106.66 | 9106.66 |

**B4G@Sbase** (accession number: A-BUGS-17; http://bugs.squl.ac.uk/ A-BUGS-17) and also ArrayExpress (accession number: A-BUGS-17). Hybridization data were analysed using an Affymetrix 428 scanner then quantified using BlueFuse for Microarrays 3.5 software (BlueGnome). Data analysis was performed in GeneSpring GX 7.3 (Agilent Technologies) and finally to 10% buffer A at 35 min. UV absorbance was monitored at 254 nm and fractions containing separated components were collected manually, combined as appropriate, lyophilized and analysed by matrix assisted laser desorption time-of-flight mass spectrometry (MALDI-TOF MS); covalently bound DNA-ELB-21 adduct samples were prepared by diluting with matrix (37 mg 2-methyl butanoic acid (MBA) in 1 mL acetonitrile, 45 mg ammonium citrate in 1 mL water – mix 1:1 for matrix) either 2:1, 1:1 or 1:5 (sample:matrix), then 1 μL of sample was spotted onto the MALDI target plate and allowed to dry. Samples were analysed with an Applied Systems Voyager-DE Biospectrometry Workstation MALDI-TOF mass spectrometer with a nitrogen laser in positive linear mode using delayed extraction (500 ns) and an accelerating voltage of 25000 V. Acquisition was between 4000 and 15000 Da with 100 shots/spectrum.

**Kinetics of covalent binding of drug to dsDNA**

The interaction of ELB-21 and short (12- to 14-mer) oligonucleotides incorporating putative binding sites was investigated using a combination of ion-pair reversed phase liquid chromatography (RPLC) and mass spectrometry (MS) as described earlier. Sequences of the single-stranded (ss) oligonucleotides used are given in Table S1 (available as Supplementary data at JAC Online). Data shown are the median of three biological and two technical replicates; each replicate was performed in duplicate.

**Quantitative RT–PCR (qRT–PCR)**

qRT–PCR was performed as described previously. Gene-specific primer pairs were designed for *S. aureus* RN4220 genes of interest to yield ampli- cons of 100–150 bp and the oligonucleotides used are listed in Table S1 (as Supplementary data at JAC Online). Data shown are the median of three biological and two technical replicates; each replicate was performed in duplicate.

**Results**

**Formation of covalent adducts with ds oligonucleotides**

Predictive modelling and DNA cross-linking and footprinting studies have indicated that the preferred interstrand binding sites for ELB-21 are 5′-PuGAATC-Py and 5′-PuGAATC-Py, but more recent work has identified further interstrand targets as well as at least 10 potential intrastrand sites comprising 2 to 6 bases separating same-strand guanines. To establish the preference for ELB-21 covalent adduct formation with DNA we investigated real-time covalent binding of the drug to the DNA duplexes shown in Table 1; these duplexes incorporate the major interstrand and intrastrand sites identified by our previous work. The formation of interstrand cross-links within the 5′-PuGAATC-Py sequence was investigated using the 13-mer oligonucleotide duplex-1 (Table 1). RPLC analysis of the annealed duplex formed from the ss sequences Seq-1 and Seq-2 (Table 1) resulted in two peaks with retention times (RTs) of 27.1 min and 27.5 min (Figure 2a), equivalent to denatured Seq-1 and Seq-2 as determined by MALDI-TOF MS and consistent with our previous finding that short dsDNA duplexes denature
under the HPLC conditions used. Immediately following mixing of duplex-1 and ELB-21, a major adduct peak (RT 30.9 min) was apparent (Figure 2b), confirmed by MALDI-TOF MS as the 1:1 ELB-21/Seq-1/Seq2 duplex interstrand cross-linked adduct and representing approximately 70% of the DNA in the sample. A minor (~10%) peak (RT 33.7 min) was also observed and was identified as the ELB-21/Seq-1 ssDNA adduct; its abundance declined over time. Further incubation determined that interstrand 5′-Pu-GAATC-Py adduct formation was complete (~95%) within 3 h (Figure 2c and d).

