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REVIEW

Biodegradation of azo dye-containing wastewater by activated sludge: a critical review

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Abstract

The effluent from the textile industry is a complex mixture of recalcitrant molecules that can harm the environment and human health. Biological treatments are usually applied for this wastewater, particularly activated sludge, due to its high efficiency, and low implementation and operation costs. However, the activated sludge microbiome is rarely well-known. In general, activated sludges are composed of *Acidobacteria, Bacillus*, *Clostridium*, *Pseudomonas*, *Proteobacteria*, and *Streptococcus*, in which *Bacillus* and *Pseudomonas* are highlighted for bacterial dye degradation. Consequently, the process is not carried out under optimum conditions (treatment yield). Therefore, this review aims to contextualize the potential environmental impacts of azo dye-containing wastewater from the textile industry, including toxicity, activated sludge microbiome identification, in particular using the matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) as a novel, rapid and accurate strategy for the identification of activated sludge microbiome (potential to enhance treatment yield).

Keywords Activated sludge · Textile industry · Microbiome · Biodegradation · Azo dye

Introduction

The high fluctuations in composition and other parameters such as biological oxygen demand (BOD), chemical oxygen demand (COD), colour, pH, and salinity during textile processing contribute to the complexity of textile wastewater treatment (Senthilkumar et al. 2011; Farias et al. 2017). The textile industry generates, inherently, a high volume of toxic effluent, mainly due to the chemical baths and rinsing series (Harane and Adivarekar 2017). According to Leão (2002), 150 L of water are necessary to produce 1 kg of fabric, in which 132 L (88%) are wastewaters.

The dyeing stage leads to a large amount of wastewater with high levels of COD (from the chemical used in the process), BOD (due to the direct discharge of wastewater in water sources which promotes a rapid depletion of dissolved oxygen), pH, and dyes (Holkar et al. 2016; Swati and Faruqui 2018). The incorrect disposal of textile industry effluents into water bodies interferes with the penetration of light. Hence, it harms the photosynthetic activity of water body communities (Elisangela et al. 2009). Thus, the textile industry effluent has to be properly treated before disposal into water bodies. In this sense, conventional textile industry treatments include coagulation/flocculation, biological, membrane, and advanced oxidation processes (Vajnhandl and Valh 2014; Yukseler et al. 2017). Among these techniques, the dye biodegradation by the activated sludge process is drawing attention due to its low cost (implementation and operation) and high efficiency (Haddad et al. 2018). Regarding activated sludge, the effectiveness of COD and BOD reduction can reach up to 90% (Pereira et al. 2010; Waghmode et al. 2019).

Activated sludges are composed of microbial communities. However, there are few reports on their characterization (El et al. 2016; Zhu et al. 2018; Cao et al. 2019). The evaluation of activated sludges as microbial consortia is essential to comprehend the interactions among the microbial community and optimize biodegradation (Köchling et al. 2017). Nevertheless, experiments of dye-biodegradation by isolated strains from activated sludges makes easier the elucidation of biodegradation mechanisms (Khehra et al. 2005).

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Therefore, this review describes the main biodegradation aspects of textile effluent. Then, it correlates the MALDI-TOF MS as a promising methodology for identifying activated sludge microbiome and, consequently, improving the treatment yield.

Potential impacts of azo dyes

Azo dyes are chemically composed of aromatic groups and azo chromophore (-N=N-). They are highly water-soluble. It is worth noting that azo dyes are widely applied by textile industry corresponding ≥ 50% out of the worldwide dye production (Brüschweiler and Merlot 2017). However, they hamper conventional textile wastewater treatment plants due to their recalcitrance.

