

Molecular screening of Antibiotic Resistance Genes in Blue-Green Algae and pathogenic Bacteria Isolated from Local Environmental and clinical sources

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ABSTRACT

Background: Blue-green algae can adapt to different environmental conditions through physiological and biochemical responses. Their tolerance to antibiotics may also be associated with specific resistance mechanisms, including antibiotic-inactivating enzymes encoded by resistance genes. This is due to their possession of resistance genes, including the *bla* gene, which encode the β -lactamase enzyme responsible for breaking down penicillin. **Objective:** The study aimed to detect the presence of antibiotic resistance genes in local isolates of blue-green algae and compare them with pathogenic bacterial isolates. **Methodology:** Eight isolates of blue-green algae were obtained from the Euphrates River and purified on BG11 medium, while four pathogenic bacterial isolates were obtained from Ramadi Teaching Hospital and identified using microscopic examination and standard biochemical tests. Deoxyribonucleic acid (DNA) was extracted from all samples, and PCR was used to detect six resistance genes: *bla*, *cat*, *erm*, *npt*, *aadA*, *gmr*. **Results:** The results showed a great similarity in the patterns of resistance genes between algae and bacteria, particularly the *bla* gene, which appeared in most species of blue-green algae and pathogenic bacteria. The *erm* and *cat* genes were also detected in a large number of the isolates examined. Among the samples studied, *Chroococcus* sp. and *Escherichia coli* were the two species with the most resistance genes. The genus *Oscillatoria* sp. however, was less resistant, as the results showed that it possessed only two genes: *gmr* and *aadA*. Other resistance genes, such as *bla* and *cat*, were not detected in this species. **Conclusion:** The nucleotide sequences of blue-green algae and pathogenic bacteria were compared using the MEGA_X program, and the results revealed a high percentage of similarity, reaching 95%, between species belonging to different families. Research has shown that pathogenic bacteria and cyanobacteria are 95% similar in *gmr*, 92% similar in *bla* and 77% in *sul*.

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Keywords: Cyanobacteria, Blue Green Algae, Antibiotic resistance genes, Biocontamination, Horizontal gene transfer.

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INTRODUCTION

Cyano-green algae create defense mechanisms against antibiotics—known as resistance mechanisms so that they can survive. Cyanobacteria possess various defense mechanisms that enable them to survive in the presence of antibiotics. These mechanisms may include limiting antibiotic entry into cells, reducing antibiotic activity, and interfering with cellular processes involved in protein production (1). The global problem caused by antibiotic resistant cyanobacteria could cause higher mortality rates. Antibiotic-inactivating enzymes are produced by various mechanisms, one of which is β -lactamase that degrades antibiotics like penicillin (2).

Cyanobacteria are microorganisms that live in a variety of ecosystems. They can be found in several types of habitats, including moist soils and aquatic soils. Blue-green algae come in many forms and types. They can be unicellular (single-celled), filamentous (thread-like), aggregative, and colonial. In addition, they have one circular chromosome.

Their genome lengths have been shown to range from 1.4 to 12 million bases (bp). Cyanobacteria possess DNA recombination and repair mechanisms that contribute to genome maintenance and adaptation to environmental conditions (3). Certain types of cyanobacteria can be engineered for helpful use to enable the introduced genes of industrial use (4). Blue-green algae can form a phenomenon called blooms. Some cyanobacteria produce enzymes that may contribute to the degradation of antibiotics in the environment can harm aquatic organisms like fish and cause destruction to the aquatic ecosystem. When humans consume fish or come into contact with blue-green algae while swimming, it can Exposure to harmful cyanobacterial blooms during swimming may have adverse effects on human health (5). There are several reasons to believe that cyanobacteria may contain resistance genes (ARGs). Plasmids are one of the mobile genetic elements that may facilitate horizontal gene transfer (6). Horizontal gene transfer is a major mechanism by which antibiotic resistance genes are transferred between microorganisms (7) Cyanobacteria have been suspected to determine their antibiotic resistance by plasmids, because their sensitivity to antibiotics also depends on the type and concentration of the antibiotics (8). There are three main methods for DNA transfer between microorganisms: conjugation, transformation, and transduction. Antibiotic resistance genes are transferred between some species of blue-green algae and bacteria. This gene transfer may be associated with mobile genetic elements, such as plasmids, transposons, and integrons (9,10). Some cyanobacteria may pose risks to human health and the environment. The spread of antibiotic resistance is also an important environmental and public health concern. This resistance develops due to processes that enable microbes to grow and reproduce despite the presence of antibiotics. The overuse of antibiotics in medicine and agriculture is causing new bacteria to develop effective means of resistance. Blue-green algae are known to produce enzymes capable of degrading antibiotics, some cyanobacteria produce enzymes that may contribute to the degradation of antibiotics in the environment (11). The study assessed the antibiotic-resistance genes in some local freshwater cyanobacteria from Marine Biology Research Station, Kakinada. The results were then compared to ARGs from pathogenic bacteria causing infections to determine the presence and frequency of other organisms in Iraqi freshwater (12).

