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STUDYING THE IMPACT OF THE SCIENTIFIC MIRACLES OF THE HOLY QURAN ON THE PHENOTYPIC AND GENETIC INDICATORS OF SOME PATHOGENIC BACTERIAL ISOLATES

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Abstract: Background : This study explores the novel application of the Holy Qur'an and Shariah ruqyah in affecting the genome of bacteria. Conducted for the first time in Iraq and the Arab world, this research seeks to investigate the potential impact of these treatments on bacterial DNA, leveraging RAPD-PCR markers for mutation detection. Materials and Methods : Genomic DNA was extracted from four bacterial isolates using established protocols. The study employed 10 RAPD primers to identify mutations in the bacterial genomes. The bacterial samples were subjected to treatments with the Qur'an and Shariah ruqyah, and the resulting genomic changes were analyzed. RAPD-PCR reactions were conducted, and the products were separated on agarose gel electrophoresis. The mutations were identified by comparing the banding patterns of treated samples with control samples. Results and Discussion : The results indicated significant genomic alterations in the bacterial samples treated with the Qur'an and Shariah ruqyah. Staphylococcus hemolyticus exhibited the highest number of mutant bands (29) compared to the control sample, followed by Proteus bacteria (25), another strain of Staphylococcus hemolyticus (22), and Staphylococcus aureus (10). These findings demonstrate the high efficiency of RAPD markers in detecting mutations with a limited number of primers. The study revealed that the magnetic field significantly affects the genome of faba beans, causing mutations that increase with longer exposure periods. The induced mutations could potentially be utilized to improve antibiotic quality and track harmful bacterial genes, rendering them non-pathogenic. The differences in results between the strains are attributed to their different genomic backgrounds, originating from various sources. Conclusions : The findings underscore the significant impact of the Qur'an and Shariah ruqyah on bacterial genomes, suggesting their potential use as alternative therapeutic methods. The study recommends applying this approach to other pathogenic bacterial species, using specialized primers for gene-specific investigations, and integrating Qur'anic and Shariah-based treatments in medical practices. Additionally, the research emphasizes the importance of employing genetic techniques to enhance bacterial species diagnosis and determine antibiotic resistance.

This pioneering study paves the way for future investigations into the interplay between religious practices and genetic modifications in microorganisms, highlighting the absence of prior literature on this subject within the region.

Keywords: Qur'an, Ruqyah, Bacteria, Genome, RAPD-PCR, Mutations, Therapy, Antibiotics

Introduction

Miracles are extraordinary events that defy natural explanations, often perceived as manifestations of divine intervention. They typically emerge from contexts of apparent helplessness, incapacity, or impossibility, challenging our understanding of the physical world. The Qur'an, central to Islamic belief, represents one of the clearest examples of such a miracle. It challenges skeptics to produce a text of comparable depth and complexity, a challenge that has stood unmet for centuries, thereby affirming its unique divine origin and emphasizing the extraordinary nature of its content [1]. This concept extends to what are known as 'scientific miracles' in the Qur'an, which refers to verses that allegedly contain knowledge that aligns with modern scientific discoveries—insights that were unknown at the time of the Qur'an's revelation. This suggests that the Qur'an anticipated many principles of contemporary science, lending a miraculous quality to its teachings [2-4]. Moreover, Qur'anic recitation is believed to impact listeners on a physiological level, where specific sound frequencies have therapeutic effects. This aligns with modern medical practices that use sound frequencies to treat various conditions, suggesting a fascinating overlap between spiritual practice and scientific methodology. The Qur'an itself posits that the divine creation is a perfect system, immutable and precisely regulated, as highlighted in the text: "The nature of God, on which people are weaned, does not change" (Romans 2). This divine constancy supposedly extends to the effects of Qur'anic recitation, which some studies suggest can enhance the body's resistance to various ailments, including cancer and viral infections [1]. The psychological impact of the Qur'an is equally profound. It includes vivid descriptions and metaphors, such as the potential effect of its message on a mountain: "If We had sent down this Qur'an upon a mountain, you would have seen it humbled and crumbled from fear of Allah..." (Qur'an, Hashr: 21). This illustrates not only the strength and transformative power of the divine word but also its capacity to inspire awe and reflection in those who engage with it [1]. Delving into microbiology, the discussion on bacteria reveals the incredible complexity and ubiquity of these organisms. For instance, fertile soil can contain billions of bacteria per gram, illustrating the rich microbial diversity that plays critical roles in maintaining ecological and physiological balances. Bacteria are categorized based on their structural features into groups such as cocci (spherical) and bacilli (rod-like), each adapted to specific functions and environments. The study of these microorganisms not only deepens our understanding of the biological processes essential for life but also highlights the interconnectedness of all living systems. Staphylococcus aureus, a particularly notable pathogen, exemplifies the challenges and dangers associated with bacterial infections. Capable of causing a wide range of conditions—from minor skin infections to life-threatening diseases like pneumonia and osteomyelitis—this bacterium underscores the critical importance of rigorous hygiene and infection control practices in healthcare settings. The adaptability of bacteria like Pseudomonas aeruginosa is further showcased by research conducted in space. Under microgravity conditions aboard the International Space Station, this bacterium has been observed forming unique biofilm structures, demonstrating its ability to thrive and adapt in extreme environments. Such studies not only provide insights into bacterial behavior but also inform approaches to infection control on Earth and beyond. The integration of microbiological research with medical science, especially in understanding and combating infections, highlights the ongoing need for innovative approaches to manage antibiotic resistance and develop effective