As we have obtained evidence that ELB-21 may form intrastand cross-links,3 we investigated the potential for intrastrand adduct formation using duplex-2 (Table 1); this duplex differs from duplex-1 with respect to replacement of 9-cytosine with a guanine residue on the 5′ strand, yielding 5′-Pu-GAATG-Py. Analysis of the annealed duplex under RPLC conditions revealed two peaks (RT 27.1 min and RT 28.2 min), confirmed by MALDI-TOF MS to be Seq-3 and Seq-4, respectively (Figure 3a). A prominent peak was apparent at RT 29.8 min immediately (0 h) after mixing of ELB-21 and duplex-2 (Figure 3b), confirmed by MALDI-TOF MS as the 1:1 ELB-21/Seq-3/Seq4 duplex interstrand adduct. During the time course of these experiments, two further peaks emerged at RT 34.2 min and RT 36.3 min (Figure 3b–d), although the RT 29.8 min peak remained prominent throughout and accounted for 90% of the adducts formed at completion. Adduct formation with 5′-Pu-GAATG-Py progressed very rapidly and was complete within 1 h (Figure 3c). Even at 0 h, it was noticeable that the ratio of the unreacted oligonucleotides Seq-3 and Seq-4 changed in favour of Seq-4, indicating preferential ELB-21 reactivity with the 5′-Pu-GAATG-Py-containing strand Seq-3 (Figure 3b). The chromatograms indicated that ELB-21 initially formed the duplex intrastrand cross-linked RT 29.8 min adduct with the Seq3/Seq-4 duplex, consuming both ssDNA species at an equal rate. However, in contrast to the duplex-1 interstrand cross-linked adduct, which is stable under RPLC conditions due to the covalent bonding of both oligonucleotide strands,19 a fraction of the intrastrand ELB-21/Seq-3(Seq-4) adduct dissociated as the ELB-21/Seq-3 intrastrand adduct (RT 34.2 min; m/z 4609) and the free Seq-4 strand (RT 28.2 min), causing a relative increase in the RT 28.2 min Seq-4 peak in comparison to the RT 27.1 min Seq-3 peak. MALDI-TOF MS data (not shown) indicated that the RT 36.3 min peak corresponded to the 2.1 ELB-21/Seq-3 adduct, with one ELB-21 unit attached to each of the guanine residues of the 5′-Pu-GAATG-Py binding site (Figure 3b).

Similar experiments were conducted with the self-complementary 5′-Pu-GAATC-Py duplex-3 (Seq5/Seq5) and 5′-Pu-GAATG-Py duplex-4 formed from Seq-6 and Seq-7. The latter contains an intrastand binding site as a consequence of the replacement of cytosine-8 in Seq-5 with a guanine residue. Figure 4 shows that ELB-21 immediately formed a covalent adduct (RT 28.7 min) with duplex-3 and the reaction was essentially complete within 3 h. The formation of covalent adducts between ELB-21 and duplex-4 was evident immediately after mixing, but the reaction failed to go to completion, even after 24 h (Figure S, Supplementary data). Thus, in contrast to experiments with the predicted2 pentanucleotide binding sequences 5′-Pu-GAATC-Py (Figure 2) and 5′-Pu-GAATG-Py (Figure 3), ELB-21 preferentially formed interstrand, rather than intrastand, cross-links with these tetranucleotide sequences. The experiments demonstrate that ELB-21 can form cross-linked adducts with binding sites that are smaller than the ideal binding sequences.
Figure 3. Formation of ELB-21 intrastrand adducts with dsDNA 13-mer duplex-2. Ion-pair RPLC chromatograms of (a) duplex-2, showing denaturation to Seq-3 (RT 27.1 min) and Seq-4 (RT 28.2 min) under RPLC conditions; (b) immediately (0 h) after mixing of ELB-21 with duplex-2, showing the rapid appearance of intrastrand 5′-Pu-GAATG-Py adduct (RT 29.8 min). Seq-3, which contains the 5′-Pu-GAATG-Py intrastrand binding site, has almost disappeared; (c) 1 h after mixing of ELB-21 with duplex-2, showing emergence of two minor peaks (RT 32.4 min and RT 36.3 min) in addition to a major peak (RT 29.8 min). Seq-3 is completely absent, indicating completion of the reaction; (d) 12 h after mixing of ELB-21 with duplex-2. Peaks were characterized using MALDI-TOF MS.