METHODOLOGY

Algal and Bacterial Isolates

Eight isolates of blue-green algae were obtained from Al-Anbar Governorate. The samples were collected and processed in the graduate laboratories of the Department of Life Sciences, University of Anbar, for the purpose of this study. The isolates were purified using decimal dilution techniques, as described by Parvin *et al.* (13). Purification was confirmed after isolation by culturing the isolates on Nutrient agar to ensure the purity of the cultures and the absence of bacterial and fungal contamination. The purified isolates were then cultured in BG11 medium (HiMedia Laboratories, India) according to the manufacturer's instructions, using 100 mL of BG11 medium. Good growth was achieved, and the resulting biomass was collected. The algae were incubated at 26°C under a 12 h light/12 h dark photoperiod.

Four pathogenic bacteria (*E. coli*, *Pseudomonas aeruginosa*, *Klebsiella pneumoniae*, and *Staphylococcus aureus*) were isolated from urine and sputum samples from Ramadi Teaching Hospital. These collected isolates were cultured on Nutrient Broth medium, then incubated at 37°C for 24 hours. Identification of the samples was carried out using the 16S rRNA gene, which showed a similarity of up to 95% with the NCBI Database. Comparative analysis of antibiotic-resistance genes was performed between the isolated cyanobacteria and pathogenic bacteria to assess similarities in their resistance-gene profiles, following the comparative genomic approach described (14).

DNA Extraction

Using Geneaid Biotech Presto Mini gDNA Bacteria Kit, Taiwan, DNA was extracted separately from blue green algae and bacteria. The extracted DNA was confirmed using a 1% agarose gel 80 V for 45 minutes. The extracted DNA was stored at temperature -20°C.

Polymerase Chain Reaction

Six antibiotic resistance genes were detected using PCR. The antibiotic resistance genes were *gmr*, *aadA*, *Bla*, *Cat*, *erm*, *npt*, responsible for resistance to the following antibiotics Gentamicin (Gm), Streptomycin (Sp), Ampicillin (Ap), chloramphenicol (Cm), Erythromycin (Em), Kanamycin. (Km). (Table 1) below shows the PCR's primer sequence, name and product. A thermocycler was used to perform PCR (Table 2) and the products were run on 1% agarose gel. Agarose gels were visualized using a UV transilluminator.

