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Enhanced Decolorization of Textile Dyes by Gamma Radiation Induced *Bacillus cereus* Isolated from Wastewater

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Abstract: Two bacterial (MAM-B11 and MAM-B22) were isolated from textile wastewater I and II respectively. These two isolates were identified by 16 S rRNA as *Bacillus cereus* MAM-B11 and *Bacillus cereus* MAM-B22. The two bacterial strains were exposed to different doses of gamma radiation. As gamma radiation doses increased, the viability of the *B. cereus* MAM-B11 and MAM-B22 decreased gradually. Dose (15.0 kGy) reduced the viability of both MAM-B11 and MAM-B22 by 3.7 log cycles. Mutants MAM-D6 and MAM-D13 resulted from exposure of the parent strain *B. cereus* MAM-B11 to dose 2.0 kGy for both of the two mutants were the most efficient mutants in decolorizing textile dyes (Isma Fast red, Fantacell olive, Dycrofix Red, Dycrofix Violet, Jakazol Black, Drimarene Blue and Jakofix Yellow). However, Mutants (MAM-D1, MAM-D15, MAM-D17 and MAM-D18) resulted from exposure of parent strain *B. cereus* MAM-B22 to doses 8.0, 8.0, 10.0 and 4.0 kGy respectively. These mutants were more efficient in decolorizing textile dyes. They decolorized Isma Fast dye more than parent strains by a range between 1.0% to 14.0%, Fantacell olive dye by a range between 1.0% to 25.0%, Dycrofix Red dye by a range between 26.0% to 88.0%, Dycrofix Violet dye by a range between 3.0% to 238.0%, Jakazol Black dye by a range between 3.0% to 9.0%, Drimarene Blue dye by a range between 7.0% to 33.0% and Jakofix Yellow dye by a range between 17.0% to 210.0%. Parent strains and their mutants decolorized textile wastewater I efficiently (more than 95.0%).

Keywords: Textile wastewater, Dyes, Gamma radiation, *B. cereus* mutants.

1.Introduction

Synthetic dyes are essential for textile, paper, pharmaceutical, cosmetics and food industries. Over 800,000 tons/year of more than 100,000 dyes are produced worldwide [**1**]. Azo dyes account for up to 70% of dyestuffs applied in textile processing, due to the ease and cost-effectiveness in their synthesis, stability and availability of variety of colors compared to natural dyes [2, 3, 4]. At least 10.0−15.0% of this group of chemicals which characterized by the presence of one or more −N=N− of the used dye is released as effluent into the open streams presenting eco-toxic danger [5, 6, 7]. Water pollution with dyestuff is clearly visible and prevents penetration of light into water which directly interfered with survival of aquatic organisms. Many reactive azo dyes are toxic to aquatic life and are carcinogenic and mutagenic to humans, so efficient treatment methods must be developed [8, 9, 10, 11]. Physicochemical treatment of dye containing wastewater generates large amounts of sludge and are very expensive. However, microbial treatments using bacteria and fungi have been shown to be more efficient, more cost effective and eco-friendly [12, 1].

Some azo dyes biodegrading strains that belonged to the genus of *Bacillus* have been isolated and used for decolorization of different textile dyes.

[4], decolorized azo dye reactive black B by *Bacillus cereus* HJ-1. While, reactive black B was decolorized by another *Bacillus* strain YZU-1 [6]. However *Bacillus amyloliquefaciens* degraded Congo red [7].
[13] isolated a new strain of *Bacillus pumilus* W3 having the ability to decolorize dyes. [14] used the newly isolated *Bacillus* sp. MZS-10 for decolorizing Azure B dye.
Bacillus cereus is a spore forming Gram-positive bacterium, found in soil, water, air and wastewater as a natural habitat. *Bacillus cereus* is radio-resistant and posing a battery of extracellular enzymes that helps this bacterium to tolerate and survive in harsh conditions [15, 16] and [17, 18].Gamma (γ) radiation has a narrow range of length and high energy penetrating power resulting from nuclear disintegration of certain radioactive substances such as isotopes Cobalt 60 (Co^{60}) and Cesium 137 (Cs^{137}) [19]. The origin of ionizing radiation resistance in the prokaryotes is obscure and this resistance cannot be explained as an adaptation to environmental radiation. It has been suggested that DNA repair mechanism may have evolved not to count the damage of ionizing radiation but rather to compensate

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for desiccation, another naturally occurring stress that generate a pattern of DNA damage similar to that produced by ionizing radiation [20]. Gamma radiation can effect protein finger printing and enzymatic activity of *Bacillus cereus* [21,22] and induced mutants having more abilities to degrade pollutants than their parent strains and enhanced production of laccase and manganese peroxidase enzymatic activities [23,24,25].In the present study, the main aim is to isolate bacterial strain (s) having the ability to decolorize a variety of textile dyes from textile wastewater and exposing this strain (s) to different doses of gamma radiation to select mutant (s) able to enhance decolorization percentage of textile dyes that polluted water streams in Egypt to be used as eco-friendly technology to get clean environment.

2. Materials and methods

2.1. Sampling site and collection

Textile wastewater I and II were used to isolate bacterial strains. Textile wastewater were collected as effluent samples from El-Mahalla El-Kubra Company, Delta, Egypt. Textile wastewater were collected in 1.0 liter sterile screw capped glass bottles and shipped on ice in ice box and transferred to the laboratory within 4.0 hours to be used for bacterial isolation.