Figure 4. Formation of ELB-21 interstrand adducts with dsDNA 12-mer duplex-3. Ion-pair RPLC chromatograms of (a) duplex-3, showing denaturation to Seq-5 (RT 24.6 min); (b) immediately (0 h) after mixing of ELB-21 with duplex-3, showing the rapid appearance of interstrand 5′-Pu-GATC-Py duplex adduct (RT 28.7 min); (c) 3 h after mixing of ELB-21 with duplex-3, showing the emergence of a minor peak at RT 34.2 min in addition to the major peak at RT 28.7 min; (d) 12 h after mixing of ELB-21 with duplex-3. Peaks were characterized using MALDI-TOF MS.
Finally, to investigate binding to an extended sequence, two oligonucleotides were designed with one additional A/T base pair between the two guanines of duplexes 1 and 2. Thus duplex-5 (Seq-8/Seq-9) offered the extended interstrand Pu-GAAATC-Py cross-linking site and duplex-6 (Seq-10/Seq-11) offered the extended intrastrand Pu-GAAATG-Py site (Table 1). After incubation of ELB-21 with duplex-5, a minor peak at RT 29.8 min and a major peak at RT 33.4 min were apparent (Figure 5). The identities of the peaks were confirmed by MALDI-TOF MS; the minor RT 29.8 min peak was found to be the interstrand ELB-21/Seq-8/Seq-9 adduct and the RT 33.4 min peak at duplex-6 resulted in the rapid emergence of a major peak at RT 29.8 min and two minor peaks at RT 33.6 min and RT 34.1 min (Figure 6a). As anticipated, the RT 29.8 min peak was identified as the interstrand ELB-21/Seq-10/Seq-11 duplex adduct. Both the RT 33.6 min and RT 34.1 min peaks gave mass values corresponding to ELB-21/Seq-10 adducts. Based on previous studies with non-nucleophilic inosine-containing oligonucleotides, which are unable to form covalent linkages with PBD, the RT 33.6 min peak was identified as the intrastrand cross-linked ELB-21/Seq-10 adduct and the RT 34.1 min peak was identified as the ELB-21/Seq-10 monoalkylated adduct. The intrastrand cross-linked duplex adduct was the most abundant in this experiment (Figure 6).

Thus the rank order of ELB-21 binding sequences was determined in this study to be 5′-Pu-GAAATG-Py > 5′-Pu-GAAATC-Py > 5′-Pu-GATC-Py > 5′-Pu-GATG-Py > 5′-Pu-GAAATG-Py > 5′-Pu-GAAATC-Py.

**Antistaphylococcal effects of ELB-21**

ELB-21 displayed potent antibacterial activity against 38 MRSA isolates, with an MIC\textsubscript{90} value of 0.03 mg/L, the MIC for EMRSA-16 was confirmed as 0.015 mg/L (Table 2). The agent exhibited potent bactericidal activity against EMRSA-16 and other bacteria, with an immediate reduction in viable count following exposure to the drug and it induced genes associated with prophages εSa2 and εSa3, common residents within S. aureus clinical isolates. These observations raised the possibility that the bactericidal effect associated with ELB-21 is due to ‘lysis from within’ determined by activation of resident prophages. We therefore examined the effect of ELB-21 on the viability, optical density and prophage induction of prophage-carrying and prophage-cured strains of S. aureus in comparison to MMC, a well-established inducer of prophage.

The addition of ELB-21 at concentrations of 2–4×MIC to 3 h mid-logarithmic EMRSA-16 cells produced an immediate and large reduction in viability; at 1×MIC the bactericidal effect was much less pronounced (Figure 7b). Cell viability began to decline approximately 1 h after addition of the drug; with supra-inhibitory concentrations, a threefold reduction in cfu/mL was evident after 8 h (Figure 7a). Phage release occurred 3 h after drug exposure and the pfu/mL increased up to 5 h, time-points which are coincident with maximal reduction in OD\textsubscript{600}.
phage numbers declined rapidly following this delayed burst (Figure S2, Supplementary data). Interestingly, more infectious phage particles were induced by 1×MIC compared with 4×MIC; only one morphological phage type, typical of the Siphoviridae, was evident after extensive transmission electron microscopy (TEM) investigation of ELB-21-induced supernatants. Growth of the surviving fraction of EMRSA-16 cells was evident after 24 h incubation. The response was comparable to that induced by MMC (Figure 7c and d), except that recovery of MMC-exposed bacteria was not evident after 24 h (Figure 7d).