Table (1): The primers which were used to detect the ARGs in the samples

Gene	Primer Name	Primer sequence 5'. → 3'	PCR product Length (bp)	Reference
<i>gmr</i> (Gm)	<i>gmr</i> F <i>gmr</i> R	TCCAGAACCTTGACCGAAC ATCACTTCTTCCCGTATGCC	654	(12)
<i>aadA</i> (Sp)	<i>aadA</i> . F <i>aadA</i> R	TACCAAGGCAACGCTATGTT C ATCAGAGGTAGTTGGCGTCA T	400	(12)
<i>bla</i> (Ap)	<i>bla</i> F <i>bla</i> R	TTTGCCTTCCTGTTTTTGCTC AACTTTATCCGCCTCCATCC	593	(12)
<i>cat</i>) Cm)	<i>cat</i> F <i>cat</i> R	ATCCCAATGGCATCGTAAAG ATCACAAACGGCATGATGAA	553	(12)
<i>erm</i> (Em)	<i>erm</i> F <i>erm</i> . R	CGCATCCGATTGCAGTATAA TCGTCAATTCCTGCATGTTT	885	(12)
<i>npt</i> Km)	<i>npt</i> F <i>npt</i> R	TGAATGAACTGCAGGACGAG AATATCACGGGTAGCCAACG	515	(12)
16S rRNA	16S rRNA F 16S rRNA R	CTGAAGATGGGTGGGGT CGTATTACCGCGGCTGCT	294	(25) (15)

Table (2): PCR amplification conditions used for the detection of antibiotic resistance genes.

PCR	Temperature	Times	Number of cycles
Initial Denaturation	95°C	5 min.	1
Denaturation	95°C	1 min.	35
Annealing	56°C	1 min.	
Extension	72°C	1 min.	
Final Extension	72°C	5 min.	1

Statistical analysis

Categorical data including the presence and prevalence of antibiotic resistance genes ARGs across Cyanophyta species and pathogenic bacterial isolates were expressed as frequencies and percentages. Differences in gene frequencies between Cyanophyta and pathogenic bacteria as well as among the individual target genes *bla*, *cat*, *erm*, *aacCI*, *aadA*, and *npt* were evaluated using the Pearson Chi-Square test. Fisher's Exact Test was additionally performed to account

for the small sample size and expected cell counts less than 5. All statistical analyses were performed using SPSS software version 26.0 IBM Corp Armonk NY USA. A p -value less than 0.05 were considered statistically significant.

DNA Sequencing

The purified PCR products were sent to Macrogen, South Korea, for DNA sequencing using the Sanger sequencing system. The obtained nucleotide sequences were analyzed using Chromas software and compared with sequences in the GenBank database of NCBI using BLASTn to determine sequence similarity and confirm the identity of the studied isolates.

RESULTS

The samples were identified as *Spirulina platensis*, *Anabaena lutea*, *Oscillatoria nigro-viridis*, *Langhya aestuarii*, *Wolleea Saccata*, *Limnospira Fusiformis*, *Chroococcus* sp., and *Oscillatoria* sp. The samples studied were identified by 16S rRNA gene amplification. The samples were blasted with NCBI database to match the sequences with the GenBank sequences; more than 95 percent matches rate was obtained. Previous studies have shown that cyanobacteria have the ability to continue living despite the presence of antibiotics (15) (16). The current study demonstrated that blue-green algae and bacteria can resist antibiotics. ARGs were investigated in the Cyanophyta and pathogenic bacteria studied. The *bla* gene was found in all blue-green algae and pathogenic bacteria except for the *Oscillatoria* sp and *Wolleea saccata*, as shown in Figure (1).

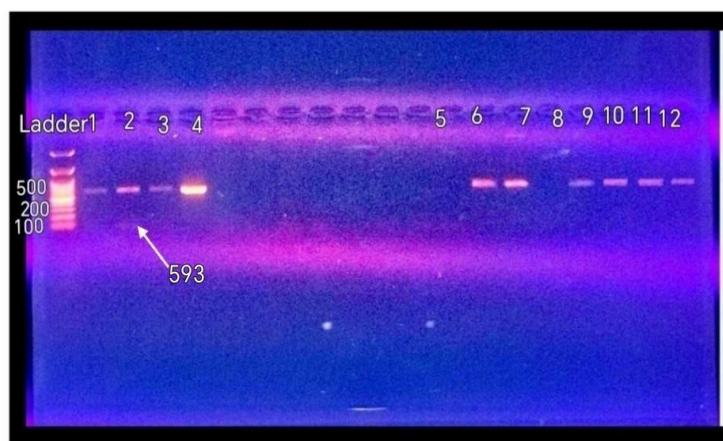


Figure (1): Electrophoresis of the PCR products of the *bla* gene on a 1% agarose gel at 80 mV for 45 minutes. L: 100-bp DNA ladder; lanes 1–12: *Chroococcus* sp., *L. fusiformis*, *O. nigro-viridis*, *A. lutea*, *W. saccata*, *S. platensis*, *L. aestuarii*, *Oscillatoria* sp., *S. aureus*, *K. pneumoniae*, *E. coli*, and *P. aeruginosa*.

