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Original Article

Characterization of a reactive yellow-2 decolorizing zinc tolerant bacterial strain *Pseudomonas* sp. LT10 isolated from textile industry wastewater

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Abstract

The textile effluents contain the synthetic dyes, which are mostly discharged into water resources without prior treatment. These dyes are very harmful for aquatic life and microorganisms but also for human beings. These harmful effects become further severe because the metal ions are present along with the dyes. Hence, there is need to deal these pollutants simultaneously. Therefore, present study was carried out to isolate and characterize a bacterium, which showed efficient color removal of reactive yellow-2 (RY2) in occurrence of zinc (Zn). For this purpose, Zn tolerant bacterial strains were isolated and examined for efficient color removal of RY2 in occurrence of Zn. Among the isolated bacterial strains, degrading capabilities of most effective strain, *Pseudomonas* sp. strain LT10 were characterized under different conditions. In existence of Zn, the strain LT10 exhibited significant decolorization of RY2 and other azo dyes. Moreover, yeast extract as a carbon co-substrate, showed efficient color removal of RY2 at pH 7.5-8.5 by the strain LT10. Moreover, the strain LT10 also revealed considerable decolorization of RY2 even at high levels of Zn. On the basis of results, it can be concluded that *Pseudomonas* sp. LT10 can be an efficient bioresource for treating textile wastewaters containing azo dyes and metal ions.

Keywords: Synthetic dyes, Reactive Yellow-2, Decolorization, Bacteria, Zn tolerance

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Introduction

Textile sector plays a significant role in the economy of several countries and contemporarily becoming central cause of environmental pollution worldwide due to release of enormous amounts of wastewater (Mondal et al., 2017). The consumption of water in textile industries is very high and almost 90% of the total consumed water is released as wastewater (Verma et al., 2012; Imran et al., 2015). Textile wastewater contains many types of dyes, which act as major pollutants in wastewater (Imran et al., 2015).

These dyes are recalcitrant in nature and impart intense color to textile wastewater (Mondal et al., 2017). The unsuitable disposal of textile wastewater causes reduction in penetration of sunlight in aqueous ecosystem, which results in reduced photosynthetic activity and causes acute toxicity in aquatic flora and fauna (Imran et al., 2015; Mondal et al., 2017).

Azo dyes are the synthetic dyes, which contain nitrogen to nitrogen double bond and the most frequently used dyes in textile and pharmaceutical industry (Imran et al., 2015). According to some estimates, about 50% of the applied dyes is released as wastewater during the textile dyeing processes (Carliell et al., 1995; Kusic et al., 2011). Their release in environment cause displeasing odor and color in the water bodies (Chacko and Subramaniam, 2011). These dyes also reported to alter COD, BOD and TOC for aquatic organisms (Saratale et al., 2009: Chacko and Subramaniam, 2011). It has been stated that few azo dyes and their metabolites are toxic and mutagenic in nature, causing serious threats to living organisms including human beings (Phugare et al., 2011). These dyes not only affect germination, growth and production of plants but also disturb microbial activities in soil (Ghodake et al., 2009; Imran et al., 2015). Plants growth is also suppressed by high concentration of these dyes (Dawkar et al., 2008; Khadhraoui et al., 2009; Phugare et al., 2011). In case of exposure to human beings, several problems including diarrhea, dermatitis, irritation of respiratory track and mucous membrane ulceration have been reported to be caused (Mittal et al., 2005). Even though high molecular weight and aromatic ring structure enable the azo dyes to resist degradation process, there is a need to remediate the effluents containing these dyes.