treatments. This includes exploring the mechanisms of pathogenesis, the efficacy of antimicrobial agents like Rifampicin, and the potential of vaccines against microbial structures such as fimbriae. The aim of this study is to provide a scientific groundwork for the usefulness of the Holy Quran and Islamic Ruqayyah in the treatment of microorganisms that cause disease. Through the use of both numerical statistical analysis and molecular tools, the research project will evaluate the influence that these spiritual practices have on the susceptibility of bacteria to antibiotics as well as their resistance to antibiotics. To be more specific, we will take use of RAPD-PCR technology in order to investigate the changes that occur in the genetic material of bacteria that have been subjected to Quranic recitation. Our objective is to present empirical data that supports the healing potential of the Quran from both a scientific and a medical perspective. In addition, the research will investigate the more general idea of "sound healing" or sound therapy in order to confirm this time-honored practice via the use of cutting-edge scientific techniques

Methods

Sample collection

Four patient samples, ranging in age from 3 to 62 years, were collected from Tikrit Teaching Hospital in Salah al-Din for this study. Two samples were obtained from patients with otitis media by inserting a swab into the ear canal and rotating it to collect the specimen [5]. Additionally, two samples from patients with urinary tract infections were collected following a specific protocol that included hand washing and sterilization, followed by capturing the midstream urine to minimize contamination, and then these samples were stored in disposable plastic collection bottles [6]. The collected samples were then cultured on mannitol salt agar plates and incubated at 37 degrees Celsius for 24 hours. After the initial growth period, bacterial colonies were isolated for further purification and diagnostic analysis [7].

Agricultural Media used

Table 1 :Culture Media Table

Sequence	Name of Culture Media	Description
1	Nutrient Agar	General-purpose medium for non-fastidious bacteria
2	Brain-heart Infusion Broth	Used for cultivating fastidious organisms and preparing the inocula for antimicrobial susceptibility testing
3	Mannitol Salt Agar	Selective and differential medium for the isolation of Staphylococcus aureus
4	Mueller-Hinton Agar	Commonly used for antibiotic susceptibility testing
5	MacConkey Agar	Selective and differential medium used for the isolation of gram-negative bacteria from clinical, dairy, and other samples

Tools and devices used

Table 2: Laboratory Equipment Table

Sequence	Equipment Name	Description
1	Autoclave	Sterilizes equipment and media using high-pressure saturated steam
2	Sensitive Balance	Measures precise weights of small samples

3	**Incubator**	**Maintains controlled temperature environments for culturing samples**
4	**Test Tube**	**Holds, mixes, or heats small quantities of substances**
5	**Refrigerator**	**Stores biological samples and chemicals at low temperatures**
6	**Flask + Beaker**	**Used for mixing, transporting, and reacting chemicals in the lab**
7	**Water Bath**	**Heats samples in water at a consistent temperature**
8	**Distiller**	**Purifies liquids by heating to vapor and then cooling to liquid**
9	**Hot Plate**	**Heats samples and solutions to high temperatures**
10	**Micropipette**	**Precisely measures and transfers small volumes of liquids**
11	**Centrifuge**	**Separates substances of different densities by spinning them at high speed**
12	**Bunsen Burner**	**Provides a single open gas flame for heating, sterilizing, and combustion**
13	**Loop**	**Transfers microorganisms without contamination**
14	**pH Meter**	**Measures the acidity or alkalinity of a solution**
15	**Eppendorf Tubes**	**Small plastic tubes used for multiple types of laboratory applications**
16	**Hood**	**Enclosed workspace in a lab to handle harmful substances safely**
17	**Vortex Mixer**	**Rapidly mixes solutions using a circular shaking motion**

Methods of preparation of Media

The implant Media were prepared according to the manufacturer's instructions provided on the packaging. They were then sterilized at a temperature of 121°C and a pressure of 15 psi for 15 minutes. After sterilization, the circles were poured and incubated at 37°C for 24 hours to ensure sterility before being stored in a refrigerator at 4°C until needed.

Preparation of Nutrient Medium: The nutrient medium was prepared following the specifications of the manufacturing company. This involved dissolving 28 grams of the medium in 1 liter of distilled water, followed by sterilization. The sealed medium was then used to cultivate Pseudomonas aeruginosa [Collee et al., 1996].

Preparation of MacConkey Medium: The MacConkey medium was prepared as per the provider's instructions, which included dissolving 50 grams of the medium in 1 liter of distilled water. This mixture was then sterilized and used as a growth medium for Proteus bacteria [Nester et al., 2001].

Preparation of Brain Heart Infusion Medium: This medium was formulated by dissolving 37 grams of the medium in 1 liter of distilled water, followed by sterilization. The sealed medium serves as an enrichment medium, facilitating the activation and development of bacteria prior to treatment [Macfaddin, 2000].

Preparation of Mannitol Salt Agar Medium: Mannitol salt agar medium was prepared by

dissolving 111 grams of the medium in 1 liter of distilled water and then sterilizing it with a sealant. This medium is specifically used for the cultivation of Staphylococcus aureus [Collee et al., 1996].

Preparation of Mueller-Hinton Agar Medium: For the Mueller-Hinton agar medium, 38 grams of the medium were dissolved in 1 liter of distilled water and sterilized with a seal. This medium is employed to assess the sensitivity of samples before and after treatment [Vall et al., 1999].

Mode of operation

1. Initial Inoculation: Four test tubes, each containing 5 ml of Brain Heart Infusion Broth (BHIB), were inoculated with bacteria using a sterilized loop heated by a gasoline flame. The inoculated tubes were then incubated at 37°C for 24 hours under sterile conditions.

