Potentiating activity of rhein in targeting of resistance genes in methicillin-resistant \textit{Staphylococcus aureus}

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**ABSTRACT**

**Objective:** To investigate the synergistic effect between rhein (RHE) and oxacillin against \textit{Staphylococcus aureus} (MRSA) at the gene level. **Method:** A minimum inhibitory concentration and checkerboard dilution test were conducted to evaluate antibacterial activity. Reverse transcriptase polymerase chain reaction was conducted to investigate the gene expressions. **Results:** RHE exhibited a minimum inhibitory concentration of 62.5-250.0 μg/mL against various MRSA strains and the reference strain, respectively. As revealed by the checkerboard assay, a combination of RHE and oxacillin exhibited synergistic or partially synergistic effects against MRSA strains. RHE decreased the expressions of \textit{mecA}/\textit{blaZ} in a dose-dependent manner. RHE also decreased the expressions of the regulator genes \textit{mecI}/\textit{blaR1} and \textit{mecI}/\textit{blaR1}.

**Conclusions:** We suggest that RHE affects the activity of \textit{mecI}/\textit{blaR1}, which is located in the cell membrane of MRSA and results in the suppression of \textit{mecA}/\textit{mecI}/\textit{mecR1} and \textit{blaZ/blaI/blaR1} gene expressions.

**1. Introduction**

Methicillin-resistant \textit{Staphylococcus aureus} (\textit{S. aureus}) (MRSA) causes infections ranging from skin and soft tissue infection to more severe diseases, including bacteremia, osteomyelitis, arthritis, pneumonia, sepsis, and pericarditis\textsuperscript{[1]}. \textit{β}-Lactams, which are antibiotics that disrupt cell wall synthesis by targeting the four \textit{S. aureus} penicillin-binding proteins involved in the transpeptidation of peptidoglycan, were commonly used to treat bacterial infection\textsuperscript{[2]}. However, MRSA has recently developed two major resistance mechanisms against \textit{β}-lactam antibiotics. First, bacteria produce \textit{β}-lactamases, a family of enzymes that inactivate \textit{β}-lactam antibiotics, such as penicillins, carbapenems, and monobactams by hydrolyzing their \textit{β}-lactam rings\textsuperscript{[3]}. Second, the production of penicillin-binding protein 2A (PBP2a) is a major determinant of \textit{β}-lactam resistance. PBP2a has a low affinity for \textit{β}-lactams, thereby allowing it to maintain its transpeptidation activity in the presence of \textit{β}-lactam antibiotics\textsuperscript{[4]}. \textit{β}-lactamase and PBP2a are encoded by \textit{blaZ} and \textit{mecA}, respectively; these are located in a mobile genetic element known as the Staphylococcal cassette chromosome mec (SCCmec). The transcription of \textit{mecA} and \textit{blaZ} is regulated by the \textit{mec-mecR1} and \textit{bla-mepR1} systems, respectively. The mec and bla operons are controlled by two-component systems comprising the repressors \textit{mecI} and \textit{blaI} and the sensors \textit{mecR1} and \textit{blaR1}. The

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genes for mecA blaZ, its repressors mecI/blaI, and the transducing-sensors mecR1/blaRI are clumped together, either on a plasmid or within the bacterial chromosome. In the absence of β-lactam, the DNA repressor MecI/BlaI suppresses mecA blaZ by binding to the conserved DNA motif TACA/TGTA, which is located in the promoter region of mecA blaZ. However, when exposed to β-lactam antibiotics, acylation of BlaRI/MecRI, which is a transmembrane and signal transduction protein, is subsequently followed by autoproteolytic cleavage on the cytoplasmic side of the cell membrane. The cleaved intracellular fragment of MecRI/BlaiI then moves to the bacterial chromosome where it removes its cognate repressor MecI/BlaI by proteolysis. Transcription of the mecA/ mecRI and blaZ/blaRI/blaI genes begins once the repressor dissociates from the promoter region[5-7].