Several physic-chemical technologies including adsorption, coagulation, chemical transformation and irradiation have been described to be exploited for remediation of textile wastewaters (Chacko and Subramaniam, 2011). However, physicochemical technologies are not preferred because of their higher cost and not being environmental friendly. Biological technologies involve microbial decolorization of textile wastewaters and preferred due to their less cost and environment friendly nature (Tripathi and Srivastave, 2011; Mahmood et al., 2012; Imran et al., 2015; Maqbool et al., 2018). As few fungal species have also been found in dye removal process (Hussain et al., 2017) but the bacterial strains are given priority because of their shorter life span and rapid degradation process (Verma and Madamwar, 2003; Elisangela et al., 2009; Imran et al., 2015). Previous scientist have isolated a number of bacteria belonged to different genera and studied their potential for decolorization of various azo dyes e.g., *Enterobacter* (Roy et al., 2018), *Acinetobacter* (Meerbergen et al., 2018), *Arthrospira maxima* (Afreen et al., 2016), *Staphylococcus aureus* (Ayed et al., 2017), *Shewanella* (Imran et al., 2014) and *Serratia* (Najme et al., 2015). Moreover the existence of metal ions including zinc, cadmium, chromium, copper, nickel etc. significantly affect the dye decolorizing activity of bacterial strains (Hafeez et al., 2018; Maqbool et al., 2018). As these metal ions are also a component of the textile wastewaters, hence, there is need to isolate and characterize bacterial strains able to decolorize azo-dyes while tolerating the existence of such metal ions.

Zinc (Zn) is one of the heavy metals, which has been stated as a contaminant in the wastewaters produced from different industries including the textile dyeing units. However, presence of Zn in the textile wastewaters influence growth and activity of azo dyes degrading bacterial strains (Hussain et al., 2013; Imran et al., 2015). Therefore, it is a prerequisite to isolate bacterial strains proficient in not only decolorizing azo dyes but also show resistance towards existence of Zn in the media. Therefore, this study was carried out to isolate and characterize a Zn tolerant bacterium for decolorization of azo dyes in occurrence of Zn.

Material and Methods

Dyes, chemicals and culture media

The azo-dyes used in present experimental study were obtained either from Sigma-Aldrich (Germany). Analytical grade chemicals and reagents were used and purchased from Sigma- Aldrich. Zinc tolerant bacteria were isolated by using mineral salt media (MSM), which contained NaCl (1 g L^{-1}), $MgSO_4.7H_2O$ (0.5 g L^{-1}), $CaCl_2.2H_2O$ (0.1 g L^{-1}), K_2HPO_4 (1 g L^{-1}), KH_2PO_4 (1 g L^{-1}) and yeast extract (3 g L^{-1}). In general, the pH of the medium was adjusted at 7.2 and 200 mg L^{-1} of Zn using $Zn(NO_3)_2$ and 200 mg/L of RY2 were also added in MSM in order to isolate bacterial strains that have the potential of dyes decolorization in presence of zinc. Standard NaOH or HCl was used to adjust the pH of MSM whenever it was required. Nutrient agar (NA) medium with composition (g L^{-1}) NaCl (5.0), yeast extract (2), peptone (5) and agar (15) was used for determining minimum inhibitory

concentration (MIC) of Zn and other metal ions for the bacterial strains and to estimate the bacterial population density.

Isolation of Zn tolerant RY2 decolorizing strain LT10

To isolate Zn tolerant RY2 decolorizing bacterial strain, the industrial effluents were sampled from different textile industries in Faisalabad. The pH of all the collected samples was alkaline and electrical conductivity (EC) of all the samples was greater than 5 dS m^{-1}. For the isolation of Zn resistant RY2 decolorizing bacteria, enrichment culture technique was adopted using MSM broth containing 200 mg L^{-1} of Zn and 200 mg L^{-1} of RY2 dye. For enrichment, each waste water sample was inoculated into MSM broth (1:10) in individual flask and incubated in dark at 30°C in static incubator together with un-inoculated control. After an incubation period of 72 h, the aliquots were taken from each flask and subjected to centrifugation (6000 rpm for 5 minutes) and decolorization of RY2 was analyzed by making a comparison of absorbance (λ_{max} = 404 nm on a UV-Visible Spectrophotometer) of aliquots in inoculated media and controls through the following formula:

$$Decolorization\ (\%) = \frac{(Uninoculated\ control - Inoculated\ sample)}{Uninoculated\ control} \times 100$$