Table 2. Susceptibility of S. aureus strains to ELB-21 and mitomycin C (MMC)

| Bacterial strain | Description                  | MIC (mg/L) |
|------------------|------------------------------|------------|
|                  |                              | ELB-21     |
| EMRSA-16         | Hospital-acquired MRSA       | 0.015      |
| NCTC 8325        | Isolated in 1960 from sepsis patient | 0.015 |
| RN4220           | Prophage-cured derivative of NCTC 8325 | 0.03 |
| RN450            | Prophage-cured derivative of NCTC 8325 | 0.03 |
| RN451            | RN450 lysogenic for ϕ11      | 0.03       |
| RN981            | ΔrecA derivative of RN450    | 0.00015    |
| RN1030           | ΔrecA derivative of RN451    | 0.000075   |
|                  |                              | MMC        |
| EMRSA-16         |                              | 0.03       |
| NCTC 8325        |                              | 0.125      |
| RN4220           |                              | 0.25       |
| RN450            |                              | 0.25       |
| RN451            |                              | 0.25       |
| RN981            |                              | 0.0075     |
| RN1030           |                              | 0.0075     |

MMC was a far more potent inducer of prophage than ELB-21 (Figure S2, Supplementary data). To further investigate if induction of prophage contributed wholly or in part to the bactericidal or lytic profile of ELB-21, we compared the response to ELB-21 exposure of NCTC 8325, a strain carrying ϕSa2 and ϕSa3, with that of its prophage-free derivative RN4220. As shown in Figure 8, there was a clear difference in the responses of these two strains to ELB-21 and MMC at concentrations at or above the MIC (0.015–0.03 and 0.125–0.25 mg/L, respectively). The immediate reduction in OD 600 at 2 h following addition of supra-inhibitory ELB-21 concentrations (Figure 8a) was far greater than that found with the more recent clinical isolate EMRSA-16 (Figure 7a) and was accompanied by a corresponding immediate reduction in viability (Figure 8b). Similar profiles were obtained with MMC (Figure 8c and d) and, again, in contrast to ELB-21, there was no recovery of viability after 24 h incubation (Figure 8d). Although loss of viability of RN4220 was comparable to the NCTC 8325 parent strain with both ELB-21 (Figure 8f) and MMC (Figure 8h), there was no reduction in optical density for either drug (Figure 8e and g). Thus prophage induction does not account for killing of the prophage-replete parent NCTC 8325, but bacterial lysis, observed with a proportion of the bacteria, appears to be due solely to activation of resident prophages. Exposure to both ELB-21 and MMC resulted in levels of induction of resident NCTC 8325 prophages comparable to those found with EMRSA-16 (data not shown).

We have previously shown that the addition of ELB-21 to logarithmic phase EMRSA-16 cells led to a twofold or greater change in expression of 184 genes, the large majority of which were upregulated, compared to unexposed controls (Figure S6, Supplementary data). In contrast, expression of 38 genes was downregulated, compared to unexposed controls (Figure S6, Supplementary data). In addition, exposure to ELB-21 led to a significant increase in expression of genes involved in cell wall biosynthesis, including those encoding peptidoglycan biosynthetic enzymes (Figure S6, Supplementary data). Of the 38 downregulated genes, the largest proportion (15%) were coding for proteins involved in cell wall degradation (Figure S6, Supplementary data).