It is usually observed a very low degradation rate of azo dyes at primary and secondary treatment stages due to their recalcitrant behaviour, which is related to their synthetic origin and chemical structure, providing them high resistance to photo-oxidation, biological activity, and other environmental conditions. The molecular arrangement and size of these substances contribute negatively to their biodegradation since a steric effect hinders the enzymatic access necessary to start the degradation (Rittmann 2018). Therefore, the accumulation of azo dyes can occur in sediments, soils, and contaminate the drinking water supply system (Salter-Blanc et al. 2016; Xiang et al. 2016; Mullai et al. 2017). The colour reduction ≈ 50% (azo dyes) from coloured wastewater is considered adequate. However, the toxicity factor must also be considered, particularly due to the aromatic amines (Xiang et al. 2016; Brüschweiler and Merlot 2017). Heavy metals, salts, and sulfides are potentially microbial inhibitors of biological treatment system. Thus, it must be also evaluated (Sarayu and Sandhya 2012).

It is known that the chromophore azo groups present in anionic and nonionic dyes suffer reductive cleavage producing highly toxic aromatic amines (Table 1): $R\text{-}N = N\text{-}R' + 4\bar{e} + 4H^{+} \rightarrow R\text{-}NH_2 + R'\text{-}NH_2$ (Xiang et al. 2016). The chemically reduced form of dyes was already found in sediments of aquatic bodies. These molecules are carcinogenic, since they can be oxidized to *N*-hydroxylamines. Thus, the nitrenium ion generated can bind with cellular macromolecules as DNA, proteins, and RNA (Ford and Griffin 1992; Sari and Simarani 2019). Nevertheless, an activating metabolism varies according to the balance between numerous competing steps, the bioavailability of the reactive metabolite, and nutritional habits. Moreover, possible differences in individual susceptibility influence the higher complexity of the metabolic pathway, polymorphisms of enzymes associated with the metabolism of aromatic amines, and equilibrium between activating and inactivating steps (Gregory 2007; Neumann 2010).

Kumar et al. (2019) carried out the optimal process of decolourization of Acid Black 24 azo dye by *Bacillus pseudomycoides*. The authors also evaluated the genotoxicity and phytotoxicity of the degraded dye. Genotoxicity assay was carried out using *Allium cepa* (onion), evaluating the DNA damage in cells treated with dye solution performed by single-cell gel electrophoresis method. The results were obtained by comparing before and after decolourization. The untreated dye sample presented a genotoxic effect on the root cells of *Allium cepa*. Phytotoxicity experiments were also performed on seeds of *Vigna radiata* and *Sorghum vulgare* at 25 °C. After 48 h was observed the number of full seeds germinated, and with five days of incubation was calculate the length of plumule (cm) and radicle of seedlings (cm) and germination percentage. The control and treated sample results presented similar values, which indicate the production of non-toxic metabolites correlated to high degradation yields.

On the other hand, according to Waghmode et al. (2019) higher phytotoxicity was observed with *Phaseolus mungo* and *Sorghum vulgare* after a sequential photocatalytic and biological treatment consisting of ZnO as the photocatalyst and a microbial consortium of *Brevibaccilus laterosporus* and *Galactomyces geotrichum*. Through HR-MS and GC–MS analysis, degradation products were analyzed after bacterial treatment. Many products with a fragmentation pattern inferring asymmetrical/symmetrical cleavage in azo bonds were found, probably due to the demethylation and desulfonation mechanisms. It was also observed that the produced metabolites in the activated sludge can be correlated to microbial species (Tabasum et al. 2019).

The toxicity of a treated textile effluent was analyzed by Carvalho et al. (2020), using *Vibrio fischeri* as a toxicity indicator, monitoring cell luminescence inhibition (30 min). The dilution factor (effluent) required to not affect bacteria metabolism was also used as a comparison parameter, in which the acute toxicity is correlated to 50% reduction in the bacteria bioluminescence. In the conventional up-flow anaerobic sludge blanket (UASB) effluent, it was obtained a dilution factor between 14 and 16, which can be associated with the presence of aromatic amines, (strong toxicity levels). Whereas the results of UASB effluent micro aerated on top indicated that aromatic amines were converted into nontoxic compounds.