When <50% of added RY2 was decolorized, samples were taken from 1st enrichment and mixed with freshly prepared MSM broth (1:10) amended with RY2 and Zn. The second batch of enrichment cultures was treated in the same way as the first batch and again decolorization was estimated as described above. After five cycles, sample from each culture was spread on MS+Zn+RY2 agar plates through dilution plate technique and incubated in dark at 30°C. After 72 h, 35 dissimilar bacterial colonies were selected on the base of their rapid growth and different morphology and purified through repeated streaking method using MSM agar plates. The single purified colonies were examined for color removal of RY2 in occurrence of Zn in MSM broth medium. The purified 35 bacterial isolates were transferred to MS broth media containing Zn (200 mg/L). After 24 h, growth of each bacterial isolates was checked by measuring their optical density (OD) at 600 nm. 2.0 mL of each bacterial culture was inoculated distinctively in triplicates containing 18 mL of MS broth media with an addition of Zn (200 mg/L) and RY2 (200 mg/L). All the samples together with un-inoculated control were incubated at 30°C in static incubator. After 48h incubation, samples from all cultures were taken and centrifuged at 6000 rpm for 5 min, supernatants were analyzed for RY2 color removal as already described above. All the 35 isolates were also assessed for their Zn tolerance by estimating the MIC of Zn against them. For this purpose, all the isolates were grown on NA plates containing different concentrations of Zn (200 to 3000 mg L^{-1}). The minimum concentration of Zn at which some bacterial isolate could not grow was considered MIC of Zn for that bacterial isolate. From this screening, the isolate LT10 showed highest decolorization of RY2 and exhibited high MIC value of Zn, and therefore selected for further characterization.

Amplification and sequencing of 16S rDNA of strain LT10

The amplification and sequencing of 16S rDNA gene was done for identification of the isolate LT10. The 16S rDNA gene amplification of the isolate LT10 was done by the process as reported by Maqbool et al. (2016). The purification and sequencing of the amplified 16S rDNA gene was done by Macrogen (Seol, South Korea). By using the online BlastN program of National Center for Biotechnology Information (NCBI), the 16S rDNA sequence of LT10 was compared with other known sequences. Phylogenetic analysis of this sequence based on multiple alignments followed by construction of phylogenetic tree through neighbor joining method was carried out as previously reported by Maqbool et al. (2016).

Optimization of decolorizing ability of LT10 at different incubation conditions

Color removal of RY2 by LT10 at different pH

The potential of strain LT10 for RY2 color removal (200 mg/L) in MSM containing Zn (200 mg L^{-1}) was evaluated at different pH including 5.5, 6.5, 7.5, 8.5 and 9.5. For this purpose, pH of the MSM broth media was maintained using standard HCl and NaOH solutions. The MSM liquid media adjusted with RY2 (200 mg/L) and Zn (200 mg/L) were inoculated with the bacterial culture of LT10 to obtain OD_{600} of 0.1. The triplicates of inoculated media together with controls were preserved in static incubator. The aliquots were taken after consistent incubation period (24, 48, 72, 96 and 120 h), subjected to centrifugation (6000 rpm for 5 min) and used for measuring RY2 decolorization through UV-visible spectrophotometer as described above.

Color removal of RY2 by LT10 in the presence of varying carbon co-substrates

The ability of the strain LT10 for color removal of RY2 (200 mg/L) in MS broth media altered with Zn (200 mg/L) was evaluated in the presence of varying carbon (C) co-substrates including glucose, lactose, sucrose, maltose, yeast extract and D-Mannitol. Therefore, the media altered with RY2 (200 mg/L) and Zn (200 mg L^{-1}) were separately added with 3 g L^{-1} of the individual carbon co-substrates and then bacterial cells of LT10 were added in MSM to obtain OD_{600} of 0.1. The triplicates of inoculated samples together with their respective controls were placed in static incubator at 30°C. The aliquots were drawn after 16 and 40 h of incubation, subjected to centrifugation (6000 rpm for 5 minutes) and used for measuring RY2 decolorization through UV-visible spectrophotometer as explained above.

Decolorization of RY2 by LT10 at different concentrations of Zn

The capability of the LT10 bacterial isolate for decolorization of RY2 (200 mg/L) was also evaluated at varying concentrations of Zn including 200, 500, 800, 1000, 1500 and 2000 mg/L of Zn in the MS broth media. The separate MS broth media containing RY2 (200 mg/L) and above different concentrations of Zn were subjected to inoculation with the bacterial cells of LT10 to achieve OD_{600} of 0.1. The triplicates of inoculated media together with their respective controls were placed in static incubator at 30°C in dark. The aliquots were drawn after planned intervals, subjected to centrifugation (6000 rpm for 5 min) and used for measuring RY2 decolorization as already described above.

