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Accessibility
Antimicrobial and Efflux Pump Inhibitory Activity of Caffeoylquinic Acids from *Artemisia absinthium* against Gram-Positive Pathogenic Bacteria

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Abstract

**Background:** Traditional antibiotics are increasingly suffering from the emergence of multidrug resistance amongst pathogenic bacteria leading to a range of novel approaches to control microbial infections being investigated as potential alternative treatments. One plausible antimicrobial alternative could be the combination of conventional antimicrobial agents/antibiotics with small molecules which block multidrug efflux systems known as efflux pump inhibitors. Bioassay-driven purification and structural determination of compounds from plant sources have yielded a number of pump inhibitors which acted against gram positive bacteria.

**Methodology/Principal Findings:** In this study we report the identification and characterization of 4′,5′-O-dicaffeoylquinic acid (4′,5′-ODCQA) from *Artemisia absinthium* as a pump inhibitor with a potential of targeting efflux systems in a wide panel of Gram-positive human pathogenic bacteria. Separation and identification of phenolic compounds (chlorogenic acid, 3′-O-dicaffeoylquinic acid (4′,5′-ODCQA) was based on hyphenated chromatographic techniques such as liquid chromatography with post column solid-phase extraction coupled with nuclear magnetic resonance spectroscopy and mass spectroscopy. Microbial susceptibility testing and potentiation of well known pump substrates revealed at least two active compounds; chlorogenic acid with weak antimicrobial activity and 4′,5′-ODCQA with pump inhibitory activity whereas 3′,5′-ODCQA was ineffective. These initial findings were further validated with checkerboard, berberine accumulation efflux assays using efflux-related phenotypes and clinical isolates as well as molecular modeling methodology.

**Conclusions/Significance:** These techniques facilitated the direct analysis of the active components from plant extracts, as well as dramatically reduced the time needed to analyze the compounds, without the need for prior isolation. The calculated energetics of the docking poses supported the biological information for the inhibitory capabilities of 4′,5′-ODCQA and furthermore contributed evidence that CQAs show a preferential binding to Major Facilitator Super family efflux systems, a key multidrug resistance determinant in gram-positive bacteria.


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Introduction

Multi-drug resistant microbial infections caused by Gram-positive bacteria such as *Staphylococcus aureus* and *Enterococcus faecalis* represent an exponentially growing problem affecting communities worldwide. Efflux mechanisms have become broadly recognized as major components of resistance to many classes of antibiotics [1,2]. Some efflux pumps selectively extrude specific antibiotics while others, referred to as multidrug efflux pumps (MEPs), expel a variety of structurally and functionally diverse compounds [3] in addition to a variety of other physiological roles [4]. A novel and promising approach to deal with multidrug resistance is to improve the clinical performance of various antibiotics by employing efflux pump inhibitors (EPIs) [5,6]. Plants
have been explored comprehensively as potential sources of antimicrobials [7,8]. It has been established that disabling MEPs in Gram-negative species using a combination of MEP mutants and synthetic EPIs leads to a striking increase in the activity of numerous plant compounds [9]. Several Berberis medicinal plants (Berberis repens, B. aquifolium, and B. fremontii) that produce the plant antimicrobial berberine also synthesized an inhibitor of the Staphylococcus aureus NorA MEP identified as 5'-methoxyhydrocadin (5'-MHC) [10]. Identification of 5'-MHC intensified the search for natural EPIs of plant origin. Bioassay driven purification and structural determination of compounds from various plant sources yielded a number of EPIs acting against Gram-positive bacteria with activities similar to 5'-MHC [11,12,13,14,15,16]. Gram-negative bacteria and fungi comprise the main groups of plant pathogens, and it is important to determine whether the antimicrobial/EPI synergy is a general mechanism of plant defense.

Artemisia is a fairly large genus within the family of the Asteraceae (Composite), with more than 200 individual species [17]. Artemisia absinthum, best known as the principal ingredient in the infamous Absinthe drink, has been used medicinally since the times of ancient Greece, and also in western European systems of traditional medicine [17]. It was recently reported that the essential oils occurring in flowers and aerial parts from A. absinthum have antimicrobial properties [17]. Moreover aqueous extracts of A. absinthum are rich in caffeoyl and dicaffeoylquinic acids, which are known to inhibit HIV-1 integrase from integrating the reversibly transcribed viral DNA into host cell DNA [18]. Furthermore, these components are hepatoprotective, anti-histaminic, hypocholesterolemic, anti-spasmodic, and potentially antimicrobial. They also demonstrate high antioxidative activity [19] due to their o-quinoine moieties. Caffeoylquinic acids could inhibit oxidative damage to both low-density lipoprotein [20] and linolenic acid [21] by scavenging reactive oxygen species (ROS) related to cancer and cardiovascular diseases. It has been reported that chlorogenic acid (5-O-caffeoylquinic acid) had inhibitory effects on carcinogenesis in the large intestine, liver, and tongue, and exhibited protective effects on oxidative stress in vivo [22].

The effort to discover plant EPIs, a process ranging from identifying a hit to isolating a pure compound, presents a distinct bottleneck: the lack of comprehensive, chemically and biologically representative natural product extract libraries. Analysis of natural product extracts is time-consuming and laborious, consisting of the isolation of different components of the extract and the successive identification of these compounds by spectrometric data acquisition. We have identified EPI activity against Gram-positive bacteria in A. absinthum extracts. We dramatically expedited the analysis of A. absinthum aquatic infusions using analytical techniques (LC-SPE-NMR and LC-MS), revealing caffeoylquinic acids as key components. Subsequent antimicrobial susceptibility testing of berberine uptake and a competitive efflux assay employing the pure compounds was conducted. An array of pathogens, including knock out and over expression MEP mutants, strongly supported the hypothesis that 4',5'-CDCQA behaves as a designated EPI for the major facilitator super family (MFS) MEPs of the Gram-positive bacteria: S. aureus, and Enterococcus faecalis.