2.Centrifugation: The next day, the bacterial samples were transferred to sterile laboratory tubes and centrifuged at 6,000 rpm for 10 minutes.

3. Supernatant Removal: After centrifugation, the supernatant was discarded, retaining the pellet at the bottom of the tubes.

4.Saline Wash: Each tube then received 5 ml of saline solution. The tubes were vortexed, centrifuged twice under the same conditions to ensure thorough washing, and then incubated again at 37°C for another 24 hours.

5.Dilution Preparation: For each bacterial strain, five test tubes were prepared with 9 ml of saline solution each. 1 ml of the original bacterial culture was added to the first tube to achieve a 0.1 dilution. Subsequent 1 ml transfers from each preceding tube to the next achieved dilutions of 0.01, 0.001, and 0.0001.

6.Plating for Colony Count: From each dilution, 0.1 ml was plated onto sterile Petri dishes with culture media appropriate for each bacteria type: MacConkey agar for Proteus, mannitol salt agar for Staphylococcus aureus and S. haemolyticus, and nutrient agar for Pseudomonas aeruginosa. These were then incubated at 37°C for 24 hours to facilitate colony counting, aiming for colony counts between 30 and 300.

7.Exposure to Qur'anic Recitation: Samples from each dilution were transferred to sterile Eppendorf tubes and exposed to continuous Qur'anic recitation by Qari Hassan and Shariah papers for a period of 24-48 hours during their incubation.

8. Post-Treatment Incubation: After the exposure period, 0.1 ml from each treated tube was again plated onto new sterile Petri dishes with the corresponding media. The plates were incubated at 37°C for 24 hours to count and compare bacterial growth post-treatment.

9.Analysis: Both pre-treatment and post-treatment bacterial colonies were subjected to antibiotic sensitivity testing to evaluate the efficacy of the Qur'anic treatment.

10.Molecular Analysis: DNA extraction was performed on samples before and after treatment to validate the bacteriological findings and to assess any molecular changes induced by the exposure to Qur'anic recitation.

How the allergy test works

1.Preparation of Media: Sterile Petri dishes are prepared by pouring Mueller-Hinton agar into them and allowing the agar to solidify.

2.Inoculation: A 0.1 ml sample from the bacterial culture, both pre-treatment and post-treatment, is transferred onto the surface of the solidified agar using a pipette.

3. Spreading the Sample: The bacterial inoculum is evenly spread across the surface of the agar using a sterile cotton swab to ensure uniform coverage.

4. Placement of Antibiotic Disks: Antibiotic-impregnated disks are placed on the agar using sterile forceps. These disks are spaced adequately apart to prevent overlapping of inhibition zones that might result from antibiotic diffusion.

5. Incubation: The plates are then incubated at 37°C for 24 hours to allow sufficient time for bacterial growth and antibiotic activity.

6.Measurement and Interpretation: After incubation, the inhibition zones around each antibiotic disk are measured in millimeters using a ruler. The diameters of these zones are then

interpreted to determine the sensitivity of the bacteria to the antibiotics, based on standard guidelines established by Kirby et al., 1996.

Molecular study

Materials and devices used

Table 3: List of Chemicals Used

No.	Chemical Name
1	Polyvenalpyroldin (PVP)
2	Agarose
3	Di, sodium ethylene diamin tetra acetic acid (Na2EDTA)
4	Ether
5	Isopropanol
6	Cetyltrimethylamonium bromide (CTAB)
7	Tris-base
8	Tris-HCl
9	Isoamyl alcohol
10	Boric acid
11	Hydrochloric acid
12	Ammonium acetate
13	Sodium acetate
14	Bromophenol-blue
15	Ethidium bromide
16	Hypo cloraat sodium
17	Ethanol
18	Glycerol
19	Sodium chloride
20	Chloroform
21	Liquid Nitrogen
22	Beta mrcabtoethanol
23	Sodium hydroxide
24	Filter paper

Table 4: List of Equipment Used

No.	Equipment Name	Origin
1	Magnetic stirrer	Biosan
2	Gel electrophoresis	Labnet International Inc., Taiwan
3	Portable autoclave	Daihan Lab Tech, Korea
4	Vortex	Heidolph, Germany
5	Thermocycler	Applied Biosystems, Singapore
6	Cooling Centrifuge	Eppendorf, Germany
7	Microfuge	Sigma, Germany
8	Gel Documentation System	Korea
9	Nanodrop	Thermo Scientific, Germany
10	Microwave	Shownic, Indonesia
11	Shaking water bath	Julabo, Germany
12	Digital Camera	Sony, Japan
13	Micropipettes (p10, p20, p100, p1000)	Herchman Laborgarate, Germany
14	Spectrophotometer	Julabo, Germany
15	pH-meter	Hanna Instruments, Italy
16	Analytical balance	Sartorious, Germany

17	**Water distiller**	**Distiller (wsc\4d)**

Sample collection of Molecular study
Genomic DNA Extraction
DNA Extraction and Purification:

- **Methodology:** DNA was isolated following protocols from Weigand et al., 1993, and Huang et al., 2013.
- **Purification Process:** Purification was necessary if DNA strands appeared not perfectly white and contained faint colors, likely due to the high concentrations of phenols, alkaloids, sugars, and proteins present in pea plants. A new purification method was implemented in this study, which provided excellent results using the same extraction materials and solutions but varying the procedural techniques.