Color removal of structurally different azo dyes by LT10 in the presence of Zn

The strain LT10 was also studied for its potential to remove color of different azo dyes such as RY2, RR120, RO16, RB5, CRD, OD, BD and VD in MSM broth media altered with Zn (200 mg/L). For this purpose, all these dyes were individually added (@ 200 mg/L) in the separate MS liquid media containing Zn (200 mg/L) and then inoculation with the cells of LT10 was carried out to achieve OD_{600} of 0.1. The triplicates of inoculated media along with their respective un-inoculated controls were placed in static incubator. The supernatants from all samples were drawn after 24, 48, 72, 96, 120 and 144 h, subjected to centrifugation (6000 rpm for 5 minutes) and used for determining decolorization of each azo-dye using spectrophotometer at particular λ_{max} values (RY2 = 404 nm, RB5 = 597 nm, RR120 = 535 nm, RO16 = 494 nm, CRD = 540 nm, OD = 496 nm, BD = 580 nm, VD = 510 nm) for each dyes. The decolorization of each dye was estimated using the equation already given above.

Results

Isolation, screening and identification of LT10

This study demonstrated the isolation of several bacteria from textile wastewater samples collected from various textile industries located in Faisalabad. Among the isolated bacteria, 35 different bacterial isolates were examined for color removal RY2 as well as their ability to tolerate Zn in MSM medium. All the 35 isolates were found to decolorize (>10%) RY2 in MSM altered with 200 mg/L of Zn but with varying extents ranging from 10.9 ± 1.2% to 90.8 ± 2.5% (Table 1). Such variation might be due to variation in decolorizing capabilities of the isolates and their involved enzymatic systems. Such variation has also been described in different studies dealing with bacterial decolorization of several azo dyes (Maqbool et al., 2016; Hafeez et al., 2018; Maqbool et al., 2018). However, this study is different from others because in this study the decolorization was conducted in the existence of 200 mg/L of Zn. It was also observed that 13 out of these 35 isolates including LT1, LT2, LT3, LT6, LT7, LT8, LT9, LT10, LT16, LT25, LT28, LT33 and LT34 were found to decolorize >50% of the initially added RY2 within 48 h. Among these isolates, the highest decolorization of RY2 was observed by the isolate LT10 as it had decolorized more than 90% of RY2 within 48 h. Furthermore, it was observed that LT10 also had the ability to tolerate the presence of Zn because it was found to grow in MS medium even at 3000 mg/L of Zn. Although some other isolates including LT14 and LT25 could also grow at this high concentration of Zn but they did not show a very good potential for RY2 decolonization.

From this study, the isolate LT10 was selected for further experiments because it exhibited highest RY2 decolorization at 200 mg/L of Zn as well as a good capability to resist the presence of greater concentration of Zn. Based on BlastN analysis of its amplified 16S rDNA gene (NCBI GeneBank Accession No. KY492394), LT10 bacterial isolate was found to exhibit maximum resemblance with bacteria belonged to genus Pseudomonas.

Table-1. Growth of the Zn resistant isolates at varying Zn concentrations and removal of RY2 by the isolates in the presence of 200 mg L^{-1} of Zn