**Results and Discussion**

Antimicrobial and EPI activity of extracts

The experimental approach to detect EPI activity was to test the combined action of a plant extract (the non-alkaloid fraction) with berberine added at a sub inhibitory concentration. Extracts that inhibited cell growth in the presence of berberine and had no activity when added alone were likely to contain an EPI. Chloroform extracts of leaves from A. absinthium had no antimicrobial activity alone at up to 500 μg/ml (Table 1), but inhibited Staphylococcus aureus, Enterococcus faecalis and Bacillus cereus growth completely in the presence of 30 μg/ml berberine (15 μg/ml berberine for Bacillus cells), a concentration one-eighth the MIC for this substance (data not shown).

The three main components of the extract consisting 40% of the total mass were identified via LC-UV-SPE-NMR [23] and LC-MS. The molecular ion in the ESI negative mode of the first peak was m/z = 353 and the MS2 gave a characteristic chlorogenic acid fragmentation pattern [24]. The structure was confirmed by the respective 1H-NMR analysis. The second and third main components of the extract were co-eluted from the chromatographic column. By the spectral data obtained it was concluded that two dicaffeoylquinic acid isomers were present (3',5'-CDCQA and 4',5'-CDCQA) (Figures S1, S2).

**Antimicrobial and EPI activity of CQAs**

The A. absinthum extract was tested against a panel of human and plant pathogenic bacteria both for direct antimicrobial and EPI activity. The extract exhibited neither antimicrobial activity

<p>| Table 1. Antimicrobial susceptibility for A. absinthum and acquired CQA derivatives. |
|-----------------------------------|-----------|--------------|--------------|--------------|--------------|--------------|</p>
<table>
<thead>
<tr>
<th>Strain *</th>
<th>Extr</th>
<th>3',5'-CDCQA</th>
<th>4',5'-CDCQA</th>
<th>5'-CQA</th>
<th>1',3'-CDCQA</th>
<th>1',5'-CDCQA</th>
</tr>
</thead>
<tbody>
<tr>
<td>S. aureus 8325-4</td>
<td>256</td>
<td>&gt;128</td>
<td>&gt;128</td>
<td>128</td>
<td>&gt;128</td>
<td>&gt;128</td>
</tr>
<tr>
<td>norA</td>
<td>256</td>
<td>&gt;128</td>
<td>&gt;128</td>
<td>64</td>
<td>&gt;128</td>
<td>&gt;128</td>
</tr>
<tr>
<td>NorA++</td>
<td>256</td>
<td>&gt;128</td>
<td>&gt;128</td>
<td>&gt;128</td>
<td>&gt;128</td>
<td>&gt;128</td>
</tr>
<tr>
<td>CA-MRSA</td>
<td>256</td>
<td>&gt;128</td>
<td>&gt;128</td>
<td>&gt;128</td>
<td>&gt;128</td>
<td>&gt;128</td>
</tr>
<tr>
<td>B. cereus</td>
<td>128</td>
<td>&gt;128</td>
<td>&gt;128</td>
<td>&gt;128</td>
<td>&gt;128</td>
<td>&gt;128</td>
</tr>
<tr>
<td>E. faecalis</td>
<td>256</td>
<td>&gt;128</td>
<td>&gt;128</td>
<td>64</td>
<td>&gt;128</td>
<td>&gt;128</td>
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<tr>
<td>norA</td>
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<td>256</td>
<td>&gt;256</td>
<td>32</td>
<td>&gt;256</td>
<td>&gt;256</td>
</tr>
<tr>
<td>E. coli</td>
<td>&gt;256</td>
<td>&gt;256</td>
<td>&gt;256</td>
<td>&gt;256</td>
<td>&gt;256</td>
<td>&gt;256</td>
</tr>
<tr>
<td>C. albicans</td>
<td>&gt;256</td>
<td>&gt;256</td>
<td>&gt;256</td>
<td>&gt;256</td>
<td>&gt;256</td>
<td>&gt;256</td>
</tr>
</tbody>
</table>

All MIC determinations were performed in triplicate.

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nor EPI activity in *Escherichia coli* or *Candida albiscans* (concentration range 150–500 μg/mL). It showed no apparent direct antimicrobial activity (MICs in the range of 128–256 μg/mL for all Gram-positive bacteria tested), but completely inhibited growth in concentrations lower than 50 μg/mL when berberine was added in sub inhibitory concentrations (30 μg/mL for *S. aureus* and *E. faecalis*, and 15 μg/mL for *B. cereus*).

We obtained 5’-caffeoylquinic (5’-OCQA) acid and peracetyldervatives 1’,3’-, and 1’,5’-ODCQA, 3’,5’-ODCQA and 4’,5’-ODCQA, and tested their direct antimicrobial and EPI activity (Table 1). 5’-OCQA was the only molecule with weak direct antimicrobial activity against the Gram-positive bacteria (*B. cereus* and *E. faecalis*, MIC 64 μg/mL). There was a 4-fold difference between MICs in *S. aureus* 8325-4 and the isogenic NorA mutant providing supporting evidence for 5’-OCQA as a potential substrate of MFS efflux systems. All other derivatives were virtually inactive with significantly higher MICs (>128 μg/mL) against all microorganisms in the panel tested.