2.2. Bacterial isolation

Each wastewater was serially diluted with sterile saline and appropriate three successive dilutions were used to inoculate L.B (Tryptone, 10.0; yeast extract, 5.0; sodium chloride, 5.0 g/L) agar plates [26] in duplicates for each dilution. L.B inoculated plates were incubated at 30.0 ^{0}C for 48.0 hours, then separated single colonies on the surface of L.B plates were picked up and stored on L.B agar slants at 4.0 ^{0}C for further investigation.

2.3. Determination of maximum absorbance (λmax) of color for each textile dye

Scanning for each dye had been determined using spectrophotometer (LW-V-200 RS, UV/VIS, Germany) with quartz cuvette between 200.0 and 800.0 nm. The maximum absorbance of colour (λ_{max}) had been recorded as indicated in Table (1) and Figure (1).

2.4. Effect of gamma radiation on the most potent bacterial isolates

According to [18], The most potent bacterial isolates (MAM-B11) isolated from textile wastewater I and (MAM-B22) isolated from wastewater II and identified by 16 S rRNA (previous data under publication) as *Bacillus cereus* MAM-B11 and MAM-B22, were inoculated in L.B broth medium and incubated at 30.0 ^{0}C for 24.0 hours in shaking incubator (150.0 rpm). The well grown cultures were centrifuged for 15.0 min. at 8000.0 rpm. The pellets were washed twice with sterile saline (0.85% NaCl) and resuspended in sterile saline. Bacterial Cells suspended in saline (pool) were distributed in 5.0 ml aliquots in scrow capped test tubes and exposed to different doses of gamma radiation, (0, 1.0, 2.0, 4.0, 6.0, 8.0, 10.0 and 15.0 kGy) from Indian Chamber of Co^{60} at National Center for Radiation Research and Technology (NCRRT), Nasr City, Cairo, Egypt. Dose rate was 1.0 kGy/ 20.0 min. at the time of experiment at ambient temperatures. The non-irradiated control (0) and irradiated ones were serially diluted with sterile saline. An appropriate three successive dilutions were inoculated on the surface of L.B agar plates. Double pates and three replicates were used for each dilution for each strain. The inoculated plates were incubated at 30.0 ^{0}C for 48.0 hours. The count was determined. Dose response curve had been also determined.

2.5. Selection of the most promising mutants able of decolorizing textile dyes

From plates of the previous step (Dose response curve), colonies that showing any morphological changes (shape, color, surface, size, ---- etc.) had been picked up. Each colony has been grown in L.B broth medium and used to inoculate Nutrient Broth (peptone, 10.0; beef extract, 10.0; sodium chloride, 5.0 g/L) medium [27]. The Nutrient broth (N.B) medium containing 200.0 and 400.0 mg/L of each textile dye. Three replicates were used for each concentration, each mutant strains and each parent strains. Decolorization of each textile dye had been determined after two and six days of incubation at 30.0 ^{0}C in shaking incubator (150.0 rpm). The non-irradiated controls represents the parent strains (MAM-B11and MAM-B22). M 9 synthetic medium [28] were used instead of N.B medium for decolorization of Jakazol Black dye, because there was nearly no decolorization of Jakazol Black dye in N.B medium.

2.6. Decolorization of textile dyes in textile wastewater I by B. cereus parent strain and their mutants

The most efficient mutants resulted from the two isolated parent strains (*Bacillus cereus* MAM-B11 and MAM-B22) were used to inoculate (10.0% v/v in L.B medium) of wastewater I and then incubated in in shaking incubator (150.0 rpm) for 5.0 days at 30.0 ^{0}C. The decolorization percentage had been determined.

Decolorization assay: according to [29] and[30]. The decolorization was assessed by measuring the absorbance of the supernatant at different time intervals at the respective wavelength by using UV-VIS Spectrophotometer. The percentage of decolorization was calculated from the differences between initial and final absorbance values.

The percentage decolorization was calculated from the following equation:

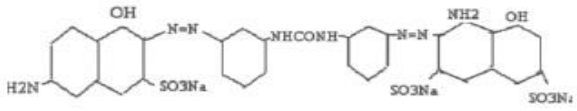
% Decolorization= (Initial OD−Final OD ×100)/ Initial OD

Initial OD= the initial Absorbance of dye concentration

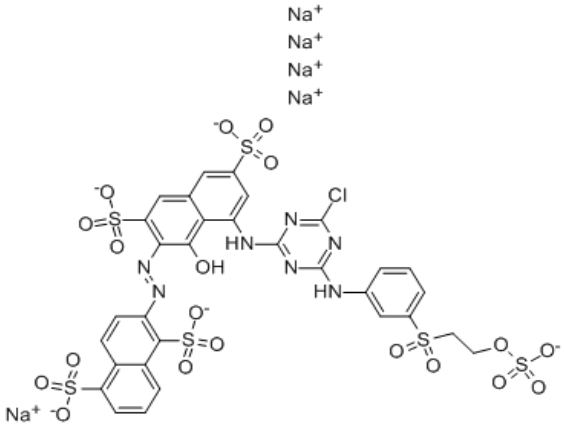
(Control)
Final OD= the absorbance of dye concentration with bacterial suspension (Sample filtrate).

Table (1): Maximum absorbance of color (λ_{max}) for each textile dye.