Measurement of DNA Concentration and Purity:

- **Equipment Used:** NanoDrop device.
- **Procedure:** A drop of pre-extracted genomic DNA was placed on the device's sample holder, and after calibration with the same thawing solution, the device measured the DNA concentration in ng/µL and purity accurately. The sample was then diluted to a concentration of 50 ng/µL and stored frozen for later use.

Gel Electrophoresis:

- **Preparation:** Solutions, materials, and gels were prepared, and samples were loaded for electrophoresis according to Sambrook et al., 1989 (Al-Sakmani, 2017).

RAPD-PCR Reactions:

- **Procedure:** RAPD reactions were conducted based on Williams et al., 1990, using ten primers for analyzing four bacterial species.
- **Reagents:** Reactions utilized the Green Master Mix supplied by Promega, USA.
- **Primers:** Provided by Operon Technologies, USA, detailed in a specific table.
- **Water:** Deionized distilled water (nuclease-free) was used in the reactions.

Materials and Equipment:

1. Reaction Mixture (Green Master Mix) - Promega, U.S.A.
2. Primers - Operon Technologies, U.S.A.
3. Deionized Distilled Water (Nuclease-Free)

Table 5 :Primers Used in RAPD-PCR Study

Primer Sequence	Primer Name	Source
GTGTGCCCCA	**P-6**	**Operon Technologies, USA**
GATGACCGCC	**P-1**	**Operon Technologies, USA**
GTCGCCGTCA	**P-7**	**Operon Technologies, USA**
ACTGGGACTC	**P-2**	**Operon Technologies, USA**
GTTGCGATCC	**P-8**	**Operon Technologies, USA**
GACAGGAGGT	**P-3**	**Operon Technologies, USA**
AACGGTGACC	**P-9**	**Operon Technologies, USA**
GGAGGGTGTT	**P-4**	**Operon Technologies, USA**
CAGCACCCA	**P-10**	**Operon Technologies, USA**
CCTTGACGCA	**P-5**	**Operon Technologies, USA**

Method of work

· **DNA Concentration Adjustment:** The concentration of DNA in all studied samples was adjusted by diluting with TE buffer to achieve the desired concentration for RAPD reactions, approximately 50 nanograms per microliter for each sample.

· **Preparation of the Master Reaction Mix:** The master reaction mix was prepared by combining

the reaction components in a sterile 2 ml Eppendorf tube. The mixture was then briefly spun in a Microfuge for 3-5 seconds to ensure thorough mixing of the components. It is essential to maintain sterile conditions within a hood, wear gloves, and keep the tubes on ice as detailed in the following table (Table 6).

Table 6 Reagents Used in RAPD Reactions

No.	Component	Final Concentration	Volume per Sample
1	Green Master Mix	1X	12.5 µL
2	Primer	10 picomoles	2.0 µL
3	Nuclease-free water	-	8.5 µL
4	DNA template	25-50 ng	2 µL

Using the RAPD-PCR reaction program, the initial mutant heat was set to be (94), and it was applied for four minutes during one cycle. This was followed by forty cycles including the mutant heat (92), which was applied for thirty seconds, the initiator link heat (36), which was applied for thirty seconds, the elongation heat (72), which was applied for one minute, and the final elongation heat (72), which was applied for seven minutes during one cycle. Following the completion of the reaction time, the tubes were removed from the thermoplastic device and placed in the freezer. This was followed by the removal of five microliters from each tube. The mixture was then loaded onto the acrose gel that had been prepared earlier at a concentration of 1.5% using the volumetric marker, as described in paragraph (3-2-6-II-2). Finally, the samples were transferred to the acrose gel. Following this step, the gel is colored by first being submerged in ethidium bromide dye for a period of one hour while being stirred. Subsequently, the gel is then photographed while being subjected to an ultraviolet radiation source using a UV-transilluminator.

Diagnosis of mutations

The differences in the genetic material (DNA) that can be obtained from the application of RAPD indicators can be used to identify the mutations resulting in the transactions and compare them with the control sample that will be obtained by converting the results that we get that appear in the gel to the characterization tables by placing (1) when the package is present and (0) when the package that appears in the transaction and is not present in the control sample expresses a mutation and vice versa, as well as the package that is absent in the transaction and is present in the control sample also expresses a mutation and comparisons can be made between the results

Result and Discussion

Genomic DNA Extraction

Genomic DNA was extracted from four bacterial isolates using the method described by Weigand et al., 1993; Huang et al., 2013. The extracted DNA was suitable for PCR reactions in terms of both quantity and purity, with good yields estimated at 100-300 micrograms per 2 ml of bacterial culture medium. The DNA extraction process using this method is straightforward, quick, and yields high quantities of DNA with acceptable purity for RAPD-PCR reactions (Source: Dr. Riyam).

Results of RAPD-PCR Markers

In this research, as detailed in Table 7 twelve random primers were used for the studied samples. Ten of these primers recognized sites on the genome and produced various bands that were detected on an agarose gel alongside a DNA ladder (100bp DNA Marker). The primers varied in their production of main/monomorphic bands and polymorphic bands, while two primers (P-11, P-12) did not recognize any sites on the genome and thus did not produce any bands on the agarose gel. This finding aligns with most researchers who have used RAPD markers to study genetic variation (Al-Asi, 2002; Al-Qaisi, 2013; Al-Zuhairi, 2014; Al-Sakmani, 2017). The primer

patterns presented in Table 4-1 identified different band patterns, with a total of 70 recognized sites on the sample genomes—7 were common across all samples and 63 were polymorphic. Primer P-7 was notable for having the highest number of recognized sites, totaling 10, whereas Primer P-10 produced the least, with only 4 sites. The total bands produced from these sites were 268, with 56 being main bands and 212 being polymorphic bands. Specifically, Primer P-7 produced the highest number of bands at 52, while Primer P-3 produced the fewest at 14. The overall variation ratio for the produced primers was 95%, indicating a significant variation among the four treatments compared to control samples, suggesting an impact on the bacterial genome. High variation post-treatment indicates the effect of the treatment (Al-Ghamdi, 2009; Blair et al., 2009).