Toxicity studies

Hemolysis experiments using sheep erythrocytes and DCQA derivatives demonstrated no hemolytic activity at 50 μM, a concentration higher than the MICs for Gram-positive and significantly higher than the concentration used for antimicrobial potention (Figure 1). There are a few brief reports discussing the toxic effect of 5’-OCQA on human oral squamous cell carcinoma (HSC-2) and salivary gland tumor (HSQ) cell lines, as compared with that against human gingival fibroblast (HGF), and erythrocytes in a mM range [25]. The toxic effect is attributed to the potential of the compound to generate reactive oxygen species (ROS). A dose-response experiment using erythrocytes was also able to detect toxicity of 5’-OCQA at fairly low concentrations, (1-5 μM) whereas 3’,5’- and 4’,5’-ODCQAs did not exhibit any cell-lytic properties at significantly higher concentrations (50 μM). This trend, together with existing studies [22,26], suggest that 5’-OCQA is toxic at high concentrations, and implies that the other derivatives appear to have a different interaction pattern with mammalian cells, suggesting that a therapeutic window may exist in both cases. 3’,5’-ODCQA and 4’,5’-ODCQA showed extremely low toxicity to the blood cells indicating that the antimicrobial activity and toxicity patterns are relatively similar related to the differences in substitution moieties.

Potentiation of antibiotics by 4’,5’-ODCQA

We conducted a checkerboard assay using berberine and CQAs against *S. aureus* 8325-4 (Table 2). This method supports evidence for synergy, competition or antagonism for selected compounds as it is reflected by the FICI index (FICI). A FICI of ≤0.5 indicates synergistic interaction. FICI is calculated as the sum of the FICs of each agent. The FIC of each agent is calculated as the MIC of the agent in combination divided by the MIC of the agent. This indicated a synergistic effect for 4’,5’-ODCQA, an’d competition for the other two derivatives. We employ a clinical MRSA strain (CA-MRSA) and conducted extensive checkerboard assays using an array of known MFS substrates and 4’,5’-ODCQA suggesting a promising range of activity both in different strains and clinically relevant compounds (Table 3). We further evaluated the ability of 4’,5’-ODCQA to potentiate designated substrates of MFS and known antibiotics against a panel of Gram-positive phenotypes (Tables 4, 5). The activity of all of the MFS substrates increased significantly in the presence of the compound against the wild-type strains tested (8-fold for berberine, and 4-8-fold for EtBr and fluoroquinolones). The addition of 4’,5’-ODCQA in the more susceptible *E. faecalis* NorA knock out mutant (Table 5) increased the susceptibility of EtBr and norfloxacin (2–4 fold). This result indicated the possible additional participation of the QacA MEP system which has been implicated in the efflux of NorA substrates [12,27]. Besides this anticipated complication, the ability of 4’,5’-ODCQA to potentiate antibiotics was significantly weaker in the case of the NorA knock out phenotypes, indicating a likely mode of action associated with this MFS efflux system. Moreover the *S. aureus* with NorA overexpression showed significant potentiation of all antimicrobials and gave susceptibilities that were comparable with the wild type counterpart in the absence of 4’,5’-ODCQA (8-fold for berberine, and 4-8-fold for EtBr and fluoroquinolones). Results were similar when a *B. cereus* were used (data not shown), implying a wider range of activity for 4’,5’-ODCQA.

4’,5’-ODCQA enhances accumulation of berberine in Gram-positive bacteria

Berberine is a useful model plant antimicrobial whose accumulation in microbial cells can be conveniently monitored by measuring the fluorescence of berberine bound to DNA. We used three different Gram-positive bacteria, *S. aureus*, *E. faecalis*, *B. cereus*, and *E. faecalis* (concentration range 128–256 μg/mL). We conducted a checkerboard assay using berberine and CQAs against *S. aureus* 8325-4 (Table 2). This method supports evidence for synergy, competition or antagonism for selected compounds as it is reflected by the FICI index (FICI). A FICI of ≤0.5 indicates synergistic interaction. FICI is calculated as the sum of the FICs of each agent. The FIC of each agent is calculated as the MIC of the agent in combination divided by the MIC of the agent. This indicated a synergistic effect for 4’,5’-ODCQA, an’d competition for the other two derivatives. We employ a clinical MRSA strain (CA-MRSA) and conducted extensive checkerboard assays using an array of known MFS substrates and 4’,5’-ODCQA suggesting a promising range of activity both in different strains and clinically relevant compounds (Table 3). We further evaluated the ability of 4’,5’-ODCQA to potentiate designated substrates of MFS and known antibiotics against a panel of Gram-positive phenotypes (Tables 4, 5). The activity of all of the MFS substrates increased significantly in the presence of the compound against the wild-type strains tested (8-fold for berberine, and 4-8-fold for EtBr and fluoroquinolones). The addition of 4’,5’-ODCQA in the more susceptible *E. faecalis* NorA knock out mutant (Table 5) increased the susceptibility of EtBr and norfloxacin (2–4 fold). This result indicated the possible additional participation of the QacA MEP system which has been implicated in the efflux of NorA substrates [12,27]. Besides this anticipated complication, the ability of 4’,5’-ODCQA to potentiate antibiotics was significantly weaker in the case of the NorA knock out phenotypes, indicating a likely mode of action associated with this MFS efflux system. Moreover the *S. aureus* with NorA overexpression showed significant potentiation of all antimicrobials and gave susceptibilities that were comparable with the wild type counterpart in the absence of 4’,5’-ODCQA (8-fold for berberine, and 4-8-fold for EtBr and fluoroquinolones). Results were similar when a *B. cereus* were used (data not shown), implying a wider range of activity for 4’,5’-ODCQA.