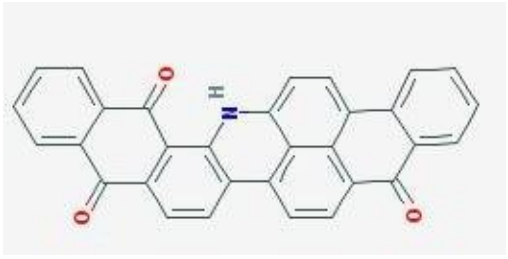
Dye	Formula	Molecular weight	λ_{max}
Isma Fast Red 8 B	$C_{29}H_{19}N_5O_8S_2.2Na$	675.63	506
Fantacell Olive TH-C50	$C_{31}H_{15}NO_3$	449.45	439
Drimarene Blue CL-R (RBBR)	$C_{22}H_{16}O_{11}N_2S_3.2Na$	626.55	590
Dycrofix Violet 5-R	$C_{20}H_{16}N_3Na_3O_{15}S_4$	735.58	557
Jakazol Black VS.BB	$C_{26}H_{21}N_5Na_4O_{19}S_6$	991.82	595
Dycrofix Red ME4B	$C_{31}H_{19}ClN_7O_{19}S_6.5Na$	1136.32	544
Jakofix Yellow MERL	$C_{28}H_{20}ClN_9O_{16}S_5.4Na$	1026.26	420



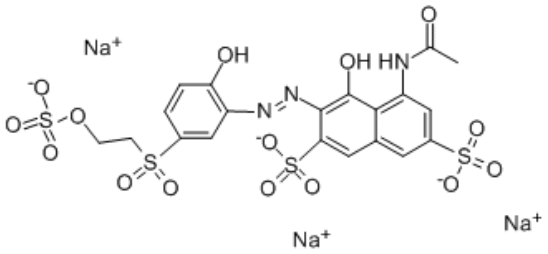
Isma Fast Red 8B dye



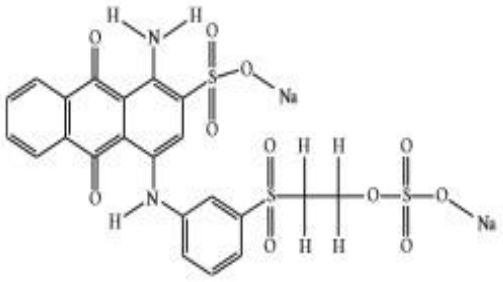
Dycrofix Red dye



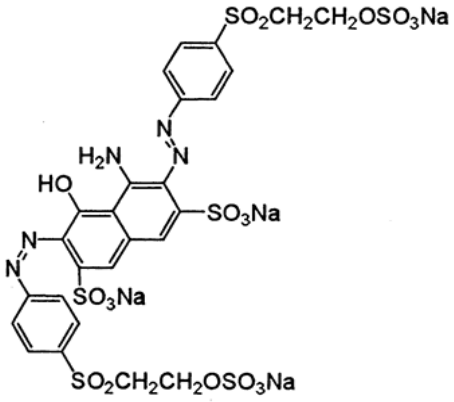
Fantacell Olive dye



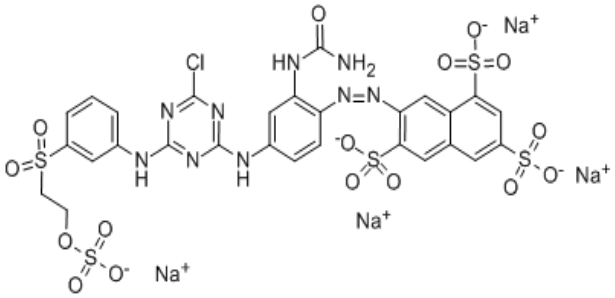
Dycrofix Violet dye



Drimarene Blue CL-R dye



Jakazol Black dye



Jakofix Yellow dye

Figure (1): Chemical structure of textile dyes.

3. Result and discussion

3.1 Effect of gamma radiation on the most potent bacterial isolates

Two bacterial strains (MAM-B11 and MAM-B22) were isolated from textile wastewater. These two isolates were identified by 16 S rRNA as *Bacillus cereus.* Exposure of *Bacillus cereus* MAM-B11 and MAM-B22 to gamma radiation with different doses reduced their viability. As the dose increased, the viability decreased exponentially (Dose response curve). Dose 15.0 kGy reduced the viability of *Bacillus cereus* MAM-B11 and MAM-B22 by 3.7 log cycles as indicated in Figures (2 and 3).

Exposure of *Bacillus cereus* strain MAM-B11 and strain MAM-B22 revealed that 15.0 kGy reduced their viability of by 3.7 log cycles. These two strains were more resistant than *Bacillus cereus* isolated from Rosetta branch of River Nile, Egypt, since 10.0 kGy reduce *B. cereus* by 5.24 log cycles [18]. The resistance of *Bacillus cereus* strains to gamma radiation can be attributed to the presence of sulfur compounds found in their cell wall and behaved as scavengers for free radicals and protect them from gamma radiation effects. Also, *Bacillus cereus* poses a powerful repair mechanisms [16, 31, 32, 18].

[21], found that 10.0 kGy gamma radiation reduced the viable count of *Bacillus cereus* NRRL 569 and ATCC 11778 by 5.5 and 2.7 log cycles respectively. However [17] reported that 10.0 kGy reduced the viable count of *Bacillus sp*. strains isolated from eye drop (MAM-40), (MAM-26) isolated from baby powder and (MAM-11) isolated from solution lenses by 4.17, 1.9 and 2.7 log cycles respectively.