Table 7 RAPD-PCR Analysis Results

No.	Primer Name	Total Sites Produced	Common Sites	Diverse Sites	Total Bands by Primer	Common Bands	Diverse Bands	Unique Bands	Missing Bands	Variation Ratio (%)
1	P-1	5	3	2	38	24	14	1	1	40
2	P-2	8	-	8	26	-	26	9	1	100
3	P-3	4	-	4	14	-	14	4	3	100
4	P-4	9	-	9	28	-	28	8	4	100
5	P-5	9	-	9	26	-	26	8	6	100
6	P-6	7	-	7	20	-	20	9	3	100
7	P-7	10	4	6	52	32	20	3	3	60
8	P-8	7	-	7	16	-	16	5	3	100
9	P-9	7	-	7	32	-	32	1	7	100
10	P-10	4	-	4	15	-	15	3	2	100
-	Total	70	7	63	268	56	212	51	33	95

Distinct packages, such as distinct band packages and missing band packages, were a characteristic that was present in the majority of different transactions (table 7,8,9). Within the scope of this investigation, a total of 84% of the prefixes were responsible for the generation of mutant distinctive packages, with 51% being one of a kind and 33% being nonexistent. In this group, the prefix P-2 had the maximum number of unique packages, which accounted for 9% of the total, while there were a total of 7% of packages that were missing. Transactions M2, M4, M3, and M1 each got forty, fourteen, thirteen, and six distinct packages, respectively, in terms of the proportion of shipments that were unique. It was transactions M4, M2, M3, and M1 that were responsible for the missing shipments. In all, these shipments amounted to eleven, nine, and four. His analysis of these transactions reveals that the DNA genetic material has been altered by the scientific marvels of the Qur'an and Islamic tradition. The missing packages are considered as a discriminating trait, and his research suggests that this has occurred. This allegation is further supported by the fact that there is a noticeable difference between these respective programs. Within the context of the missing packages, this discovery is consistent with the findings of a large number of scholars who came before it (al-Asi, 2002; al-Qaisi, 2013; Al-Zahiri, 2014). A mutation in a website that identified just the person who initiated the transaction was also responsible for masking the appearance of the package and erasing the identification of the transaction starter.

The prefixes varied in the sizes of the resulting packets, their sizes ranged from (250-3000bp), the lowest molecular size was (250 bp) in the initiator P-5 and the highest molecular size was (3000bp) in the initiator P-4.

Table 8:Distinctive Mutations for Bacterial Treatments

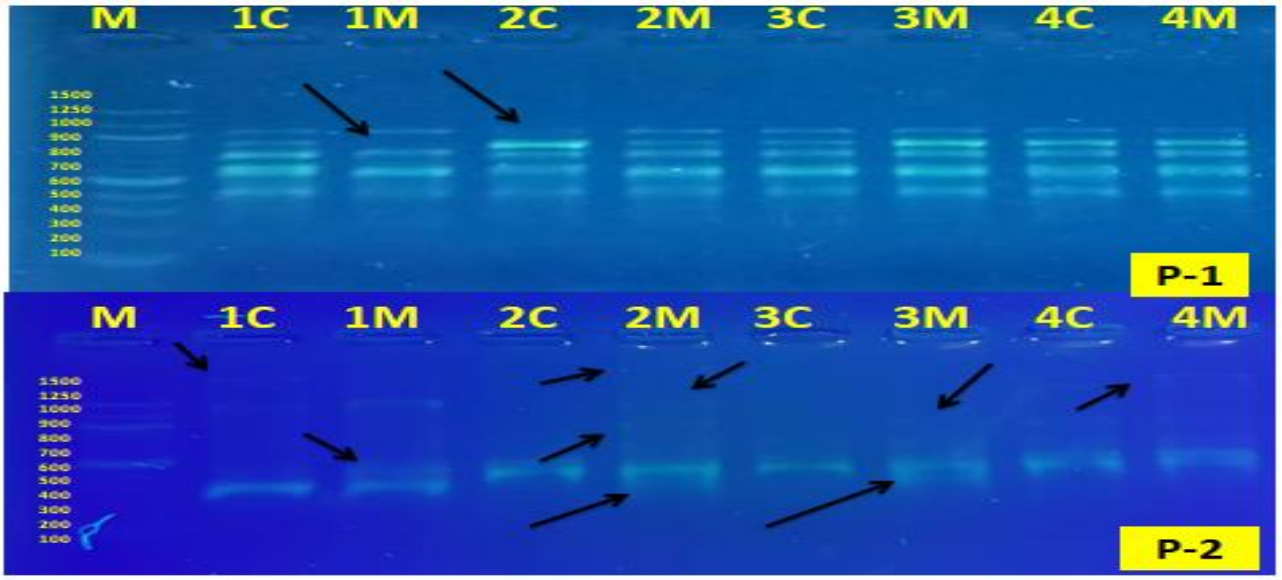
Primer Name	Molecular Weight (bp)	Staphlococcus aureus (Unique)	Staphlococcus aureus (Absent)	Staphlococcus hemolyticus (Unique)	Staphlococcus hemolyticus (Absent)	Pseudomonus aeruginosa (Unique)	Pseudomonus aeruginosa (Absent)	Proteus (Unique)	Proteus (Absent)
P-1	400-1100	-	1	1	-	-	-	-	-
P-2	300-2000	1	1	5	-	2	-	1	-
P-3	400-1000	-	-	1	-	1	3	3	-
P-4	600-3000	1	1	3	1	4	1	-	1
P-5	250-2750	1	-	4	2	1	3	2	1
P-6	400-2900	2	-	3	1	1	2	3	-
P-7	275-2850	-	1	1	-	-	-	2	2
P-8	300-2500	-	-	1	1	1	-	2	2
P-9	300-2000	-	-	1	3	-	-	-	4
P-10	700-1500	1	-	-	1	3	-	1	1
Total	-	6	4	20	9	13	9	14	11