To overcome β-lactam resistance, antibiotics with different modes-of-action or agents that inhibit drug resistance should be used concurrently. Therefore, antibacterial agent combination therapy appears useful because it can enhance antibacterial activity and reduce drug resistance[8]. Rhein (RHE) is a lipophilic anthraquinone compound found in rhubarb (Rheum palmatum L.), Reynoutria japonica (Houtt.), and Fallopia multiflora, and is extensively used in treating various clinical disorders, such as hepatic disease, osteoarthritis, atherosclerosis, various cancers, and diabetic nephropathy (Figure 1). RHE was identified as a major metabolite of diaceterein, a prodrug used in treating osteoarthritis[9-12]. In addition, RHE has been reported to possess antibacterial activity and synergistic effects against MRSA when combined with antibiotics such as ampicillin (AM) or oxacillin (OX)[13].

However, there is no reports which state that RHE inhibits the drug resistance mechanism of MRSA at the molecular level. Here, we investigated the synergistic effect of RHE combined with antibiotics on MRSA drug resistance at the gene level.

2. Materials and methods

2.1. Chemicals

RHE (4,5-dihydroxyanthraquinone-2-carboxylic acid), 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT), dimethyl sulfoxide (DMSO), AM, and OX were purchased from Sigma-Aldrich (St. Louis, MO, USA). Mueller-Hinton (MH) broth and MH agar were purchased from Difco Laboratories (Baltimore, MD, USA).

2.2. Bacterial strains and growth conditions

Strains 25923 and 33591 were purchased from the American Type Culture Collection (ATCC). Clinical isolates of bacterial strains (DHCR 1-15) were obtained from the Department of Plastic Surgery of Wonkwang University Hospital (Iksan, Korea). Before experimentation, all bacteria were stored in 30% glycerol and were frozen at -70 °C. All strains were maintained on MH agar plates or nutrient agar, and antibacterial assays were conducted using MH broth. Bacterial growth was monitored as a function of turbidity by measuring optical density (OD) at 600 nm[14,15].

2.3. Determination of minimum inhibitory concentration (MIC)

MICs were determined using the method described in the Clinical and Laboratory Standards Institute (CLSI)[16]. The RHE MIC determinations with MRSA were performed using 96-well microtiter plates. Briefly, RHE was dissolved in DMSO followed by MH broth. The suspension was diluted with RHE. The bacterial concentration was adjusted to 5×10^7 CFU/mL of an overnight bacterial culture was inoculated into each well. The final volume in each well was 150 μL, and the DMSO concentration was 5% (which has no influence on bacterial growth). The DMSO concentration used is extremely important, because high concentrations can influence the activity of RHE. The samples were then incubated at 37 °C for 24 h. Twenty microliters of 1 mg/mL 3-(4,5-dimethylthiazol-2-y1)-2,5-diphenyltetrazolium bromide (1 mg/mL) was added to the suspension and incubated at 37 °C for 30 min. Clear yellowish-colored wells indicated inhibition of microbial growth, whereas dark blue-colored wells indicated the absence of inhibition. The MIC was defined as the lowest concentration producing no visible growth, as observed through the naked eye[17].

2.4. Checkerboard dilution test

The checkerboard dilution test was used to measure the synergistic effects of RHE and OX. OX was mixed in MH broth and serially diluted with RHE. The bacterial concentration was adjusted to 1.5×10^8 CFU/mL. Suppression of microbial growth was checked for after incubation for 24 h at 37 °C. Each experiment was conducted in triplicates. The interaction between RHE and OX was determined using the fractional inhibitory concentration index.

Figure 1. Chemical structure of rhein.
2.5. Reverse transcriptase polymerase chain reaction (PCR)

MRSA (ATCC 33591) was cultured in MH broth until an OD600 of 0.35-0.45 was reached; the culture was then treated with various concentrations of OX and RHE and incubated for 20 min at 37 °C. RNA was extracted using the E.Z.N.A.® bacterial RNA kit (Omega Bio-tek, Norcross, GA, USA), in accordance with the manufacturer’s instructions. Single-strand cDNA synthesis was performed using the Quantitate Reverse Transcription Kit, in accordance with the manufacturer’s instructions. PCR was performed using the Maxime PCR PreMix (20 μL; iNtRon Biotechnology, Inc., Seongnam, Korea), primers, cDNA sample, and sterile distilled water. Primer sequences of mecA, mecI, mecR1, blaZ, blaI, blaR1, and 16s rRNA are presented in Table 1. After PCR, equal amounts of the PCR products (12 μL) were subjected to 1.5% agarose gel electrophoresis; bands were visualized under ultraviolet light.