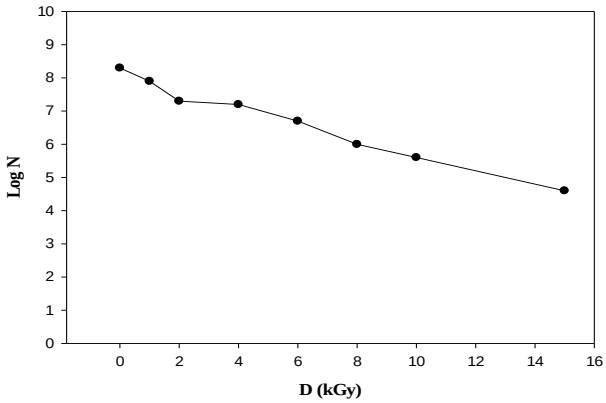


Fig. (2): Dose response curve of strain MAM-B11.

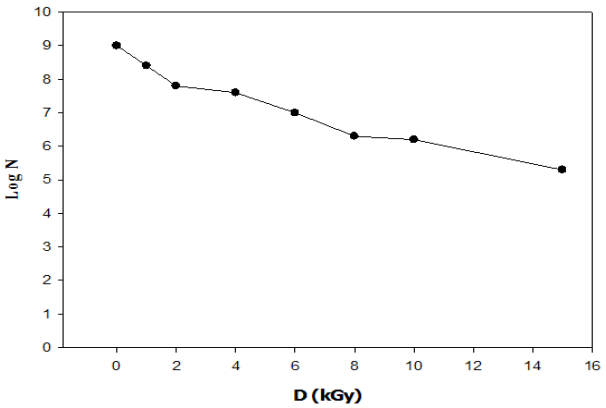


Figure (3): Dose response curve of strain MAM-B22.

3.2 Decolorization of textile dyes in textile wastewater I by B. cereus parent strains and their mutants

Mutant MAM-D6 resulted from exposure to 2.0 kGy gamma radiation decolorized Isma Fast dye more than

parent strain MAM-B11 by 1.0%, 10.0% and 5.0% at 200.0 and 400.0 mg/L after 48.0 hours and 400.0 mg/L after 6.0 days respectively. Another Mutant MAM-D13 of the same parent exposed also to 2.0 kGy gamma radiation, decolorized Isma Fast more by 0.9%, 14.0% and 7.0% for the same concentrations at the same incubation periods respectively as indicated in Table(2).

Mutant MAM-D1 resulted from parent strain MAM-B22 and exposed to 8.0 kGy gamma radiation decolorized Isma Fast more by 2.0%, 13.0% and 6.0% at 200.0 and 400.0 mg/L for 48.0 hours and 400.0 mg/L after 6.0 days respectively. Another mutant MAM-D15 which exposed to 8.0 kGy gamma radiation resulted from parent strain MAM-B22 decolorized also Isma Fast more by 3.0%, 11.0% and 5.0% at the same concentrations and incubation periods as shown in Table (2).

Mutant MAM-D13 removed Jakofix Yellow dye more by 17.0%, 88.0% and 50.0% of 200.0 mg/L after 48.0 hours and 400.0 mg/L after 6.0 days respectively than parent strain MAM-B11 as indicated in Table (3).

However, mutants MAM-D1, MAM-D15 and MAM-D18 which exposed to 4.0 kGy gamma radiation, resulted from parent strain MAM-B22 removed 82.0%, 79.0% and 97.0% of 200.0 mg/L Jakofix Yellow after 48.0 hours respectively. It also removed more Jakofix Yellow by 84.0%, 99.5% and 210.0% of 400.0 mg/L after 48.0 hours respectively. Meanwhile, the same mutants (MAM-D1, D15 and D13) removed more Jakofix Yellow than their parent strain MAM-B22 of 400.0 mg/L after 6.0 days by 41.0%, 47.0% and 51.0% respectively as shown in Table (3).

Mutant MAM-D13 resulted from parent strain MAM-B11 removed 25.0% and 6.0% of 200.0 and 400.0 mg/L of Fantacell Olive dye more than parent strain after 48.0 hours However, the removal was more by 18.0% and 11.0% but after 6.0 days respectively as indicated in Table (4).

Mutants MAM-D1 and MAM-D15 resulted from parent strain MAM-B22 removed Fantacell Olive more by 9.0% and 1.0% of 200.0 mg/L after 48.0 hours respectively. Also, the results recorded more removal 16.0% and 11.0% after 6.0 days for 200.0 mg/L respectively. In case of 400.0 mg/L Fantacell Olive, mutants MAM-D1 and MAM-D13 removed more dye than parent strain MAM-B22 by 7.0%, 3.0%, 8.0% and 5.0% respectively after 48.0 hours and 6.0 days incubation as shown in Table (4).

Mutant MAM-D13 resulted from parent strain MAM-B11 removed Dycrofix Red dye more than parent strain by 88.0%, 72.0%, 26.0% and 45.0% from 200.0 mg/L after 48.0 hours and 6.0 days. And 400.0 mg/L after 48.0 hours and 6.0 days respectively as indicated in Table (5).