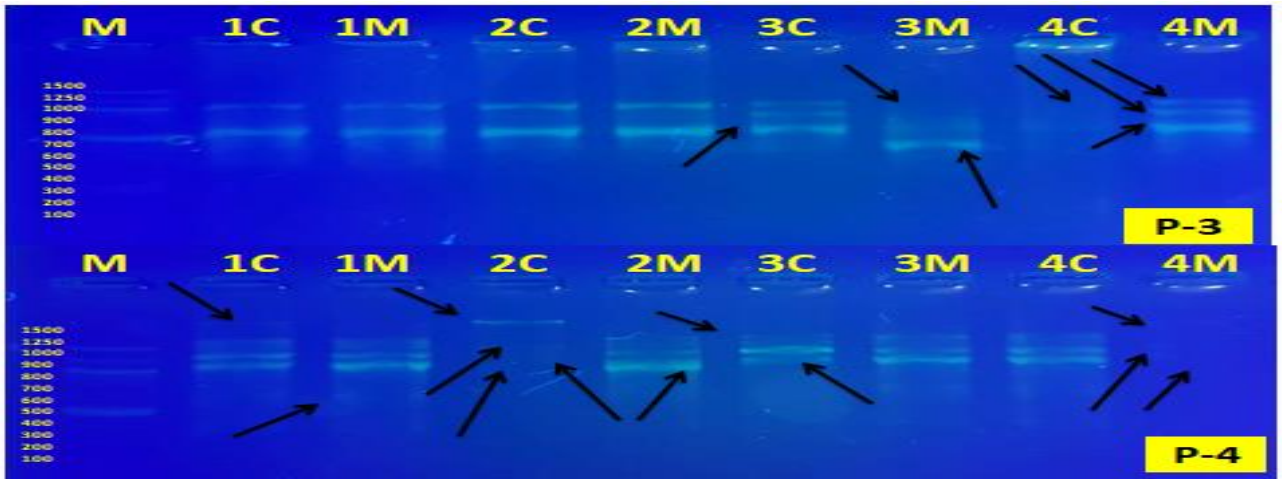
Table 9 : Distinctive Mutations for Bacterial Treatments