### Figures

**Figure 6.** Formation of ELB-21 intrastrand adducts with dsDNA 14-mer duplex-6. Ion-pair RPLC chromatograms of (a) duplex-6, showing denaturation to Seq-10 (RT 26.8 min) and Seq-11 (RT 28.2 min); (b) immediately (0 h) after mixing of ELB-21 with duplex-6, showing the rapid appearance of the major intrastrand Pu-GAAATG-Py duplex adduct (RT 29.8 min); (c) 3 h after mixing of ELB-21 with duplex-6; (d) 24 h after mixing of ELB-21 with duplex-6, showing that the duplex intrastrand ELB-21/Seq-14/Seq-15 adduct at (RT 29.8 min) remains the major product of the incubation.
which were upregulated, almost half were induced prophage genes as well as genes associated with the SaPI4 pathogenicity island. To determine the transcriptional response of ELB-21 in a prophage-free background, we exposed mid-logarithmic MH broth-grown RN4220 to the agent at a concentration of 0.5 MIC. One hour after addition of ELB-21, 27 genes were found to be up-regulated (Table S2, Supplementary data) and 32 genes down-regulated (Table S3, Supplementary data) at least twofold compared with drug-free RN4220 cultures. Ten of the genes activated by exposure to the drug are involved in DNA damage repair and the pattern of ELB-21-mediated induction of SOS-associated proteins was comparable to that induced by MMC. Other ELB-21-activated genes included small numbers encoding membrane proteins, transporter components and metabolic enzymes. No clear pattern of down-regulation by ELB-21 emerged, with a variety of regulatory, transport, membrane and metabolic proteins affected (Table S3), and may reflect specific binding to primary sequences at subinhibitory concentrations within these genes. Interestingly, the number of RN4220 genes down-regulated by the PBD dimer was twice that found with EMRSA-16, an isolate carrying prophages ϕSa2 and ϕSa3. The pattern of genes with increased expression following exposure to ELB-21 was markedly similar to that associated with induction by a subinhibitory concentration of MMC (Table S2), even though the latter compound is considered to be a less specific DNA binding agent than PBD dimers such as ELB-21. Thus exposure to MMC at 0.5 MIC resulted in the twofold or greater up-regulation of 25 genes and down-regulation of 16 (Tables S2 and S3), with a higher degree of complementarity between ELB-21 and MMC for up-regulated compared with down-regulated genes. Changes in the expression of eight genes by ELB-21 and MMC, as determined by microarray analysis, were validated by qRT–PCR (Table S4, Supplementary data); there was a high degree of correlation between the two methods.

That the relative susceptibility of DNA repair-competent staphylococci is critically dependent on induction of the SOS response was emphasized by large decreases in MIC values for both ΔrecA mutant RN1030 and prophage-cured ΔrecA mutant RN981; both ΔrecA mutants were more than 100-fold more susceptible to ELB-21 than the parent strains (Table 2).
Figure 8. Response of *S. aureus* NCTC 8325 (a–d) and the prophage-cured derivative RN4220 (e–h) to subinhibitory and supra-inhibitory concentrations of ELB-21 and mitomycin C (MMC). ELB-21 (a, b, e, f) and MMC (c, d, g, h) were added to mid-logarithmic phase cultures (OD$_{600}$≈0.1; 2 h), OD$_{600}$ measured (a, c, e, g) and viable numbers determined (b, d, f, h). Error bars represent ±1 SD; n=3.
Discussion

PBD dimers were designed to arrest DNA replication, inhibit binding of enzymes and transcription factors to DNA and prevent transcription by stably cross-linking opposing DNA strands.\textsuperscript{2,4,27,28} The drugs are shaped to fit the minor groove of duplex DNA without distortion of the helix and to form covalent bonds with appropriately spaced guanine residues. The five-carbon diether linking moiety of ELB-21 facilitates interstrand tethering of guanines separated by 3 bp, and hydrogen bonds between the N10 protons of the PBD units and neighbouring adenine residues provide further sequence selectivity.\textsuperscript{19} ELB-21 is the most potent antibacterial in this group of compounds examined to date, displaying bactericidal killing kinetics against susceptible Gram-positive bacteria and cross-linking DNA in situ.\textsuperscript{1,7} However, recent investigation of ELB-21 binding sites using DNase I footprinting methods identified a range of further interstrand DNA binding sites both longer and shorter than the predicted target sequences and indicated that the drug forms intrastrand as well as interstrand DNA adducts.\textsuperscript{3} These observations complement those made with SJG-136, a PBD dimer with a three-carbon diether bridge that recognizes guanines on opposing DNA strands separated by 2 bp.\textsuperscript{4} It has successfully completed phase I clinical trials in patients with advanced solid tumours,\textsuperscript{30} this promising, clinically effective agent has recently been found to form interstrand and intrastrand adducts with a wider variety of DNA targets than previously recognized.\textsuperscript{18} As the nature of the adducts formed between ELB-21 and dsDNA sequences has implications for its mode of antibacterial action, the capacity of recombination-competent bacteria to repair damaged sites on DNA and the potential for resistance to this class of agent, we investigated the preferred binding patterns of ELB-21 to short oligonucleotide sequences using a new method\textsuperscript{19} that provides precise, quantitative kinetic data and mass spectrometric identification of the adducts formed.