4’,5’-ODCQA enhances accumulation of berberine

![Figure 1. Hemolytic activity of caffeoylquinic acids towards sheep erythrocytes.](https://example.com/fig1)

The CQA induced significantly more (*) hemolysis, while DCQAs induced significantly virtually no hemolysis. The data were analyzed by two-way repeated-measurement ANOVA for the factors of different derivatives and derivative concentrations followed by post hoc testing by the Holm-Sidak method (*P*<0.05). Values are means ± SEM (n = 3). Note the log scales on both the x and y axes.

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and *B. cereus*, to evaluate with a functional assay the EPI potential of CQAs. We monitored an increase in berberine fluorescence, assessing the rate of penetration and the level of accumulation of berberine in *S. aureus* cells, in response to an established NorA inhibitor ([INF]271) [28,29] and the selection of CQA derivatives (Figure 2A) compared to berberine alone. Rapid accumulation was also observed in other strains tested (*E. faecalis*, *B. cereus*, *B. cereus*, and *S. aureus* strains as well as the significantly higher than those used for antimicrobial susceptibility tests. CQA enhanced the killing effect of the in both strains whereas both DCQAs did not. Challenging biofilms with CQA derivatives in combination with sub-inhibitory concentrations of berberine, ethidium bromide, and the fluoroquinolone moxifloxacin gave a statistically significant decrease in viability of biofilms in the presence of added 5'-OCQA. The killing effect was increased 2 to 4 logs in the presence of 50 μg/ml. *E. faecalis* than *S. aureus* for all antimicrobials tested. CQA enhanced the killing effect of the compounds used in a less dramatic fashion when it was added in both biofilm species at the same concentration. By contrast 3',5'-ODCQA had no apparent effect in either microorganism tested, regardless of the antimicrobial employed. Quantification of biofilm formation and subsequent inhibition with or without treatments was followed by reduction of OD600 after Crystal Violet staining and Colony Forming Units (CFU) determinations. Results from the CV stained biofilms were compatible with CFU determinations but were omitted in the presentation for simplicity.

### Table 4. Potentiation of antimicrobials by 4',5'-ODCQA in *S. aureus*.

<table>
<thead>
<tr>
<th>Antibiotic (Dye)</th>
<th>FIC (antibiotic or dye)</th>
<th>FIC (4',5'-ODCQA)</th>
<th>FICI</th>
</tr>
</thead>
<tbody>
<tr>
<td>CIPRO</td>
<td>0.20</td>
<td>0.00078</td>
<td>0.0039</td>
</tr>
<tr>
<td>NOR</td>
<td>0.10</td>
<td>0.00039</td>
<td>0.0039</td>
</tr>
<tr>
<td>LEVO</td>
<td>0.40</td>
<td>0.00156</td>
<td>0.0039</td>
</tr>
<tr>
<td>BERB</td>
<td>0.0312</td>
<td>0.0625</td>
<td>0.50</td>
</tr>
<tr>
<td>EtBr</td>
<td>0.0625</td>
<td>0.0156</td>
<td>0.0625</td>
</tr>
</tbody>
</table>

*Evaluated by the checkerboard method recommended by the CLSI and expressed as the FIC index (FICI). A FICI of <0.5 indicates synergistic interaction. FICI is calculated as the sum of the FICs of each agent. The FICI of each agent is calculated as the MIC of the agent in combination divided by the MIC of the agent alone.

**Table 5. Potentiation of antimicrobials by 4',5'-ODCQA in *E. faecalis*.

<table>
<thead>
<tr>
<th>OGRF1 (MIC μg/mL)</th>
<th>norA−/− <em>E. Faecalis</em> (MIC μg/mL)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>+4',5'-ODCQA</td>
</tr>
<tr>
<td>BERB</td>
<td>512</td>
</tr>
<tr>
<td>EtBr</td>
<td>128</td>
</tr>
<tr>
<td>CIPRO</td>
<td>2</td>
</tr>
<tr>
<td>NOR</td>
<td>1</td>
</tr>
<tr>
<td>MOXI</td>
<td>1</td>
</tr>
<tr>
<td>LEVO</td>
<td>1</td>
</tr>
</tbody>
</table>

The strains OGRF1(wt) and the knock out NorA mutant were used. All MIC determinations were performed in triplicate. 4',5'-ODCQA was added at a final concentration of 10 μg/mL.

**Table 6.**

*Antimicrobial Potential of Caffeoylquinic Acids*

In order to gain structural insights into the interaction of the potential EPIs (*5′-OCQA*, *4',5'-ODCQA* and *3',5'-ODCQA*) with two MES a. an ABC transporter [30] and b. a MFS transporter[31] we used HADDOCK [32]. High quality models could be obtained for all six protein-ligand complexes. Docking results are consistent with our antimicrobial susceptibility tests and the high-throughput competitive efflux assays performed in this study: All CQAs can successfully enter the binding site of both efflux pumps (Figure 5) remaining in the binding pockets throughout the simulation runs. In addition, CQAs are predicted to have different interaction energies with each efflux system: Their preferential binding to the MFS transporter is governed by hydrophobic interactions uniformly found in all solutions (Table 6). Conversely, when interacting with the ABC transporter, electrostatic forces (ionic interactions and hydrogen bonds) are dominant.