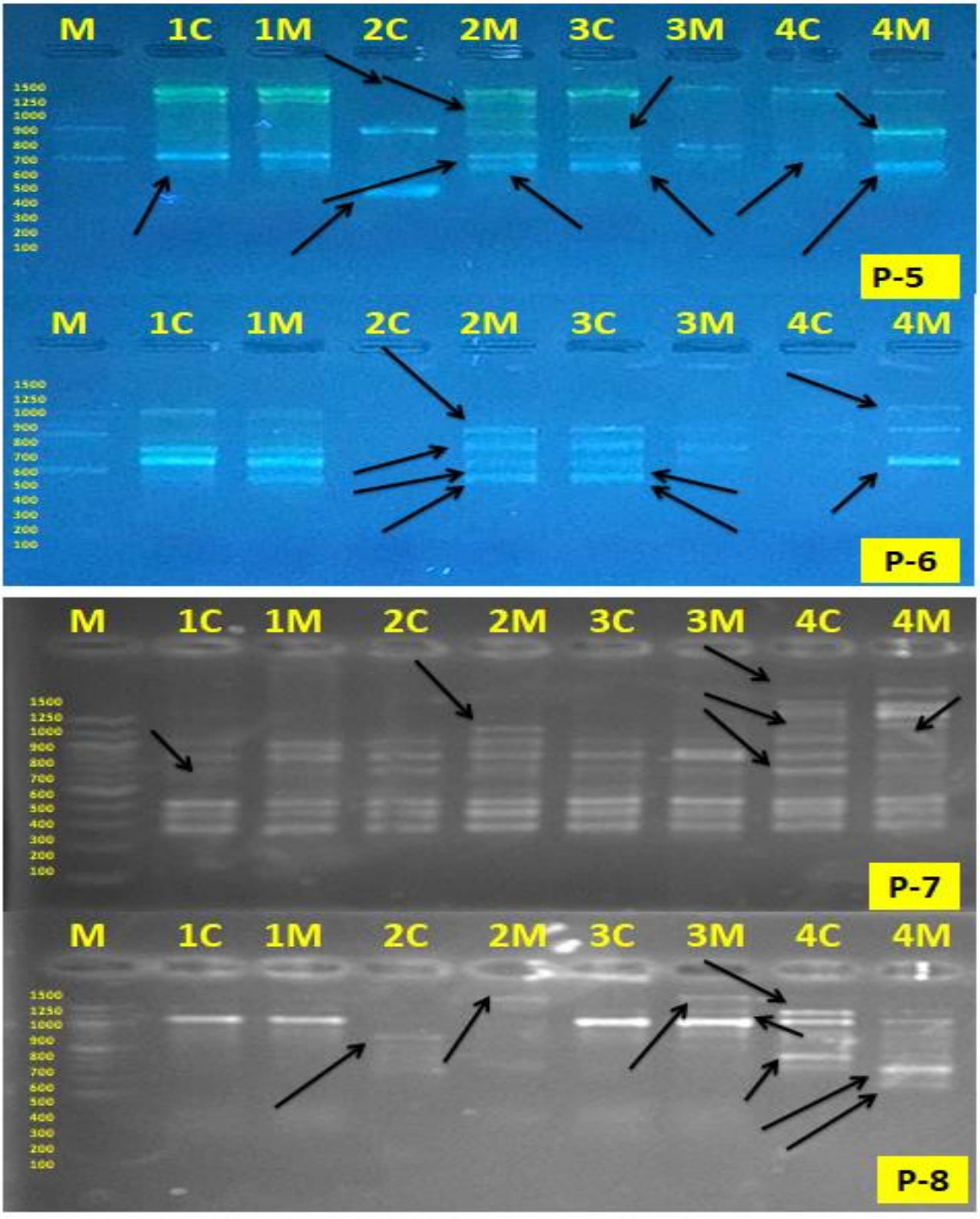
Primer Name	Proteus (4M)	Proteus (4C)	Pseudomonus aeruginosa (3M)	Pseudomonus aeruginosa (3C)	Staphlococcus hemolyticus (2M)	Staphlococcus hemolyticus (2C)	Staphlococcus aureus (1M)	Staphlococcus aureus (1C)	Molecular Weight (bp)
P-1	1	1	1	1	1	0	1	1	1100 bp
	1	1	1	1	1	1	0	1	1000 bp
	1	1	1	1	1	1	1	1	800 bp
	1	1	1	1	1	1	1	1	600 bp
	1	1	1	1	1	1	1	1	400 bp
P-2	0	0	0	0	1	0	0	0	2000 bp
	1	0	0	0	0	0	0	1	1500 bp
	0	0	0	0	1	0	1	1	1250 bp
	1	1	1	0	1	0	0	0	1050 bp
	1	1	0	0	0	0	0	0	600 bp
	1	1	1	1	1	0	0	0	500 bp
	1	1	1	0	1	1	1	0	400 bp
	0	0	0	0	1	0	1	1	300 bp
P-3	1	0	0	1	1	1	1	1	1000 bp
	1	0	0	1	0	0	0	0	900 bp
	1	0	0	1	1	1	1	1	600 bp

	0	0	1	0	0	0	0	0	400 bp
P-4	0	0	0	0	0	1	0	1	3000 bp
	1	1	1	1	1	0	1	1	2750 bp
	0	1	1	0	0	0	1	1	2500 bp
	0	0	0	1	0	0	0	0	1500 bp
	1	1	1	0	1	0	1	1	1000 bp
	1	1	1	0	0	0	0	0	900 bp
	0	0	0	0	1	0	1	1	800 bp
	0	0	1	0	0	0	0	0	700 bp
	0	0	0	0	0	0	1	0	600 bp
P-5	1	1	1	1	1	0	1	1	2750 bp
	0	0	0	1	1	0	1	1	2500 bp
	0	0	0	0	1	0	0	0	1100 bp
	1	0	0	0	0	1	0	0	1000 bp
	0	0	0	1	0	0	0	0	900 bp
	0	0	1	0	0	0	0	0	800 bp
	0	1	1	1	0	0	1	1	500 bp
	1	0	0	1	1	0	1	0	400 bp
	0	0	0	0	0	1	0	0	250 bp
P-6	1	0	0	0	0	0	0	0	3000 bp
	0	0	0	0	0	0	1	1	2500 bp
	1	0	0	0	0	1	1	0	1150 bp
	0	0	1	1	1	0	0	0	1000 bp
	0	0	1	0	0	0	1	1	700 bp
	1	0	0	1	1	0	1	1	600 bp
	0	0	0	1	1	0	1	0	400 bp
P-7	1	0	0	0	0	0	0	0	3000 bp
	1	1	0	0	0	0	0	0	2750 bp
	1	1	0	0	0	0	0	0	2500 bp
	1	0	0	0	1	0	0	0	1500 bp
	0	1	1	1	1	1	1	1	1000 bp
	1	1	1	1	1	1	1	1	900 bp

	0	1	1	1	1	1	0	1	650 bp
	1	1	1	1	1	1	1	1	400 bp
	1	1	1	1	1	1	1	1	350 bp
	1	1	1	1	1	1	1	1	250 bp
P-8	0	0	1	0	1	0	0	0	2500 bp
	0	1	1	0	0	0	0	0	1500 bp
	1	1	1	1	0	0	1	1	1000 bp
	1	1	1	1	0	1	0	0	800 bp
	0	1	0	0	0	0	0	0	550 bp
	1	0	0	0	0	0	0	0	350 bp
	1	0	0	0	0	0	0	0	300 bp
P-9	1	1	1	1	0	1	1	1	2000 bp
	1	1	1	1	0	0	1	1	1750 bp
	0	1	1	1	1	1	1	1	1100 bp
	0	1	1	1	0	0	0	0	1000 bp
	0	1	1	1	1	0	0	0	800 bp
	0	1	0	0	0	1	1	1	500 bp
	0	0	0	0	0	1	0	0	300 bp
P-10	1	1	1	0	0	1	1	1	1500 bp
	1	1	1	0	0	0	1	1	1000 bp
	0	1	0	0	0	0	1	0	800 bp
	0	0	0	0	0	0	1	1	700 bp