Meanwhile, mutants MAM-D1, MAM-D15 and MAM-D18 resulted from parent strain MAM-B22 removed more Dycrofix Red than parent strain by 65.0%, 51.0% and 29.0% from 200.0 mg/L after 48.0 hours respectively. These mutants removed Dycrofix Red than parent strain by 63.0%, 44.0% and 48.0% respectively after 6.0 days at 200.0 mg/L. In case of the same mutants at 400.0 mg/L Dycrofix Red, they removed this dye more than the parent strain by 37.0%, 33.0% and 37.0% of 400.0 mg/L after 48.0 hours and removed more of Dycrofix Red after 6.0 days by 31.0%, 28.0% and 30.0% than that removed by parent strain as shown in Table (5). So, in all mutants, the removal percentage after 6 days more than the removal after 48.0 hours.

Mutants MAM-D6 and MAM-D13 resulted from parent strain MAM-B11 removed more Dycrofix Violet at concentration 400.0 mg/L by 22.0%, 20.0%, 21.0% and 17.0% after 48.0 hours and 6.0 days respectively as indicated in Table (6) than the parent strain. In case of mutants MAM-D15 and MAM-D17 resulted from parent strain MAM-B22 removed more Dycrofix Violet than parent strain in both 200.0 mg/L and 400.0 mg/L after 48.0 hours and 6.0 days as shown in Table (6).

The results revealed that mutants MAM-D15 and MAM-D17 which exposed to 10.0 kGy gamma radiation removed 132.0% and 138.0% from 200.0 mg/L Dycrofix Violet after 48.0 hours respectively and removed more Dycrofix Violet by 117.0% and 123.0% from 200.0 mg/L than parent strain respectively as cleared from Table (6). The same mutants MAM-D15 and MAM-D17 removed Dycrofix Violet at 400.0 mg/L more than their parent strain (MAM-B22) by 55.0%, 56.0%, 34.0% and 35.0% after 48.0 hours and 6.0 days respectively.

The results of mutants MAM-D6 and MAM-D13 resulted from parent strain MAM-B11 and Mutants MAM-D1, MAM-D17 and MAM-D18 resulted from parent strain MAM-B22 revealed that mutants removed more Jakazol Black than their parent strains by a range between 3.0% to 9.0% from 200.0 mg/L and 400.0 mg/L after 48.0 hours and 6.0 days as indicated in Table (7).

Mutants MAM-D6 and MAM-D13 removed more Drimarene Blue dye than parent strain MAM-B11 by 16.0% and 7.0% of 200.0 mg/L and 19.0% and 9.0% of 400.0 mg/L after 6.0 days as cleared in Table (8). However, mutants MAM-D1 and MAM-D15 removed more Drimarene Blue than their parent strain MAM-B22 by 23.0% and 33.0% from 200.0 mg/L and by 27.0% and 25.0% from 400.0 mg/L after 6.0 days as indicated in Table (8).

Mutants MAM-D6 and MAM-D13 resulted from exposure to gamma radiation of the parent strain *Bacillus* cereus MAM-B11 and mutants MAM-D1, MAM-D15, MAM-D17 and MAM-D18 resulted from exposure of *Bacillus cereus* parent strain MAM-B22 removed Textile dyes (Isma Fast, Jakofix Yellow, Fantacell Olive, Dycrofix Red, Dycrofix Violet, Jakazol Black and Drimarene Blue) more efficiently than their parent strains.

Mutants of parent strains MAM-B11 and MAM-B22 removed textile wastewater I more efficiently than their parent strains as indicated in Table (9).

The enhanced removal of the seven textile dyes may be attributed to enhanced production of oxidizing enzymes produced by *Bacillus cereus* due to induction of more enzymes by gamma radiation. Low doses of gamma radiation induced the enzymatic activity of microbial cells, consequently enhanced decolorization of textile dyes. The previous results were in a harmony with the results reported by [22, 21, 23, 24, 25].

Doses of gamma radiation enhanced the production of Laccase and MnP. enzymes produced by *P. Ostreatus* and *P. Sajor-Caju* with consequently enhanced the removal of dyes. [23, 24, 25]. Also gamma radiation enhanced the production of xylanases produced by *Bacillus megaterium* mutants [22].

Bacillus sp. YZU1 removed 95.0% of 100.0 mg/L of reactive Blacks in 120.0 hours and cloud Tolerate up to 500.0 mg/L. Enzymatic assays demonstrated that *Bacillus* sp.YZU1 possessed azo-reductase which played the most important role in decolorization [6]. While, [7,13] proved that laccase played the corner stone role in decolorizing Congo red, two azo dyes and two anthraquinon dyes secreted by *Bacillus amyloliquefaciens* and *Bacillus pumilus* W3.

Bacterial decolorization of textile dyes under certain environmental conditions has gained increasing attention as a method of treatment by eco-friendly manner, because it is an inexpensive and highly effective method [33]. Many dye decolorizing bacteria have been reported e.g. *Aeromonas* sp. [34], *Comamonas* sp. [35], *Enterobacter* sp. [36] and *pseudomonas* sp. [33].