### Table 3. Checkerboard assay of 4',5'-ODCQA with antimicrobials against MRSA.

<table>
<thead>
<tr>
<th>Antibiotic (Dye)</th>
<th>FIC (antibiotic or dye)</th>
<th>FIC (4',5'-ODCQA)</th>
<th>FICI</th>
</tr>
</thead>
<tbody>
<tr>
<td>CIPRO</td>
<td>0.20</td>
<td>0.00078</td>
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<tr>
<td>NOR</td>
<td>0.10</td>
<td>0.00039</td>
<td>0.0039</td>
</tr>
<tr>
<td>LEVO</td>
<td>0.40</td>
<td>0.00156</td>
<td>0.0039</td>
</tr>
<tr>
<td>BERB</td>
<td>0.0312</td>
<td>0.0625</td>
<td>0.50</td>
</tr>
<tr>
<td>EtBr</td>
<td>0.0625</td>
<td>0.0156</td>
<td>0.0625</td>
</tr>
</tbody>
</table>

The strains *S. aureus* 8325-4 (wt) and the isogenic pair of knock out and overexpression NorA mutant were used. All MIC determinations were performed in triplicate. *4',2'-ODCQA* was added at a final concentration of 10 μg/mL.

The strains *S. aureus* 8325-4 (wt) and the isogenic pair of knock out and overexpression NorA mutant were used. All MIC determinations were performed in triplicate. *4',2'-ODCQA* was added at a final concentration of 10 μg/mL.

MOXI, moxifloxacin.

doi:10.1371/journal.pone.0018127.t004
Interactions of the caffeoylquinic acids with the glycerol-3-phosphate transporter (PDB ID: 1PW4)

5'-OQA exhibits strong binding to the glycerol-3-phosphate transporter (see Table 6 and Figure 5, A). Besides the strong desolvation energy component (~40.1 ± 10.2 kcal/mol), it is also stabilized by increased electrostatics (~140.9 ± 18.3 kcal/mol). For example, two Arg residues (R45 and R269) have been observed to be crucial for the inhibition of the MFS transporter. In our results, their side chains form salt bridges with the oxygen atoms of the 5'-O-cafeoylquinic acid (distance <5.5 Å) (Figure 5A). K80, located at the transporter’s active site, forms a salt bridge with the –COOH group of 5'-OQA. Results are also very consistent as nearly all models fall into under one cluster, with an average positional root mean square displacement from the overall lowest-energy structure equal to 0.3 ± 0.1 Å.

For 3',5'-OCQA, the docking results in two low-energy conformations (Table 6). Although their interaction energies are quite similar and their location resembles that of the ‘classical inhibitor’, striking differences in their hydrogen bond network are observed (For details, see Figure S3). 4',5'-ODCQA is found in the binding site in an orientation similar to that of 3',5'-OCQA. However, the significantly larger buried surface area (BSA) and more favorable van der Waals interactions of these EPIs also follow the same principle (Table 6).

All the above mentioned results can rationalize the strong observed binding of 4',5'-ODCQA and 5'-OCQA and the lower inhibitors; in particular 3',5'-ODCQA does not show such an extent in complementarity.

Interactions of caffeoylquinic acids with the Sav1688 ABC transporter (PDB ID: 2HYD)

The ABC transporter was modeled in its open conformation (Figure 5B) (Figure S4 and Table S1), using as template the crystal structure of its close sequential and structural homologue, the P-glycoprotein in its open form (PDB ID: 3G61) [33]. All caffeoylquinic acids successfully entered the active site of the ABC transporter (Figure 5B). Besides the favorable Electrostatics (Figure 5B), the desolvation penalty is quite large (Table 6). Results are rather similar to the ones shown above for the MFS transporters with one major cluster with over 140 members. All other clusters were small in size (<10 structures were included). Binding of this molecule to the ABC transporter is, however, not as energetically favored as to the MFS transporters (for comparison of the interactions, see Table 6 and Figure 5A and 5B). For the other two EPIs, more clusters were obtained. As was already the case with the docking to the MSF transporters, in all solutions, 4',5'-ODCQA occupies a much larger area in the binding site compared to 3',5'-ODCQA; van der Waals interactions of these EPIs also follow the same principle (Table 6).

Figure 2. Berberine accumulation with caffeoylquinic acids in Gram-positive bacteria. The uptake of berberine with no addition or with the addition of 5'-OCQA, 3',5'-ODCQA, 4',5'-ODCQA, or INF271, by cells of S. aureus (A), E. faecalis (B), was measured by determination of the increase in fluorescence following binding to DNA and is expressed as relative fluorescence units (RFU). Berberine was present at a concentration of 30 μg/ml, and 5'-OQA, 3',5'-ODCQA, 4',5'-ODCQA, INF271 were added at the same final concentrations used for the MIC determinations. doi:10.1371/journal.pone.0018127.g002

Antimicrobial Potential of Caffeoylquinic Acids

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efflux pump inhibition of 3',5'-ODCQA. They suggest that, for the MFS efflux systems, all molecules could potentially inhibit the active site; however, 5'-OCQA exhibits in both cases a substantially smaller interaction region showing less complementarity. The docking of all CQAs in the binding sites of the ABC transporter, reveals an abundance of charged interactions. 3',5'-ODCQA shows a decreased complementarity within the active site compared to that of 4',5'-ODCQA. Observed interactions with residues within the active sites are similar to the ones described in the literature for other EPIs [34,35].