Isolates	Zn Concentration (mg L^{-1})					RY2 Decolorization (%)
	200	500	1000	2000	3000	
LT1	+	+	-ve	-ve	-ve	55.5 ± 2.7
LT2	+	+	+	+	-ve	71.3 ± 1.8
LT3	+	+	-ve	-ve	-ve	55.0 ± 3.1
LT4	+	+	+	+	-ve	45.5 ± 2.4
LT5	+	+	+	-ve	-ve	45.0 ± 1.9
LT6	+	+	-ve	-ve	-ve	76.5 ± 1.8
LT7	+	+	-ve	-ve	-ve	65.0 ± 2.1
LT8	+	+	+	+	-ve	66.5 ± 2.5
LT9	+	+	+	-ve	-ve	75.7 ± 3.6
LT10	+	+	+	+	+	90.8 ± 2.5
LT11	+	+	-ve	-ve	-ve	33.9 ± 2.2
LT12	+	+	+	-ve	-ve	32.0 ± 2.0
LT13	+	+	+	+	-ve	23.0 ± 1.2
LT14	+	+	+	+	+	43.7 ± 2.5
LT15	+	+	-ve	-ve	-ve	40.0 ± 1.9
LT16	+	+	+	-ve	-ve	60.0 ± 3.8
LT17	+	-ve	-ve	-ve	-ve	34.6 ± 2.4
LT18	+	+	+	+	-ve	20.0 ± 1.8
LT19	+	+	+	+	-ve	15.7 ± 1.0
LT20	+	-ve	-ve	-ve	-ve	10.9 ± 1.2
LT21	+	-ve	-ve	-ve	-ve	15.0 ± 1.1
LT22	+	+	+	+	-ve	18.0 ± 2.9
LT23	+	-ve	-ve	-ve	-ve	20.8 ± 2.0
LT24	+	+	-ve	-ve	-ve	30.0 ± 1.5
LT25	+	+	+	+	+	55.0 ± 2.4
LT26	+	+	+	-ve	-ve	44.9 ± 4.2
LT27	+	+	-ve	-ve	-ve	34.0 ± 2.7
LT28	+	+	+	+	-ve	55.1 ± 3.6
LT29	+	-ve	-ve	-ve	-ve	20.4 ± 2.7
LT30	+	+	+	+	-ve	24.6 ± 1.9
LT31	+	+	+	+	-ve	15.5 ± 2.6
LT32	+	+	+	+	-ve	30.3 ± 2.4
LT33	+	+	-ve	-ve	-ve	50.0 ± 1.1
LT34	+	+	+	-ve	-ve	50.3 ± 3.4
LT35	+	+	-ve	-ve	-ve	18.0 ± 2.8

Likewise, LT10 strain was also found to group with the bacteria belonging to genus Pseudomonas (Figure 1). Therefore, LT10 was named as *Pseudomonas* sp. LT10 and its 16S rDNA sequence was deposited in NCBI Genebank with accession number KY492394. The previous published data indicated that few bacteria, which belong to genus Pseudomonas have already been reported for their potential to declorize several dyes (Jadhav et al., 2010; Maqbool et al., 2016; Hafeez et al., 2018). However, the bacteria isolated in this study i.e., *Pseudomonas* sp. LT10 is exceptional in the sense that it has considerable ability for RY2 decolorization even in the presence of Zn. Very recently, Hafeez et al. (2018) reported the decolorizing ability of a bacterium, which belonged to genus Pseudomonas in the presence of lead (Pb). Hence, the isolation of *Pseudomonas* sp. LT10 will be a potential addition to the existing dye decolorizing bacteria belonging to genus Pseudomonas with a special ability to decolorize even in Zn stress.

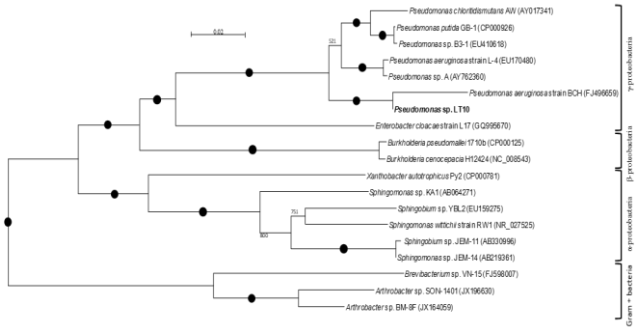

Fig-1: Phylogenetic tree based on 16S rDNA gene sequence of *Pseudomonas* sp. LT10.

Impact of pH on color removal of RY2 by strain LT10

The ability of *Pseudomonas* sp. LT10 for RY2 decolorization was evaluated at various levels of pH in MSM media altered with 200 mg/L of Zn. *Pseudomonas* sp. LT10 exhibited considerable potential for color removal of RY2 at varying pH (5.5 to 9.5) (Figure 2).