However, Gram positive spore forming bacteria of genus *Bacillus* in the recent years received more and more attention as a corner stone in decolorizing textile dyes. *Bacillus* species had been isolated from different natural and polluted habitats. Two bacterial strains (MAM-B11 and MAM-B22) were isolated from El-Mahalla El-Kubra textile factory effluents I and II respectively. These two strains were identified by 16 S rRNA sequencing analysis as *Bacillus cereus* MAM-B11 and *Bacillus cereus* MAM-B22 with 100.0% similarity with *Bacillus cereus* strain (Data shown in another paper under publication). The ability of these strains to decolorize seven different textile dyes have been investigated. The previous results were confirmed with that of other investigators as the following. [6], isolated a newly bacterium sp. YZU1 with a remarkable ability to decolorize Reactive Black 5 (RB-5) from soil samples collected around a textile factory. [4], isolated a new microbial strain from azo dye contaminated river sediment which is capable of degrading Reactive Black B dye. This strain have been identified by 16 S rRNA gene sequence analysis as *Bacillus cereus* strain HJ-1. Also, [14] isolated a newly strain (*Bacillus* sp. MZS10) and evaluated the ability of *Bacillus* sp. MZS10 to decolorize Azure B dye (Lignin−model− synthetic dye). The decolorization was discovered to be dependent on cell density of the isolate and reached 93.55% of 40.0 mg/L after 14.0 hours of cultivation.

However, [13] characterized the novel laccase –producing *Bacillus pumilus* strain W3, which has been isolated from raw gallnut honey samples.

Two azo dyes and two anthraquinonic dye could be efficiently decolorized by purified laccase. More than 90.0% decolorization was observed at pH 9.0 after incubation for 5.0 hours. Halo-tolerant strain of *Bacillus amyloliquefaciens* isolated from salt spring in Oveca spa located in Republic of Serbia. This strain that exhibited robust spore Laccase with high temperature optimum 65.0 ^{0}C. Ability to oxidize azo dye Congo red was reported. More than 85.0% of Congo red was removed by this strain [7].

The previous results revealed that the two isolated bacterial strains can be used efficiently to decolorization textile dyes and could be used efficiently in treating textile effluents.

Table 2: Effect of parent strains MAM-B11 and MAM-B22 and their mutants on Isma Fast red dye**.**

Bacterial code	Dose kGy	Isma Fast Dye Conc. (mg/L)								
		200.0 mg/L after 48.0 h.			400.0 mg/L after 48.0 h.			400.0 mg/L after 6.0 days		
		Residual Conc.	Removal Conc.	Removal %	Residual Conc.	Removal Conc.	Removal %	Residual Conc.	Removal Conc.	Removal %
Parent MAM-B11	0.0	9.33	190.66	95.33	63.21	336.78	84.2	30.55	369.45	92.36
MAM-D6	2.0	5.6	194.40	97.20	26.7	373.3	93.3	8.71	391.29	97.8
MAM-D13	2.0	7.73	192.26	96.20	13.6	386.4	96.6	1.76	398.2	99.61
MAM-D21	2.0	8.0	192.0	96.0	40.04	359.96	89.99	24.9	375.1	93.8
MAM-D22	2.0	5.86	194.14	97.10	38.63	361.36	90.34	24.6	375.4	93.9
Parent MAM-B22	0.0	13.33	186.67	93.3	61.11	338.89	84.7	28.1	371.9	92.98
MAM-D1	8.0	9.33	190.66	95.33	16.86	383.14	95.79	4.21	395.80	99.0
MAM-D15	8.0	6.66	193.33	96.61	20.72	379.28	94.8	6.5	393.5	98.4
MAM-D17	10.0	9.86	190.13	95.06	42.14	357.85	89.5	18.87	381.13	95.2
MAM-D18	4.0	9.33	190.66	95.33	17.21	382.79	95.69	4.6	395.5	98.87

Table (3): Effect of parent strains MAM-B11 and MAM-B11 and their mutants on Jakofix Yellow dye.

Bacterial code	Dose kGy	Jakofix Yellow Dye Conc. (mg/L)								
		200.0 mg/L after 48.0 h.			400.0 mg/L after 48.0 h.			400.0 mg/L after 6.0 days		
		Residual Conc.	Removal Conc.	Removal %	Residual Conc.	Removal Conc.	Removal %	Residual Conc.	Removal Conc.	Removal %
Parent MAM-B11	0.0	28.74	142.51	71.26	208.2	191.7	47.9	146.7	253.3	63.3
MAM-D6	2.0	22.94	154.12	77.06	81.23	318.77	79.7	46.39	353.61	88.84
MAM-D13	2.0	16.04	167.90	83.96	39.29	360.71	90.18	19.41	380.59	95.15
MAM-D21	2.0	18.51	136.02	81.51	189.8	210.2	52.5	113.6	286.39	71.6
MAM-D22	2.0	26.51	146.99	73.49	184.6	215.4	53.8	106.5	293.5	73.37
Parent MAM-B22	0.0	115.81	84.19	42.11	226.7	173.3	43.3	150.1	249.9	62.5
MAM-D1	8.0	46.33	153.67	76.8	80.5	319.5	79.88	44.97	355.03	88.76
MAM-D15	8.0	48.55	151.44	75.7	54.44	345.56	86.39	28.42	371.58	92.9
MAM-D17	10.0	44.097	155.91	77.95	91.36	308.64	77.16	46.86	353.13	88.28
MAM-D18	4.0	33.407	166.59	83.29	32.19	367.8	91.95	17.98	382.01	95.5

Table (4): Effect of parent strains MAM-B11 and MAM-B22 and their mutants on Fantacell Olive dye.