We, therefore, formulate a hypothesis consistent with the derived energetics, that CQAs show a preferential binding to MFS efflux systems, rather than to ABC transporters. The reported energies provide insights into the interaction of the EPIs with efflux systems and contribute to a working hypothesis regarding the molecular mechanisms behind their observed inhibitory activities. They should, however, be interpreted with caution and only in terms of estimates of potential of binding and not as binding affinities [36]. Studies including Surface Plasmon Resonance or Isothermal Titration Calorimetry to determine $K_d$'s or $\Delta G$'s will offer further insights in this primary hypothesis.

**Synopsis**

An array of natural product screening and synthesis campaigns led to the identification of a variety EPI chemotypes targeting NorA. The list includes catechin gallates [37], the resin glycosides and tetrasaccharide agents of *Ipomoea murucoides* [38], polyacylated oligosaccharides from the medicinal Mexican morning glory species [39], N-cafeoylphenalkylamide derivatives [40], citral derived amides [41] kaempferol glycoside from *Herissantia tiubae* (Malvaceae) [42] and a set of plant-based alkaloids against methicillin-resistant *S. aureus* (MRSA) [43]. A series of plant phenolic compounds have been functioning as ethidium bromide EPIs in *Mycobacterium smegmatis* [44]. A series of synthetic efforts have been concentrated in paroxetine and femoxetine [45], piperine and fluoroquinolone as the basis for designing structural analogues [46,47], phenothiazines [48] with emphasis on thioridazine and chlorpromazine [49]. All these explorations are focusing in the bioassay driven purification and structural determination of natural EPIs employing an EtBr efflux assay. In retrospective this venture offers a rapid methodological alternative to the direct isolation of active compounds as well as attempts to enrich the EPI discovery process with an extensive and rationalized secondary validation of lead chemotypes. The

**Figure 3. Efflux potentiation by 4',5'-O-dicaffeoylquinic acid in S. aureus (A), E. faecalis (B).** Efflux was measured using berberine by determination of the decrease in fluorescence following binding to DNA and is expressed as % fluorescence. Cells were loaded with berberine at a concentration of 100 μg/ml, and then resuspended in buffer in the absence or presence of 4',5'-ODCQA, at the same final concentrations used for the MIC determinations. doi:10.1371/journal.pone.0018127.g003
Antimicrobial and toxicity profile of caffeoylquinic acids combined with prior art and information regarding their impact in antioxidant defenses in mammalian systems suggests a potential similar role in bacteria. The direct antimicrobial activity of CQA implies an array of possibilities including effect in the cell envelope and requires a robust target based validation and investigation.

Materials and Methods

Microbial strains and culture conditions

The following bacterial strains were used in this study: S. aureus 8325-4 (wild-type); K1758 (8325-4 ΔnorA); QT1 8325-4 norR6cat (NorA is overexpressed [50], S. aureus Community Associated
(CA)-MRSA USA300 (Human isolate/ Clinical Microbiology, MGH), *E. faecalis* OGRF1 (Fus Rif; β-Cl-Phe), *E. faecalis* GW481 (OG1RF:ArmE), [51], *Escherichia coli* K12 (ATCC), prototrophic wild type reference strain *Candida albicans* DAY185 [52]. Bacterial cells were cultured in Mueller–Hinton Broth (MHB) and yeast cells in YPD (unless is otherwise stated). Cell growth was assessed with a spectrophotometer (Shimadzu, Mini 1240) at 600 nm (OD600).

**Chemicals**

All solvents used in chromatography were of HPLC grade from Lab-Scan Analytical Sciences Ltd. (Dublin Ireland); Formic acid from Merck (Haarlem, The Netherlands) and H2O was produced in-house (Milli-Q Water Purification System, Millipore). Acetonitrile-d3 (99.8%) was obtained from Cambridge Isotope Laboratories (Apledoorn, The Netherlands). Antibiotics (erythromycin, tetracycline) and antimicrobials (berberine, ethidium bromide, rhodamine 6G, chlorogenic acid) were purchased from Sigma Chemical Co. (St. Louis, Mo.). Fluoroquinolones (norfloxacin, ciprofloxacin, levofloxacin and moxifloxacin) were from the Massachusetts General Hospital Pharmacy [http://www.massgeneral.org/services/pharmacy.aspx]. INF-271 was provided by Chembridge Inc. San Diego, CA 1',3',5'-O-DCQA as well as peracetylderivatives of both DCQAs, were kindly provided by Jiri Slanina (Department of Biochemistry Faculty of Medicine Masaryk University in Brno [53] and 3',5'-O-DCQA, 4',5'-O-DCQA by Cfin Oskar Tropitzsch e.K. (Marktredwitz, Germany).

**Plant Material & Aqueous infusions**

*Artemisia absinthium*, growing wild in Epirus region (Northwestern Greece) was collected in the period from spring to summer. 2 g of dried aerial parts of *A. absinthium*, ground to pass a 0.4 mm sieve, were added to 50 ml of boiling double distilled water (DDW) and stirred for 30 min. The plant residue was then filtered, and the

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Figure 5. Docking results and interactions within the binding pockets of MES for of all CQAs. All CQAs can successfully enter the binding sites of both efflux systems (A, B). See also Table 3 for the calculated energetics.
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filtrate was lyophilized. The 40 mg of dried extract produced were analyzed for the determination of its main active components. Plant materials and aqueous infusions preparations as well as instrumentation used for the analysis of the constituents are reported in Text S1.