The *gmr* gene was detected in blue-green algae and bacteria, except for the *L. fusiformis*, *Chroococcus* sp., *S. platensis*, *E. coli*, *S. aureus*, *P. aeruginosa*, which exhibited a size of 654 bp, as shown in Figure (2).



Figure (2): Electrophoresis of the PCR products of the *gmr* gene on a 1% agarose gel at 80 mV for 45 minutes. L: 100-bp DNA ladder; lanes 1–12: *O. nigro-viridis*, *Oscillatoria* sp., *A. lutea*, *Chroococcus* sp., *W. saccata*, *S. platensis*, *L. aestuarii*, *L. fusiformis*, *K. pneumoniae*, *E. coli*, *P. aeruginosa*, and *S. aureus*.

The *cat* gene in the current study showed that blue-green algae and bacteria possess this gene, which exhibits a PCR product size of 553 bp, except for *Oscillatoria* sp., *L. aestuarii*, *S. platensis*, *A. lutea*, and *P. aeruginosa*, as shown in Figure (3).

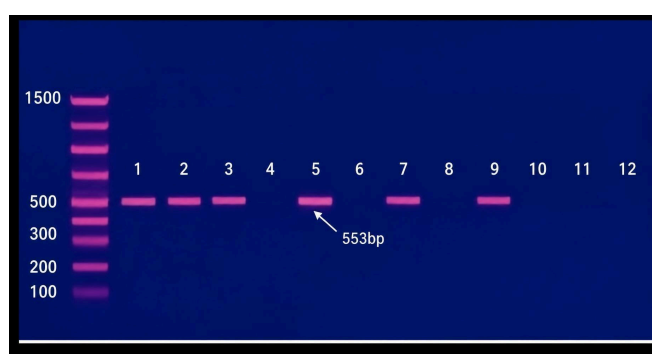


Figure (3): Electrophoresis of the PCR products of the *cat* gene on a 1% agarose gel at a potential difference of 80 V for 45 minutes. L: 100-bp DNA ladder; lanes 1–12: *O. nigro-viridis*, *Chroococcus* sp., *L. fusiformis*, *A. lutea*, *W. saccata*, *S. platensis*, *Oscillatoria* sp., *L. aestuarii*, *E. coli*, *S. aureus*, *P. aeruginosa*, and *K. pneumoniae*.

The results also showed that the kanamycin resistance gene *npt* may be possessed by some species of blue-green algae and pathogenic bacteria studied, appearing at a size of 515 bp. This gene was found in *L. aestuarii*, *Chroococcus* sp., *E. coli*, and *S. aureus*, as shown in Figure (4).

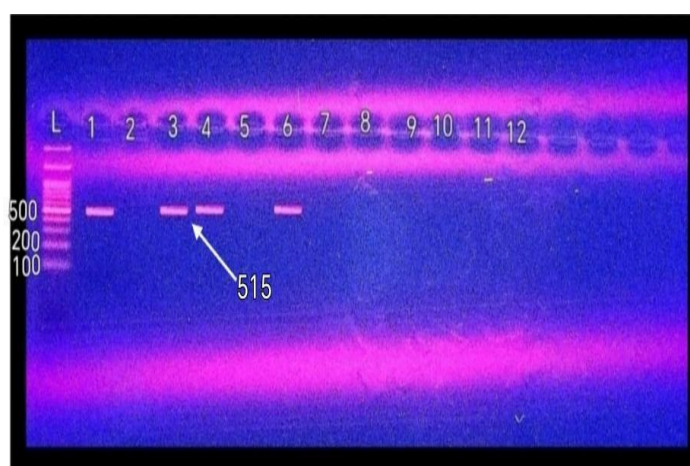


Figure (4): Electrophoresis of the PCR products of the *npt* gene on a 1% agarose gel at a potential difference of 80 V for 45 minutes. Lane L: 100 bp DNA ladder; lanes 1–12: *L. aestuarii*, *L. fusiformis*, *Chroococcus* sp., *S. aureus*, *W. saccata*, *E. coli*, *S. platensis*, *A. lutea*, *P. aeruginosa*, *K. pneumoniae*, *Oscillatoria* sp., and *O. nigro-viridis*.