Our study has provided direct evidence that ELB-21 forms interstrand cross-links at the preferred binding site S'-Pu-GGAATC-Py.\textsuperscript{3,5} cross-links were evident immediately after mixing of the drug with duplex DNA and were complete within 3 h (Figure 2), confirming the high affinity of ELB-21 for one of its designed target sequences. As anticipated from previous footprinting studies,\textsuperscript{3} the drug also avidly cross-links shorter sequences within duplex DNA, including S'-Pu-GATC-Py (Figure 4), one of the main targets for SJG-136.\textsuperscript{6} The capacity of ELB-21 to cross-link sequences longer than the preferred target, such as S'-Pu-GAAATC-Py (Figure 5), emphasizes the considerable number of potential binding sites that almost certainly contribute towards the potent antistaphylococcal activity of PBD dimers such as ELB-21.\textsuperscript{1,7} The preference of ELB-21 for formation of the intrastrand adduct Pu-GAATG-Py (Figure 6) over the interstrand cross-linking of Pu-GAAATC-Py was unexpected and represents a key finding of this study, along with the capacity of the drug to slowly form intrastrand adducts with the shorter sequence S'-Pu-GATG-Py. The observation that ELB-21 formed intrastrand adducts with duplex sequences of ideal length for interstrand cross-linking contrasts with data obtained using SJG-136;\textsuperscript{18} this PBD dimer also forms intrastrand adducts, but preferences are for sequences longer and shorter than the ideal length interstrand targets. Insights into adduct formation with SJG-136 were obtained using energy-minimized molecular models; the agent could be readily accommodated in the minor groove by participating guanines for both interstrand and intrastrand adducts but could be accommodated through binding to extended sequences only at the expense of some distortion of the DNA helix at the points of attachment.\textsuperscript{18} We anticipate similar effects with ELB-21 that may explain induction of the RecA-LexA pathway in EMRSA-16 that we have observed in this and prior studies.\textsuperscript{3}

We previously determined that exposure of EMRSA-16 to ELB-21 resulted in a pattern of gene up-regulation indicative of a DNA damage response with concomitant induction of prophage.\textsuperscript{3} The rapid bactericidal action of the drug was accompanied by delayed cell lysis that appeared to be due to release of induced phages, as strains cured of all resident prophages were rapidly killed, but not lysed, by ELB-21. In accord with other studies,\textsuperscript{31,32} a relatively low proportion of the EMRSA-16 population released viable phage particles following drug treatment, as evidenced by lysis of around 5% of bacteria and low plaque counts of culture supernatants. It is unclear in our study whether phages are released in delayed fashion from the non-viable or the viable portion of bacteria in the culture. Although ELB-21 was designed as a sequence-selective agent with the capacity to bind to a restricted set of motifs within target DNA, the response of EMRSA-16 to this agent was similar to that obtained with the non-selective DNA interactive agent MMC, suggesting that the antibacterial effects observed were due to an inadequate response to DNA damage.