### Table 1

<table>
<thead>
<tr>
<th>Primer</th>
<th>Sequence (5′→3′)</th>
</tr>
</thead>
<tbody>
<tr>
<td>blaZ-F</td>
<td>GATAAGAAGATTTGCTATGC</td>
</tr>
<tr>
<td>blaZ-R</td>
<td>GCATATGTTTTAGCTTGAC</td>
</tr>
<tr>
<td>blaI-F</td>
<td>GCAAATGGAAAATATCTTAGG</td>
</tr>
<tr>
<td>blaI-R</td>
<td>GAAAGATCCATTTTCTGACACTCTCATC</td>
</tr>
<tr>
<td>blaR1-F</td>
<td>CATGACAATGGAATGAAAGGC</td>
</tr>
<tr>
<td>blaR1-R</td>
<td>CTATGATTCCTACGATACAG</td>
</tr>
<tr>
<td>mecA-F</td>
<td>ATGAGATTGCACATGCTCC</td>
</tr>
<tr>
<td>mecA-R</td>
<td>TGGATGACGATCTGACGCC</td>
</tr>
<tr>
<td>mecI-F</td>
<td>CTGACGAAATGGAAATTATG</td>
</tr>
<tr>
<td>mecI-R</td>
<td>ACAAGTGAATGGAAATCCGCC</td>
</tr>
<tr>
<td>mecR1-F</td>
<td>AAGCAGCTTTACATGCGACA</td>
</tr>
<tr>
<td>mecR1-R</td>
<td>GAGTAAATTTTGTCTGATG</td>
</tr>
<tr>
<td>16s rRNA-F</td>
<td>CGTGCCTTATACGTAATGCA</td>
</tr>
<tr>
<td>16s rRNA-R</td>
<td>CCGTCTTTCTATTTTGACCA</td>
</tr>
</tbody>
</table>

2.6. Statistical analyses

The statistical analysis was assessed using one-way analysis of variance, followed by Scheffe’s test for multiple comparisons. Data were presented as mean±standard deviations. All calculations were assessed using SPSS statistics 23 software (SPSS Inc. Chicago, IL, USA). P<0.05 was considered statistically significant.

3. Results

3.1. Determination of antibacterial activity

To examine the antibacterial activity of RHE, AM, and OX, antibacterial susceptibility testing was conducted on MRSA using the CLSI method. AM and OX, which are β-lactam antibiotics capable of inhibiting bacterial cell wall synthesis, were used as positive controls. RHE exhibited similar MICs in all tested strains. The RHE MIC values of all tested strains (ATCC and clinical isolates) ranged from 62.5 to 250.0 μg/mL (62.5 μg/mL for ATCC 33591), whereas AM MICs ranged from 0.97 to 125.00 μg/mL. The MIC for OX against ATCC 33591 was 1 000 μg/mL; MIC values ranged from 250 to 1 000 μg/mL for other strains. The results of the MIC assay are presented in Table 2.

### Table 2

<table>
<thead>
<tr>
<th>S. aureus strains</th>
<th>MIC of RHE (μg/mL)</th>
<th>MIC of antibiotics (μg/mL)</th>
<th>FICI</th>
<th>Overcome</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>RHE alone</td>
<td>With OX</td>
<td>OX alone</td>
<td>With RHE</td>
</tr>
<tr>
<td>ATCC 33591</td>
<td>62.5</td>
<td>15.60</td>
<td>1 000</td>
<td>125.0</td>
</tr>
<tr>
<td>DHCR-1</td>
<td>62.5</td>
<td>15.60</td>
<td>1 000</td>
<td>62.5</td>
</tr>
<tr>
<td>DHCR-2</td>
<td>62.5</td>
<td>31.25</td>
<td>1 000</td>
<td>250.0</td>
</tr>
</tbody>
</table>

Synergistic combinations were investigated using the checkerboard method. The fractional inhibitory concentration indices (FICI) were interpreted as follows: synergy<0.5; partial synergy 0.50-0.75; additive effect 0.76-1.0; indifference>1.0-4.0; and antagonism>4.0. MIC: minimum inhibitory concentration.