However, this strain showed optimal decolorization at pH values of 7.5 and 8.5. After 24 hours, *Pseudomonas* sp. LT10 had decolorized 40.5%, 41.7%, 21.1%, 20.8% and 8.9% of RY2 at pH values of 8.5, 7.5, 9.5, 6.5 and 5.5, respectively.

The maximum value of RY2 decolorization by the strain LT10 was recorded after 96, 72, 72, 48 and 48 h of incubation at pH 5.5, 6.5, 7.5, 8.5 and 9.5, respectively. Slightly alkaline pH value ranging from 7.0 to 8.5 has already been stated to be most promising for color removal of dyes by several previously isolated bacteria (Imran et al., 2014; Maqbool et al.,

2016; Hafeez et al., 2018; Maqbool et al., 2018). The differential decolorization at different pH may be attributed to effect of pH either on the decolorizing enzymes or on the growth of the bacterial strain as already reported for the strain *Pseudomonas* sp. RA20 while studying the decolorization of RB5 (Hussain et al., 2013).

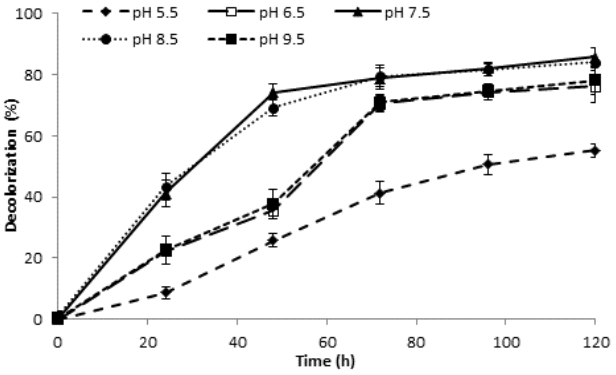

Fig-2: Removal of RY2 by *Pseudomonas* sp. LT10 at varying pH values in the presence of 200 mg L^{-1} of Zn.

Impact of different carbon co-substrates on RY2 decolorization by *Pseudomonas* sp. LT10

Over 16 h incubation period, the strain LT10 decolorized 22.5, 22.9, 13.2, 4.6, 6.8 and 5.7% of RY2 in the MSM broth amended with glucose, maltose, sucrose, lactose, yeast extract and D-Mannitol, respectively (Figure 3). However, over 40 h incubation period, it had decolorized 58.7, 44.1, 45.7, 16.8, 83.9 and 13.6% of RY2 in the MSM broth amended with glucose, maltose, sucrose, lactose, yeast extract and D-Mannitol, respectively. The increase in decolorizing abilities of bacterial strains against structurally dissimilar dyes in the existence of yeast extract has already been reported in several previous studies (Hussain et al., 2013; Imran et al., 2016; Maqbool et al., 2016; Hafeez et al., 2018). This increase in decolorization in the presence of yeast extract is attributed to its potential role not only in improving the growth of the bacterial strains but also in serving as a redox mediator for enzymes responsible for dye decolorization (Imran et al., 2016).

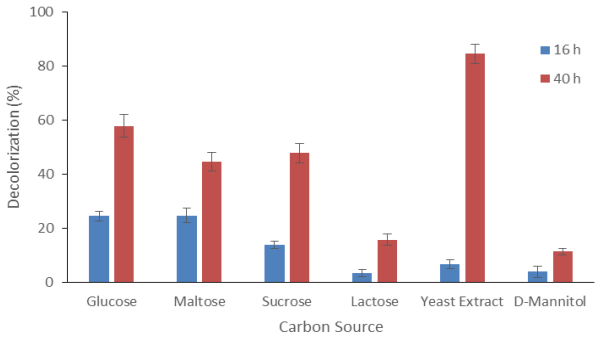

Fig-3: Removal of RY2 by *Pseudomonas* sp. LT10 in liquid culture containing different carbon co-substrates in the presence of 200 mg L^{-1} of Zn.

Decolorization of RY2 by LT10 at different levels of Zn

While studying the ability of the strain LT10 for RY2 decolorization at varying levels of Zn, it was found that this strain exhibited complete RY2 decolorization even at 800 mg/L of Zn (Figure 4).