The current study demonstrated that the *aadA* gene may be possessed by some blue-green algae and bacteria, such as *Chroococcus sp.*, *A. lutea*, *P. aeruginosa*, and *E. coli*, appearing at a size of 400 bp, as shown in Figure (5).

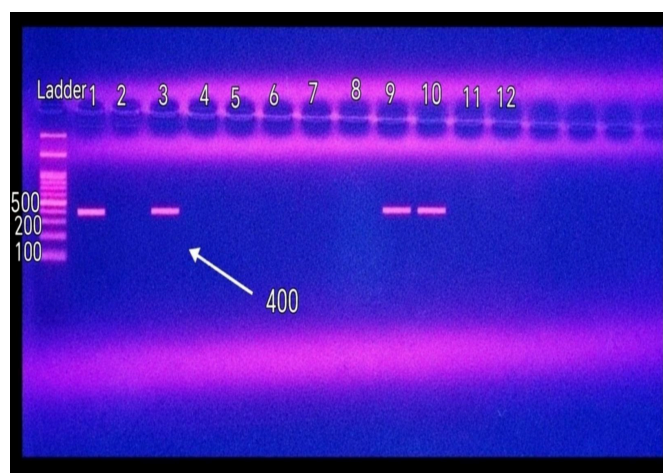


Figure (5): Electrophoresis of the PCR products of the *aadA* gene on a 1% agarose gel at a potential difference of 80 V for 45 minutes. Lane L: 100 bp DNA ladder; lanes 1–12: *Chroococcus sp.*, *W. saccata*, *A. lutea*, *L. fusiformis*, *L. aestuarii*, *Oscillatoria sp.*, *S. platensis*, *O. nigro-viridis*, *P. aeruginosa*, *E. coli*, *S. aureus*, and *K. pneumoniae*.

The findings of the present study suggest that blue green may harbor *erm* genes. algae and pathogenic bacteria, This gene has been found in *Chroococcus sp.*, *A. lutea*, *O. nigro-viridis*, *L. fusiformis*, and in bacteria such as *P. aeruginosa*, *K. pneumoniae*, and *E. coli*, with a size of 885 bp, as shown in Figure (6).



Figure (6): Electrophoresis of the PCR products for the *erm* gene on a 1% agarose gel at 80 V for 45 minutes. Lane L: 100-bp DNA ladder; lanes 1–12: 1, *Chroococcus sp.*; 2, *A. lutea*; 3, *L. fusiformis*; 4, *O. nigro-viridis*; 5, *W. saccata*; 6, *L. aestuarii*; 7, *Oscillatoria sp.*; 8, *E. coli*; 9, *K. pneumoniae*; 10, *P. aeruginosa*; 11, *P. aeruginosa*; 12, *S. aureus*.

All four pathogenic bacteria were found to possess antibiotic resistance genes (Table 3). *E. coli* carried the *bla*, *cat*, *erm*, *aadA*, and *npt* genes, while *P. aeruginosa* carried the following resistance genes: *bla*, *aacC1*, and *aadA*. *S. aureus* showed resistance through the *bla*, *cat*, and *npt* genes, while *K. pneumoniae* showed resistance through two genes: *bla* and *cat*.