### Susceptibility testing

Cells (10^6/ml) were inoculated into MHB (RPMI for *C. albicans*) and dispensed at 0.2 ml/well in 96-well microtiter plates. Growth inhibition was determined by serial 2-fold dilution of test extract or compounds in 96-well microtiter plates to determine Minimal Inhibitory Concentrations (MICs). In order to identify compounds with EPI activity, extracts and compounds were serially 2-fold diluted in combination with 30 μg/ml berberine for gram-positive bacteria, 10 μg/ml crythromycin for *E. coli*, and 10 μg/ml rhodamine 6G (R6G) for yeast cells. An EPI was defined as a compound that completely prevented cell growth in the presence of sub-inhibitory antibiotic during an 18-hr incubation at 37°C or 24-48 hr at 30°C (*B. cereus*, *C. albicans*). All tests were done in triplicate by following the Clinical and Laboratory Standards Institute (CLSI, former NCCLS, National Center for Clinical Laboratory Standards) recommendations [54,55]. Growth was assayed with a microtiter plate reader (Spectramax PLUS384, Molecular Devices) by absorbance at 600 nm. The checkerboard inhibition was determined by serial 2-fold dilution of test extract or compound in 96-well microtiter plates. Growth reached the late log phase (OD600 between 0.9 and 1), pelleted by centrifugation (2 min, 12,000 rpm), and then washed and resuspended in 25 mM PBS (pH 7.4) containing 0.05 g L^-1 folic acid, 0.01 mg L^-1 1 thiotic acid, and 4.5 mg L^-1 pyridoxine hydrochloride, 0.025 mg L^-1 riboflavin, 0.01 mg L^-1 thiamine, 0.025 mg L^-1 nicotinic acid, 0.025 mg L^-1 calcium pantothenate, 0.5 μg L^-1 vitamin B12, 0.025 mg L^-1 β-aminobenzoic acid, 0.025 mg L^-1 thiotic acid, and 4.5 mg L^-1 monopotassium phosphate. Cells were then resuspended to an OD600 of 0.8 in buffer with 10 mM glucose. Cells were then loaded with either 30 μg/ml berberine and 10 μg/ml 4',5'-ODCQA and incubated at 37°C with aeration for 20 min. Cells were then centrifuged, washed, and resuspended at an OD600 of 0.15 in HEPES buffer. Assays were performed in 96-well flat-bottom black plates (Costar) in a final volume of 200 μl. Berberine was added at 30 μg/ml, and fluorescence was measured with a Spectramax Gemini spectrophotometer (Molecular Devices) at a 355-nm excitation wavelength and a 517-nm emission wavelength.

### Berberine accumulation assays

Determination of berberine uptake was performed as described previously [9,59]. Cells were cultured with aeration at 37°C to an optical density at 600 nm (OD600) of 1.8, pelleted, and washed twice with 20 mM HEPES-NaOH (pH 7.0) buffer. The cells were then resuspended to an OD600 of 0.3 in 1 ml of HEPES buffer containing 10 μM glucose followed by incubation at 37 or 30°C for 1 h. The cells were centrifuged, washed, and resuspended at an OD600 of 0.15 in HEPES buffer. Assays were performed in 96-well flat-bottom black plates (Costar) in a final volume of 200 μl. Berberine was added at 30 μg/ml, and fluorescence was measured with a Spectramax Gemini spectrophotometer (Molecular Devices) at a 355-nm excitation wavelength and a 517-nm emission wavelength.

### Berberine competitive efflux assay

Those were performed as described [59]. *S. aureus* and *E. faecalis* cells were cultured with aeration and mild agitation until they reached the late log phase (OD600 between 0.9 and 1), pelleted by centrifugation (2 min, 12,000 rpm), and then washed and resuspended in 25 mM PBS (pH 7.4) containing 0.05 g L^-1 MgSO_4, 7 g L^-1 K_2HPO_4, 0.5 g L^-1 sodium citrate-3H_2O, 1 g L^-1 (NH_4)_2SO_4, 0.01 mg L^-1 folic acid, 0.05 mg L^-1 pyridoxine hydrochloride, 0.025 mg L^-1 riboflavin, 0.01 mg L^-1 thiamine, 0.025 mg L^-1 nicotinic acid, 0.025 mg L^-1 calcium pantothenate, 0.5 μg L^-1 vitamin B12, 0.025 mg L^-1 β-aminobenzoic acid, 0.025 mg L^-1 thiotic acid, and 4.5 mg L^-1 monopotassium phosphate. Cells were then resuspended to an OD600 of 0.8 in buffer with 10 mM glucose. Cells were then loaded with either 30 μg/ml berberine and 10 μg/ml 4',5'-ODCQA and incubated at 37°C with aeration for 20 min. Cells were then centrifuged in a 4°C cold room, washed in ice-cold PBS, and added at an OD600 of 0.3 to a chilled 96-well flat-bottom white microtiter plate (Costar) containing ice-cold 25 mM PBS and 10 mM glucose in a final volume of 200 μl. Fluorescence was measured with a Spectramax PLUS384 GeminiXS spectrophotometer (Molecular Devices) at a 355-nm excitation wavelength and a 517-nm emission wavelength.
Biofilm formation & Quantitation

Biofilm formation is assayed by the ability of cells to adhere on polystyrene surface of 24-well microtiter plates [60]. The indicated medium is inoculated from a 1:100 dilution from an overnight BHI culture. Plates are incubated at 37°C for 48 hrs. Compounds are added at the appropriate concentrations and following by additional overnight incubation at 37°C. Two identical microtiter plates were used for each independent experiment. For the first plate crystal violet (CV) solution was added to each well, the plates were incubated at room temperature, rinsed thoroughly with water and dissolved. CV-stained biofilms were solubilized in ethanol, and samples were transferred to a new polystyrene microtiter dish, and the absorbance was determined with a plate reader at 600 nm. For the second plate cells are dissolved followed by CV determination on BHI agar plates.