Bacterial code	Dose kGy	Fantacell Olive Dye Conc. (mg/L)											
		200.0 mg/L after 48.0 h.			200.0 mg/L after 6.0 days			400.0 mg/L after 48.0 h.			400.0 mg/L after 6.0 days		
		Residual Conc.	Removal Conc.	Removal %	Residual Conc.	Removal Conc.	Removal %	Residual Conc.	Removal Conc.	Removal %	Residual Conc.	Removal Conc.	Removal %
Parent MAM-B11	0.0	63.1	136.9	68.4	52.5	147.5	73.8	81.5	318.5	79.6	37.3	326.7	81.7
MAM-D6	2.0	57.1	142.9	71.4	38.5	161.5	80.7	75.8	324.2	81.04	65.7	334.3	83.6
MAM-D13	2.0	27.9	172.1	86.0	25.2	174.8	87.4	60.03	339.97	84.9	36.02	363.98	90.99
MAM-D21	2.0	45.2	154.8	77.4	31.9	168.1	84.1	71.41	328.6	82.1	41.7	358.3	89.6
MAM-D22	2.0	59.1	140.9	70.4	40.5	157.5	78.7	63.8	336.2	84.1	42.96	357.03	89.3
Parent MAM-B22	0.0	53.16	146.8	73.4	43.19	156.8	78.41	84.7	315.3	78.8	75.8	324.2	81.04
MAM-D1	8.0	39.2	160.8	80.4	16.61	183.4	91.7	61.9	338.1	84.5	49.3	350.7	87.7
MAM-D15	8.0	50.5	149.5	74.8	25.2	174.8	87.4	74.6	325.4	81.4	56.9	343.1	85.8
MAM-D17	10.0	52.5	147.5	73.8	37.9	162.1	81.1	73.3	326.7	81.7	60.03	339.9	84.9
MAM-D18	4.0	49.8	150.2	75.1	33.22	166.8	83.4	67.6	332.4	83.1	60.03	339.9	83.4

Table (5): Effect of parent strains MAM-B11 and MAM-B22 and their mutants on Dycrofix Red dye.

Bacterial code	Dose kGy	Dycrofix Red Dye Conc. (mg/L)											
		200.0 mg/L after 48.0 h.			200.0 mg/L after 6.0 days			400.0 mg/L after 48.0 h.			400.0 mg/L after 6.0 days		
		Residual Conc.	Removal Conc.	Removal %	Residual Conc.	Removal Conc.	Removal %	Residual Conc.	Removal Conc.	Removal %	Residual Conc.	Removal Conc.	Removal %
Parent MAM-B11	0.0	124.63	75.37	37.69	100.89	99.11	49.55	126.48	273.52	68.38	152.83	247.17	61.79
MAM-D6	2.0	59.35	140.65	70.33	35.01	164.99	82.49	52.70	347.29	86.82	31.62	368.37	92.09
MAM-D13	2.0	58.16	141.84	70.92	29.08	170.92	85.46	55.34	344.66	86.17	39.53	360.47	90.11
MAM-D21	2.0	106.82	93.18	46.59	85.49	117.51	58.75	105.4	294.59	73.65	86.42	313.57	78.39
MAM-D22	2.0	108.01	91.99	45.99	77.15	122.85	61.42	110.67	289.32	72.33	94.86	305.13	76.28
Parent MAM-B22	0.0	118.69	81.31	40.65	106.82	93.18	46.95	147.56	252.43	63.11	118.58	281.42	70.36
MAM-D1	8.0	65.28	134.72	67.35	47.48	152.52	76.63	51.65	348.35	87.09	31.09	368.91	92.22
MAM-D15	8.0	76.56	123.44	61.72	50.45	149.55	74.78	62.19	337.81	84.45	40.58	359.42	89.86
MAM-D17	10.0	108.01	91.99	45.99	65.88	134.12	76.06	100.13	299.87	74.97	61.66	338.34	84.58
MAM-18	4.0	94.96	105.04	52.52	60.53	139.47	69.73	53.75	346.25	86.56	34.26	365.74	91.44

Table (6): Effect of parent strains MAM-B11 and MAM-B22 and their mutants on Dycrofix Violet dye.

Bacterial code	Dose kGy	Dycrofix Violet Dye Conc. (mg/L)											
		200.0 mg/L after 48.0 h.			200.0 mg/L after 48.0 h.			400.0 mg/L after 48.0 h.			400.0 mg/L after 6.0 days		
		Residual Conc.	Removal Conc.	Removal %	Residual Conc.	Removal Conc.	Removal %	Residual Conc.	Removal Conc.	Removal %	Residual Conc.	Removal Conc.	Removal %
Parent MAM-B11	0.0	30.47	169.52	84.76	106.66	93.33	46.66	98.46	301.53	75.38	84.61	315.38	78.84
MAM-D6	2.0	47.61	152.38	76.19	20.0	180.0	90.0	29.23	370.76	92.69	17.69	382.30	95.57
MAM-D13	2.0	24.76	175.23	87.62	17.14	182.85	91.42	37.69	362.30	90.57	30.15	369.85	92.46
MAM-D21	2.0	54.28	154.71	72.85	28.57	171.42	85.71	78.46	321.53	80.38	63.07	336.92	84.23
MAM-D22	2.0	20.95	179.04	89.52	18.09	181.90	90.95	36.92	363.07	90.76	30.76	369.23	92.30
Parent MAM-B22	0.0	119.4	80.59	40.29	112.38	87.61	43.81	153.84	246.15	61.53	109.23	290.76	72.69
MAM-D1	8.0	16.19	183.8	91.9	11.42	188.57	94.29	38.46	361.53	90.38	26.92	373.07	93.26
MAM-D15	8.0	12.38	187.61	93.80	9.52	190.47	95.23	16.15	383.84	95.96	8.46	391.53	97.88
MAM-D17	10.0	6.66	193.33	96.66	3.80	196.19	98.09	14.61	385.38	96.34	5.38	394.61	98.65
MAM-D18	4.0	10.47	189.52	94.76	8.57	191.42	95.71	30.76	369.23	92.30	20.0	380.0	95.0