Table (3): The ARGs in the locally isolated Cyanophyta and Bacteria

Sample	<i>bla</i>	<i>cat</i>	<i>erm</i>	<i>aacC1</i>	<i>aadA</i>	<i>npt</i>	Resistance (%)
<i>O. nigro-viridis</i>	+	+	+	+	–	–	66.7%
<i>Oscillatoria sp</i>	+	+	–	+	–	–	50.0%
<i>L. fusiformis</i>	+	+	+	–	–	–	50.0%
<i>W. saccata</i>	–	+	–	+	–	–	33.3%
<i>L. aestuarii</i>	–	–	+	+	–	+	50.0%
<i>Chroococcus sp</i>	+	+	+	–	+	+	83.3%
<i>S. platensis</i>	+	–	–	–	–	–	16.7%
<i>A. lutea</i>	+	–	+	+	+	–	66.7%
Cyanophyta (+) (N=8)	6 (75%)	5 (62.5%)	5 (62.5%)	5 (62.5%)	2 (25%)	2 (25%)	52.1%
<i>E. coli</i>	+	+	+	–	+	+	83.3%
<i>P. aeruginosa</i>	+	–	+	–	+	–	50.0%
<i>S. aureus</i>	+	+	–	–	–	+	50.0%
<i>K. pneumoniae</i>	+	–	+	+	–	–	50.0%
Bacteria (+) (N = 4)	4 (100%)	2 (50%)	3 (75%)	1 (25%)	2 (50%)	2 (50%)	58.3%
χ^2 value	1.200	0.171	0.188	1.500	0.750	0.750	0.252
p-value	0.273	0.679	0.665	0.221	0.387	0.387	0.616
Significance	NS	NS	NS	NS	NS	NS	NS

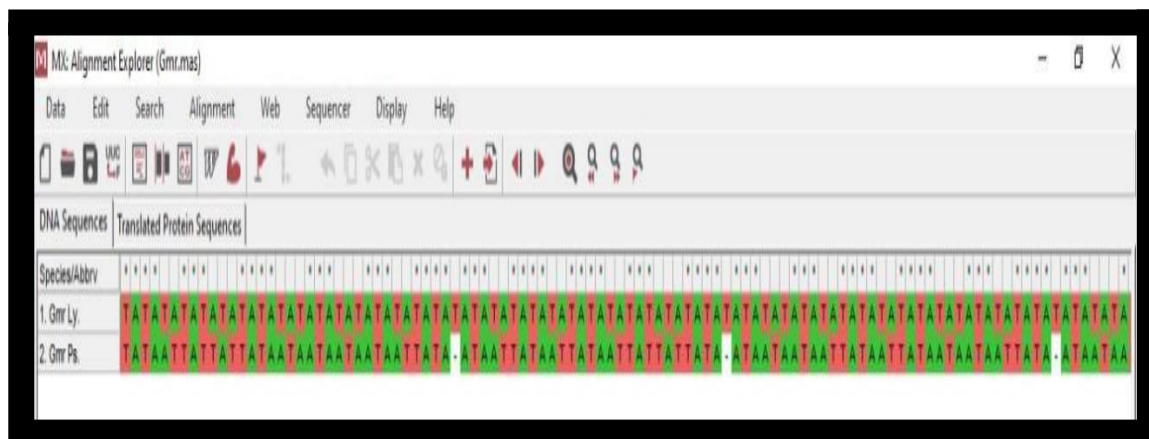
NS: Not statistically significant ($p > 0.05$).

Alignment

the nucleotide sequences of the selected antibiotic resistance genes were obtained following PCR amplification and sequencing by Macrogen. The obtained sequences were subsequently analyzed and compared with available nucleotide sequences using BLAST and MEGA X. The present study used the obtained sequences for sequence alignment and comparative analysis; however, the sequences of the resistance genes were not deposited in the NCBI GenBank

database at the time of the study. The sequence similarity analysis showed 95% similarity between *Lyngbya aestuarii* and *Pseudomonas aeruginosa* for the *gmr* gene, 92% between *Chroococcus* sp. and *Staphylococcus aureus* for the *bla* gene, 77% between *Chroococcus* sp. and *Klebsiella pneumoniae* for the *sul* gene, and 90% between *Chroococcus* sp. and *Staphylococcus aureus* for the *cat* gene Figure (7).

Figure (7): shows the similarity in the nucleotide sequence of the *gmr* gene of *L. aestuarii* and *P. aeruginosa*.