Changes in bacterial gene expression following addition of ELB-21 and MMC to mid-logarithmic S. aureus cultures further emphasized these common features of the bacterial response. We have shown\textsuperscript{3} that exposure of EMRSA-16 to subinhibitory concentrations of ELB-21 for 1 h elicited the up-regulation of more than 160 genes, almost half of which were induced prophage genes; also prominent among ELB-21-activated genes were those involved in DNA damage repair and genes encoding toxins within the SaPI4 pathogenicity island. As the bacterial transcription profile is likely to have been influenced in an unpredictable way by the activation of a large number of prophage genes and the subsequent release of viable phage particles, we determined the transcriptional response to ELB-21 and MMC of S. aureus RN4220. In this prophage-free background, only a limited number of genes were induced more than twofold, and the profiles obtained with each agent were remarkably similar. With ELB-21, the majority encoded components of the DNA damage repair system and included the positive (RecA; recombinase A) and negative (LexA) regulators of the SOS response and products of genes in the LexA regulon involved in error-prone DNA repair.

Induction of RecA by both ELB-21 and MMC in all likelihood accounts for the central features of the response of S. aureus to these agents. The extremely high susceptibility of ΔrecA strains to ELB-21 and MMC suggests that the bactericidal action of these agents occurs above the threshold of repair of damaged DNA, with growth negated by permanently stalled DNA polymerase and bacterial death due to irreversible strand breaks. During normal bacterial growth, the repressor LexA is bound to a specific DNA sequence, the SOS box, located in the promoter region of genes associated with the SOS system such as recA, lexA and uvrAB and it therefore down-regulates its own expression.
The consensus sequence for SOS boxes in *S. aureus* is CGAACAAAGTTCG (conserved regions shown in bold) which, interestingly, contains potential target sequences for ELB-21 and other PBD dimers. LexA has high affinity for A-T-rich regions but, as SOS boxes generally include G-C pairs, the affinity of LexA for each targeted promotor is variable and this facilitates some expression of SOS genes in the repressed state. The SOS response can be induced by stalled replication forks or unrepaird defects resulting in the formation of ssDNA, the ATP-dependent assembly of ssDNA-Reca nucleoprotein filaments engenders LexA autocleavage and inactivation of the repressor with consequent induction of SOS genes. During an SOS response, some genes may be rapidly induced, partly induced or remain unpressed until high or persistent DNA damage has occurred, such as cleavage between its cytotoxicity threshold; we will describe the selection of complex interactions will aid the selection of chemical agents. Further understanding of these complex interactions will aid the selection of chemotherapeutic agents for the treatment of severe infections in the human host. Although ELB-21 has the capacity to damage host cell DNA, it exerts potent antibacterial effects at concentrations below its cytotoxicity threshold, and effectively targets DNA damage in transcription and replication processes. Elaborating on its potential to supplement the current arsenal of antibiotics is so important that the systemic use of colistin is now commonplace.40

Some *S. aureus* virulence proteins, such as β-toxin (Hlb), fibronectin binding protein (Fnb) and staphylolokinase (Sak), are encoded by prophage genes and phage induction is likely to activate the expression of these virulence effectors. Indeed, ELB-21 up-regulates virulence-associated, SaP4-encoded genes hlb, tst (toxic shock syndrome toxin-1) and ssp (V8 serine protease) in EMRSA-16. Antibiotics that de-repress resident staphylococcal prophages have been shown to induce mobilization and high-frequency horizontal transmission of co-resident pathogenicity islands. Such phage-related chromosomal islands play a major role in the dissemination of genes that impact human health and bacterial adaptation to animal hosts and may affect the resolution of infections during the course of therapy with SOS-inducing chemotherapeutic agents. Further understanding of these complex interactions will aid the selection of chemotherapeutic agents for the treatment of severe infections in the human host. Although ELB-21 has the capacity to damage host cell DNA, it exerts potent antibacterial effects at concentrations below its cytotoxicity threshold, we will describe the selective toxicity profile of the compound in a future publication. Although ELB-21 has a toxicity profile that does not bear comparison with established antibiotics, the need for agents with the potential to supplement the current arsenal of antibiotics is so great that the systemic use of colistin is now commonplace. More specifically, the growing body of clinical data for SJG-136 suggests that PBD dimers elicit therapeutic effects below the toxicity threshold, and we will continue to investigate ELB-21 as a potential ‘agent of last resort’ for severe systemic Gram-positive infections.

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David Thurston is chief scientific officer at Spirogen Ltd. All other authors: none to declare.

Supplementary data
Tables S1–S4 and Figures S1 and S2 are available as Supplementary data at JAC Online (http://jac.oxfordjournals.org/).

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