Table (7): Effect of parent strains MAM-B11 and MAM-B22 and their mutants on Jakazol Black dye.

Bacterial code	Dose kGy	Jakazol Black Dye Conc. (mg/L)											
		200.0 mg/L after 48.0 h.			200.0 mg/L after 6.0 days			400.0 mg/L after 48.0 h.			400.0 mg/L after 6.0 days		
		Residual Conc.	Removal Conc.	Removal %	Residual Conc.	Removal Conc.	Removal %	Residual Conc.	Removal Conc.	Removal %	Residual Conc.	Removal Conc.	Removal %
Parent MAM-B11	0.0	30.70	169.29	84.64	21.41	178.58	89.29	46.95	353.04	88.26	35.55	364.44	91.11
MAM-D6	2.0	16.51	183.48	91.74	9.29	190.70	95.35	32.42	367.57	91.89	24.59	375.40	93.85
MAM-D13	2.0	20.38	179.61	89.80	11.09	188.90	94.45	31.30	368.69	92.17	23.25	376.74	94.18
MAM-D21	2.0	18.58	181.41	90.70	8.77	191.22	95.61	32.19	367.80	91.95	25.04	374.95	93.73
MAM-D22	2.0	22.19	177.80	88.90	11.61	188.38	94.19	33.09	366.90	91.72	26.38	373.61	93.40
Parent MAM-B22	0.0	28.12	171.87	85.93	23.22	176.77	88.38	53.21	346.78	86.69	40.02	359.97	89.99
MAM-D1	8.0	14.70	185.29	92.64	7.22	192.77	96.38	24.37	375.62	93.90	12.29	387.70	96.92
MAM-D15	8.0	21.16	178.83	89.41	35.95	164.04	82.02	27.72	372.27	93.06	18.78	381.21	95.30
MAM-D17	10.0	19.35	180.64	90.32	10.83	189.16	94.58	26.83	373.16	93.29	16.54	383.45	95.86
MAM-D18	4.0	13.93	186.06	93.03	7.48	192.51	96.25	26.38	373.61	93.40	13.86	386.13	96.53

Table (8): Effect of parent strains MAM-B11 and MAM-B22 and their mutants on Drimarene Blue dye.

Bacterial code	Dose kGy	Drimarene Blue Dye Conc. (mg/L)					
		200.0 mg/L after 6.0 days			400.0 mg/L after 6.0 days		
		Residual Conc.	Removal Conc.	Removal %	Residual Conc.	Removal Conc.	Removal %
Parent MAM-B11	0.0	57.07	142.92	71.46	125.05	274.94	68.73
MAM-D6	2.0	34.15	165.84	82.92	72.64	327.35	81.83
MAM-D13	2.0	45.84	154.15	77.07	98.39	301.60	75.40
MAM-D21	2.0	47.19	152.80	76.40	101.60	298.39	74.59
MAM-D22	2.0	52.58	147.41	73.70	102.98	297.01	74.25
Parent MAM-B22	0.0	76.85	123.14	61.57	183.44	216.55	54.13
MAM-D1	8.0	47.64	152.35	76.17	124.13	275.86	68.96
MAM-D15	8.0	35.95	164.04	82.02	128.58	271.41	67.85
MAM-D17	10.0	46.29	153.70	76.85	108.96	291.03	72.75
MAM-D18	4.0	50.78	149.21	74.60	122.29	277.70	69.42

Table (9): Effect of parent strains MAM-B11 and MAM-B22 and their mutants on textile Wastewater I.

Bacterial code Incubation 5.0 days.	Residual Conc.	Removal Conc.	Removal %
Parent MAM-B11	14.73	385.26	96.31
MAM-D6	14.03	358.96	96.9
MAM-D13	10.52	389.47	97.37
MAM-D21	12.28	387.71	96.92
MAM-D22	12.98	387.01	96.75
Parent MAM-B22	16.14	383.85	95.96
MAM-D1	11.57	388.42	97.1
MAM-D15	12.28	387.71	96.92
MAM-D17	14.03	358.96	96.9
MAM-D18	13.33	386.66	96.66

4. Conclusion

The bacterial strains isolated from indigenous microbial communities can decolorize textile dyes efficiently. *Bacillus cereus* MAM-B11 and *Bacillus cereus* MAM-B22 isolated from textile wastewater I and II respectively, they considered a potent strains for decolorizing textile dyes and the two bacterial strains were exposed to different doses of gamma radiation. As gamma radiation doses increased, the viability of the *B. cereus* MAM-B11 and MAM-B22 decreased gradually. Most of mutants resulted from exposure to radiation were more efficient than their parent strains on decolorization of textile dyes.

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