3.3. Polymerase chain reaction (PCR) analysis

RT-PCR was performed to evaluate the inhibitory effects of RHE against the MRSA resistance genes. RHE decreased the expression of mecA/blaZ in a dose-dependent manner. In contrast, their expression was increased by OX and again decreased with a combination of RHE and OX. In addition, the expression of the regulator genes mecI/blaI and mecR1/blaR1 also decreased in the presence of RHE or combined with OX (Figure 2 and 3).
4. Discussion

Drug resistant bacteria are a menace to the healthcare system, because they limit remedies to infections worldwide. Resistance can occur through the acquisition of the resistance gene by horizontal gene transfer or through spontaneous mutation. Both mecA and blaZ play an important role in the β-lactam resistance of MRSA. The chromosomal gene mecA encodes PBP2a, an alternative penicillin-binding protein having low affinity for β-lactams; PBP2a takes over the function of other PBPs that have been inactivated by β-lactam antibiotics[18]. The blaZ gene encodes β-lactamase, which inactivates penicillin by hydrolysis of the β-lactam ring[19]. Given restricted remedy in the research of novel antibacterial agent, there is notable study in targeting resistance genes to help re-establish susceptibility to commercial antibiotics[20]. Several researchers have previously reported that some antibacterial substances target these two β-lactam resistance genes, mecA and blaZ genes[21,22]. Therefore, we performed the study on antibacterial compound targeting β-lactam resistance genes.

Figure 2. Expression of PBP2α-related genes. PCR showing the expression of mecA, mecI, and mecR1 of MRSA exposed to various concentrations of rhein alone or in combination with 31.25 μg/mL oxacillin. 16s rRNA was used as a loading control, and expression levels were normalized to 16s rRNA levels. Different letters (a-e) indicate significant differences at P<0.05 based on analysis of variance followed by the Scheffe’s test for multiple comparisons. Values are presented as mean±SD.

Figure 3. Expression of β-lactamase-related genes. PCR showing the expression of blaZ, blaI, and blaR1 of MRSA exposed to various concentrations of rhein alone or in combination with 31.25 μg/mL oxacillin. 16s rRNA was used as a loading control and expression levels were normalized to 16s rRNA levels. Different letters (a-d) indicate significant differences at P<0.05, based on analysis of variance followed by the Scheffe’s test for multiple comparisons. Values are presented as mean±SD.
are expressed by the transcription of mecA and blaZ, respectively. In the presence of OX, acylation of BlaR1/MecR1, a sensor protein located in the cell membrane, is followed by the autoprolyteic cleavage of its cytoplasmic domain. The intracellular fragment of BlaR1/MecR1 travels to the SCCmec and proteolytically cleaves the Blal/MecI repressor bound to the conserved TACA/TGTA DNA motif, thereby leading to the transcription of the mec/bla system[5-7]. When RHE was added to the media containing MRSA, the gene expressions of mecA/mecR1 and blaZ/blaI/blaR1 reduced. This suggests that RHE decrease β-lactam resistance of MRSA, because it inhibits mec and bla genes located in SCCmec. When MRSA senses the presence of β-lactam antibiotics by MecR1/BlalR1, it produces resistance factors. The mec/bla genes expressions were increased by OX, again decreased with a combination of RHE and OX. It showed that RHE influences the MecR1/blaR1 located in the cell membrane of MRSA, thereby ultimately inhibiting the mec/bla system by interrupting signal transduction for transcription. Similar findings have been reported in a previous study wherein MRSA strains were treated with thioridazine, which affects membrane stability and induces conformational changes in the MecR1 and BlaR1 protein, thereby resulting in a subsequent decrease in the level of PBP2a activity via the inhibition of mecA/mecR1 and blaZ/blaI/blaR1 gene expression[21]. Chlorpromazine also was reported to have a similar effect. Chlorpromazine inhibits the expression of mecA/mecR1 and blaZ/blaI/blaR1 by affecting the cell membrane of MRSA[23]. In conclusion, RHE inhibited the gene expressions of mec/bla system because of affecting the MecR1/BlalR1 located in cell membrane of MRSA, which manifested itself as a synergistic effect between RHE and OX against MRSA. These results indicate that RHE was targeted to the expression of the resistance gene of MRSA. This study therefore demonstrates a new pharmacological activity for RHE, which could be a good candidate for clinical development as an antibacterial drug. The promising results of this study are expected to enhance the use of natural products as drugs in the future.

Conflicts of interest statement

The authors declare that there is no conflict of interest.

References