There is also a high percentage of similarity between the *bla* gene of the *Oscillatoria* sp and *S. aureus*. The percentage of similarity between the genes reaches 92%, as in Figure (8).

Figure (8): shows the similarity in the nucleotide sequence of the β – lactam for the *Oscillatoria* sp and *S. aureus*.



As for the *Sul* gene, the results of the current study showed that the percentage of nucleotide sequence similarity between *Chroococcus* sp and *K. pneumoniae* was 77%, as shown in Figure (9).

Figure (9): shows the similarity in the nucleotide sequences of the *Sul* gene of *Chroococcus* sp, and *K. pneumoniae*.

DISCUSSION

Four pathogenic bacterial isolates were used: *S. aureus*, *K. pneumoniae*, *P. aeruginosa*, and *E. coli*, and eight blue-green algae isolates: *Chroococcus* sp., *L. aestuarii*, *W. saccata*, *L. fusiformis*, *A. llutea*, *O. nigro-viridis*, *Oscillatoria* sp., and *S. platensis*. This study aimed to examine whether antibiotic resistance can be shared between pathogenic bacteria and cyanobacteria using molecular markers.

The presence of antibiotic resistance genes indicates a significant level of pollutants in the water, which may facilitate the transfer of antibiotic resistance genes from blue-green algae to bacteria. When antibiotics enter the aquatic environment, they may exert selective pressure on blue-green algae, favoring the survival and proliferation of microorganisms with antibiotic resistance. (16)(17). There are two types of antibiotic resistance. Intrinsic resistance

occurs naturally in about three per cent. Intrinsic resistance is not acquired through horizontal gene transfer. Bacteria. Induced resistance is not expressed until the antibiotic is used. Bacteria can pass on resistance genes to blue-green algae (BGA) through a specific mechanism known as horizontal gene transfer. This transfer can occur in three ways: conjugation, transformation and transduction. Mobile genetic elements which include plasmids, transposons and integrons allow for easy transfer of genes between bacteria (17)(18).

Some studies previously mentioned that the presence of plasmids in cyanobacteria determines bacterial resistance against antibiotics. These small pieces of DNA help transfer antibiotic resistance genes (ARGs) between different microorganisms through horizontal gene transfer.

According to our research, more resistant strains were observed in polluted areas as compared to the areas that were less polluted. Cai *et al.* (2019) reported that aquatic environments that are polluted can serve as hot spots for the development of the passage of antibiotic resistance between cyanobacteria and bacteria. Some cyanobacterial genera carried the *cat*, *npt*, *gmr*, *erm*, *aad*, and *bla* antibiotic resistance genes according to our study results. Cyanobacteria are resistant to antibiotics commonly used in farming, agriculture, and veterinary medicine. These antibiotics are commonly used in farming, agriculture, and veterinary medicine. The *bla* gene was the most frequently detected resistance gene in this study and was also present in most of the species examined (18)(19). This suggests that the gene responsible for beta-lactamase production is common in polluted environment. Due to the widespread use of β -lactam antibiotics such as penicillin, resistance to these antibiotics has become increasingly common in aquatic environments.

The *aadA* gene has been found in *Chroococcus* sp. and *E. coli*, which is consistent with the results of a study (19)(20). The current study showed that this gene may confer resistance to aminoglycosides and is considered common in aquatic bacteria. The gene may also be transferred between microorganisms through horizontal gene transfer, with plasmids serving as important vehicles for gene dissemination. The results of the current study indicate that blue-green algae collected from polluted environments, such as *Anabaena* and *Oscillatoria*, are more resistant to antibiotics than those collected from clean sources, which is consistent with what was reported in (20)(21). This study demonstrated that polluted environments near human-impacted sources, particularly hospital wastewater and other anthropogenic wastewater sources, may provide favorable conditions for the development and dissemination of antibiotic resistance in blue-green algae due to their exposure to antibiotics. Resistance due to the constant exposure of blue-green algae to these antibiotics. Blue-green algae can easily grow and spread in water bodies, particularly sewage and drinking water (21)(22).