M 1C 1M 2C 2M 3C 3M 4C 4M
P-1
M 1C 1M 2C 2M 3C 3M 4C 4M
P-2


M 1C 1M 2C 2M 3C 3M 4C 4M
P-3
M 1C 1M 2C 2M 3C 3M 4C 4M
P-4


M 1C 1M 2C 2M 3C 3M 4C 4M
1500
1250
1000
900
800
700
600
500
400
300
200
100
P-5
M 1C 1M 2C 2M 3C 3M 4C 4M
1500
1250
1000
900
800
700
600
500
400
300
200
100
P-6
M 1C 1M 2C 2M 3C 3M 4C 4M
1500
1250
1000
900
800
700
600
500
400
300
200
100
P-7
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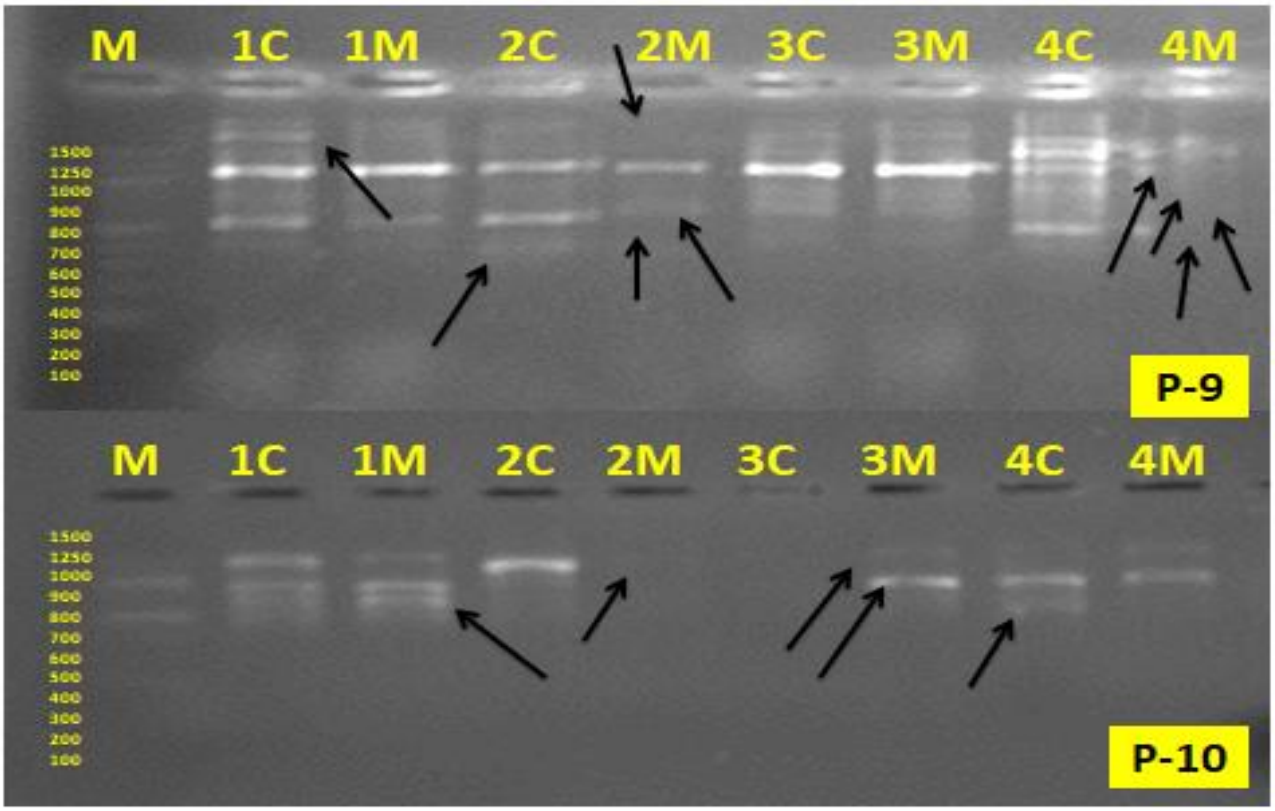
800
700
600
500
400
300
200
100
P-8



This experiment, being conducted for the first time in Iraq and the Arab world, lacks any published literature on similar research. The results indicate that the Qur'an and Sharia paper have a significant impact on the genome of bacteria across all samples. The RAPD-PCR markers have demonstrated high efficiency in identifying these mutations using a limited number of primers, specifically 10 primers. The various treatments revealed differences in the number and quality of mutant bands depending on the type of bacteria studied. Staphylococcus hemolyticus exhibited 29 mutant bands compared to the control sample, while Proteus bacteria showed 25 mutant bands. Staphylococcus hemolyticus bacteria obtained 22 mutant bands, and Staphylococcus aureus bacteria showed 10 mutant bands, all compared to their respective control samples

Conclusion

1. There are differences in the results between the two strains due to their different genomes, as they originate from different sources.
2. The magnetic field significantly affects the genome of faba beans.
4. The magnetic field induces mutations in the genome of faba beans, and the mutations increase with the length of exposure to the magnetic field.
5. The RAPD markers are efficient in detecting mutations in the genome of faba beans.

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