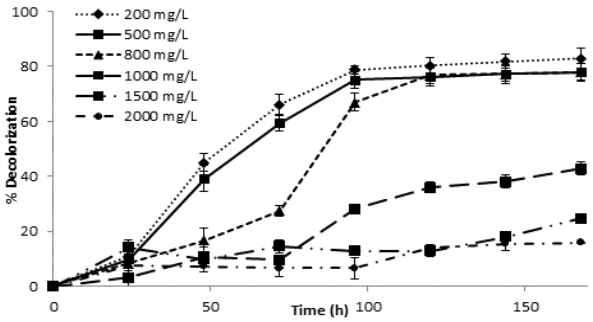

Fig-4: Effect of different levels of zinc (Zn) on removal of RY2 by *Pseudomonas* sp. LT10.

Table-2. Removal of dyes by *Pseudomonas* sp. LT10 in the presence of 200 mg L^{-1} of Zn

	Color removal %					
	24 Hours	**48 Hours**	**72 Hours**	**96 Hours**	**120 Hours**	**144 Hours**
Reactive Black-5	55.66 ± 0.02	67.20 ± 0.07	79.16 ± 0.02	75.49 ± 0.02	75.80 ± 0.07	87.24 ± 0.02
Reactive Orange-16	Nil	Nil	10.8 ± 0.1	87.79 ± 0.02	92.77 ± 0.06	93.41 ± 0.05
Reactive Red-120	0.12 ± 0.15	21.78 ± 5.23	29.79 ± 0.02	88.61 ± 0.38	93.73 ± 0.07	94.11 ± 0.02
Reactive Yellow-2	3.31 ± 0.02	11.58 ± 0.02	18.14 ± 0.02	22.44 ± 0.54	43.97 ± 0.06	70.80 ± 0.1
Congo Red direct	67.08 ± 0.12	67.30 ± 0.03	69.21 ± 0.18	71.30 ± 0.03	72.38 ± 0.03	73.40 ± 0.59
Orange direct	12.66 ± 1.9	14.14 ± 0.37	19.41 ± 0.73	22.78 ± 0.63	27.43 ± 0.37	32.91 ± 1.9
Blue Disperse	Nil	Nil	Nil	55.59 ± 0.01	55.89 ± 0.02	56.13 ± 0.11
Violet Disperse	Nil	Nil	Nil	Nil	Nil	Nil

The maximum value of RY2 decolorization by strain LT10 at 200 and 500 mg/L of Zn was obtained after 96 h. Over this incubation period, 61.3, 25.7, 11.4 and 7.6% of the primarily added RY2 was removed at 800, 1000, 1500 and 2000 mg L^{-1} of Zn. However over 168 h incubation period, 42.3, 22.6 and 16.9% RY2 was removed at 1000, 1500 and 2000 mg L^{-1} of Zn. This finding indicates that the higher concentrations of Zn in the media inhibited the decolorization activity and this inhibited might due to the impact of Zn on the enzymatic system of the strain. These findinds were in accordance to the findings of Hafeez et al. (2018) who reported that *Pseudomonas aeruginosa* strain HF5 showed efficient color removal of RR120 up to 100 mg/L of lead (Pb) over which the decolorization activity was significantly inhibited.

Color removal of structurally different dyes by strain LT10

The strain LT10 revealed very good potential for color removal of structurally dissimilar dyes in the existence of Zn as shown in Table 2. However, it was observed that the ability of LT10 to decolorize structurally different dyes was variable. This variability in decolorization capability might be due to differences in structure of the dye molecules. Such difference in color removal of structurally dissimilar dyes has already been reported in various studies (Hussain et al., 2013; Hafeez et al., 2018; Maqbool et al., 2018).

Conclusion

Based on results, it can be concluded that *Pseudomonas* sp. strain LT10 has considerable ability for color removal of RY2. However, the strain LT10 exhibited efficient decolorization color removal of RY2 in the presence of yeast extract at pH 7.5-8.5. Moreover, *Pseudomonas* sp. strain LT10 efficiently decolorized RY2 dye even at higher levels of Zn. Therefore, the strain LT10 can be considered as a potential candidate for its possible application for treatment of dye contaminated stuff.

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