When cyanobacteria grow in large quantities due to their resistance to antibiotics, they consume oxygen in the water, negatively impacting aquatic organisms, such as fish (22)(23). Recent studies show that cyanobacteria are not just environmentally detrimental. They also contribute to the spread of antibiotic resistance genes in aquatic environments. This is important today as environmental pollution is contributing to the development of antibiotic resistance in aquatic creatures and humans (23)(24). The transfer of antibiotic resistance genes is on the rise in human-altered environments like wastewater, and hospital effluents facilitating the spread of resistance in aquatic species and humans (24)(25).

CONCLUSION

Blue-green algae are also carriers of antibiotic resistance genes similar to pathogenic bacteria. The findings emphasize the key area of focus of this study as there was a high degree of similarity between the antibiotic resistance genes of pathogenic bacteria and those of blue-green algae.

ETHICAL APPROVAL

This study was approved by the Ethical Approval Committee, University of Anbar (Approval No. 258, dated December 26, 2024).

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التحري الجزيئي عن جينات مقاومة المضادات الحيوية في الطحالب الخضر المزرقّة والبكتيريا المرضية المعزولة من المصادر البيئية والمرضية

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الخلاصة

خلفية الموضوع: الطحالب الخضر المزرقّة هي كائنات قادرة على العيش في البيئات المائية والبرية، وتمتلك القدرة على التكيف مع بيئات مختلفة بفضل آلياتها، بما في ذلك مقاومتها للمضادات الحيوية. ويعود ذلك لامتلاكها لجينات مقاومة، بما في ذلك جين *bla*، الذي ينتج إنزيم البيتا-لاكتاماز المسؤول عن تكسير البنسلين. **الهدف من الدراسة:** هدفت الدراسة إلى الكشف عن وجود جينات مقاومة المضادات الحيوية في عزلات محلية من الطحالب الخضر المزرقّة ومقارنتها مع عزلات بكتيرية ممرضة. **المواد وطرق العمل:** تم الحصول على ثمانية عزلات من الطحالب الخضر المزرقّة من نهر الفرات وتنقيتها على الوسط BG11، بينما تم عزل أربعة بكتيريا ممرضة من مستشفى الرمادي التعليمي وتشخيصها باستخدام الفحص المجهرى والاختبارات البيوكيميائية القياسية. تم استخراج الحمض النووي من جميع العينات، واستخدمت تقنية PCR للكشف عن ست جينات مقاومة وهي: *bla*, *cat*, *erm*, *npt*, *aadA*, *gmr*. **النتائج:** أظهرت النتائج وجود تشابه كبير في أنماط جينات المقاومة بين الطحالب والبكتيريا، وخصوصاً جين *bla*، الذي ظهر في معظم أنواع الطحالب الخضر المزرقّة والبكتيريا الممرضة. كما ظهرت جينات *erm* و *cat* في عدد كبير من العينات المدروسة، وكان كل من *Chrococcus sp* و *Escherichia coli* هما النوعان اللذان امتلکا أكبر عدد من جينات المقاومة. بينما كان جنس *Oscillatoria sp* أقل مقاومة، إذ أظهرت النتائج أنه يمتلك جينين فقط: *gmr* و *aadA*، بينما غابت عنه جينات المقاومة الأخرى مثل *bla* و *cat*. **الاستنتاج:** تم مقارنة تسلسلات النيوكليوتيدات للطحالب الخضر المزرقّة والبكتيريا الممرضة باستخدام برنامج MEGA_X، وكشفت النتائج عن نسبة تشابه عالية تصل إلى 95% بين الأنواع التي تنتمي لعوائل مختلفة. أظهرت الأبحاث أن البكتيريا الممرضة والطحالب الخضر المزرقّة متشابهة بنسبة 95% في جين *gmr*، و92% في جين بيتا لاكتام، و77% في جين *sul*.

الكلمات المفتاحية: الطحالب الخضراء المزرقّة، الجينات المقاومة للمضادات الحيوية، التلوث البيولوجي، النقل الجيني الأفقي.