Statistics

For the toxicity experiments studies values are means of three separate experiments and bars are SEM. For biofilm inactivation studies, between means were tested for significance by a paired two-tailed t test. The significance level was set at p<0.05.

Structure-activity relationships and comparative protein-ligand docking studies

Two efflux pump crystal structures [34,35] were selected to perform comparative docking of caffeoylquinic acids to their binding sites: the glycerol-3-phosphate transporter from Escherichia coli [35] (PDB ID: 1PW4) was the representative structure from the MFS, and Sav1866 from Staphylococcus aureus [34,35] (PDB ID: 2HYD), is an ABC transporter of Gram-positive bacteria. 2HYD was crystallized in the closed conformation. Since 2HYD shares very high structural similarity with P-glycoprotein [34,61], the open conformation was generated by flexible structural alignment with FATCAT (http://fatcat.burnham.org/) against the corresponding P-glycoprotein crystal structure [61] (PDB ID: 3G61). This approach concluded in a good quality model (see Figure S3 and Table S1).

For the docking trials, HADDOCK version 2.1 [62] was used. HADDOCK is a highly successful modeling approach that makes use of biochemical and/or biophysical interaction data such as chemical shift perturbation data, mutagenesis data, or bioinformatic predictions and thus, incorporates structural knowledge of the target to drive the docking procedure. The docking was performed with default parameters using the web server version of HADDOCK [63]. All calculations were performed with CNS1.2 [64]. Non-bonded interactions were calculated with the OPLS force field [65] using a cutoff of 8.5 Å. The electrostatic potential (Eelec) was calculated by using a shift function, while a switching function (between 6.5 and 8.5 Å) was used to define the Van der Waals potential (Evdw). The HADDOCK score is used to rank the generated poses. It is a weighted sum of intermolecular electrostatic (Eelec), van der Waals (Evdw), desolvation (AGsolv) and ambiguous interaction restraints (AIR) energies with weight factors of 0.2, 1.0, 1.0 and 0.1, respectively.

The ambiguous interaction restraints to drive the docking were defined as follows. The ligand was treated as an active residue for all stages of the docking, while the residues within the protein binding site were only defined as active for the rigid-body docking stage and considered as passive the subsequent semi-flexible refinement stage. This strategy allows to effectively pulling the ligand within the binding site during rigid-body docking while allowing a more thorough exploration of the binding pocket during the refinement stage. Residues considered active for 1PW4 were 30, 42, 45, 46, 134, 165, 166, 269, 289, 290, 299, 362 and 393, whereas for 2HYD*, the active residues were 26, 252, 255, 288, 291, 295, 604, 608, 611, 612, 614, 648, 722, 837, 966, 969, 970, 973, 974 and 986. Passive residues were defined automatically via the web-server, as those surrounding the active ones.

Supporting Information

Figure S1 400 MHz 1H-NMR spectrum of 1, in CD3CN. The spin system corresponding to 5’-O-DCQA is revealed. The H-2/ and H-6/signals of the quinic moiety are overlapped by the CD3CN-H2O residual signals and, therefore, they are eliminated. (TIFF)

Figure S2 400 MHz 1H-NMR spectrum of 2A and 2B, in CD3CN. The spin system of 3’,5’-O-DCQA (2A) is mainly indicated while that one of 4’,5’-O-DCQA (2B) is suggested in italics. The signals of the aromatic protons of 2B are greatly overlapped by those of the 2A isomer and, thus, are not indicated in the spectrum. (TIFF)

Figure S3 View of protein-ligand hydrogen bonds in the top two clusters of the modelled complex of 3’,5’-O-DCQA with 1PW4: (A) top ranking cluster, (B) second, most populated cluster. The different orientations of the 3’,5’-O-DCQA is reflected in the differences in the hydrogen bonding pattern. For example, 3’,5’-O-DCQA, show a different pattern of hydrogen bonds of the carbonyl groups, interacting in one case with the side chains of Y38, Y42 and W261 whereas in the second cluster the observed hydrogen bonds are different and fewer in number. This figure was generated with PyMol (www.pymol.org). (TIFF)

Figure S4 Ramachandran plot of the model of Sav1688 in the open conformation. The plot is based on an analysis of 118 structures of resolution of at least 2.0 Å and an R-factor no greater than 20%. A good quality model would be expected to have over 90% in the most favoured regions. Plot statistics: Residues in most favoured regions [A,B,L], 1001 (95.5%). Residues in additional allowed regions, [A,B,L,P], 43 (4.1%). Residues in generously allowed regions, (∼A, ∼B, ∼L, ∼P), 2 (0.2%). Residues in disallowed regions, 2 (0.2%). Number of non-glycine and non-proline residues, 1048 (in total: 100.0%). Number of end-residues (excl. Gly and Pro), 4. Number of glycine residues (shown as triangles), 74. Number of proline residues, 30. Total number of residues: 1156. (TIFF)

Table S1 PSVS (http://psvs-1_4-dev.nesg.org/) validation statistics of the modelled open form (2HYD*) and, for comparison, of the crystal structure 2HYD. (TIFF)

Text S1 Plant materials and aqueous infusions preparations as well as instrumentation used for the analysis of the constituents of Artemisia absinthium extracts. (DOC)

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Author Contributions

Conceived and performed the experiments: YCF KL GPT. Performed the experiments: YCF PLK VE HH. Analyzed the data: YCF PLK AMJB MRH GPT. Contributed reagents/materials/analysis tools: JV AM JB KL MRH. Wrote the paper: YCF MRH GPT.