Aromatic amines from the azo-dye degradation have mutagenic effects in *Salmonella* and *Mammalian*. Methyl Red, which is naturally mutagenic, has already been associated with *N*,*N*-dimethylphenylenediamine (DMPD) formation, a toxic and mutagenic aromatic amine (Wong and Yu 1999). Consequently, methodical optimization studies simultaneously with metabolite toxicity testing should be implemented for each system, considering dye, microbe, enzyme, or mediator (Sen et al. 2016).

Table 1 Reports about the decolorization capability of bacteria from textile-activated sludge

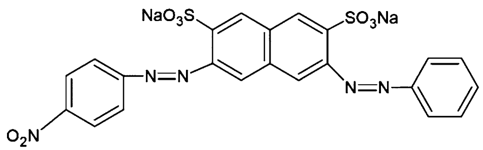
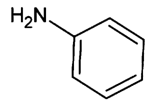
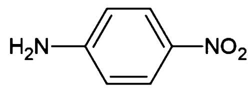
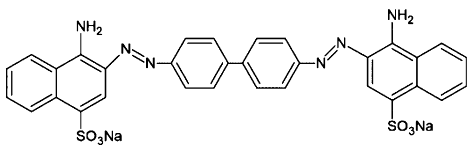
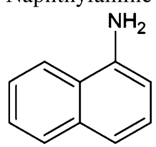
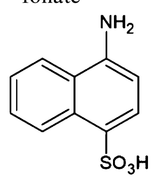
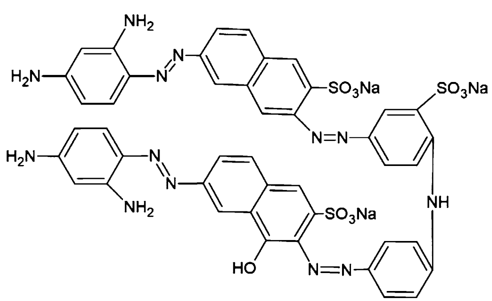
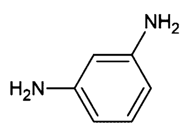
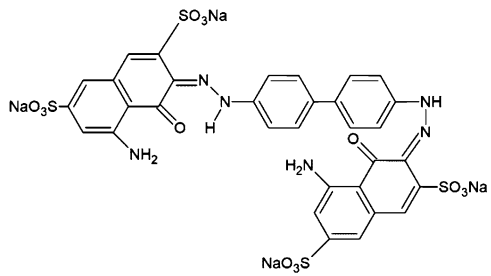
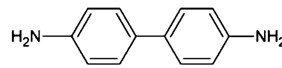
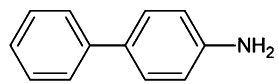
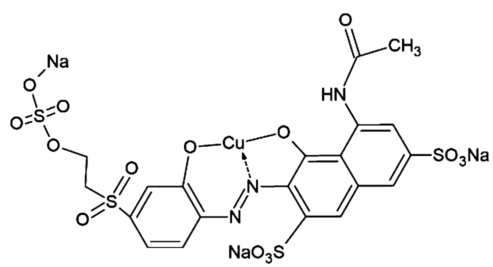
Dye	Corresponding aromatic amines	Toxicity/ecotoxicity of aromatic amines	Microbiome	Degradation system	Decolorization rate	References
Amino Black (AB) 	Aniline  4-Nitro-aminobenzene 	Naphthylamine has an occupational carcinogen potential and can be absorbed into the body by ingestion, inhalation, and through the skin. It is toxic to aquatic life with long-lasting effects 4-nitro-aminobenzene is expected to have high mobility in soil	*Bacteroides* and *Lactococcus*	Decolorization reaction by anaerobic condition, and mineralization process under aerobic environment	85.1% 85.2%	Zhu et al. (2018), Tomioka et al. (2015), Varanasi (1989)
Congo Red (CR) 	Naphthylamine  4-Aminonaphthalene-1-sulfonate 					
Direct Black 22 (DB22) 	Benzene-1,3-diamine 	Suspected carcinogen behaviour. According to its structure, there is a high adsorption potential with suspended solids and sediment in the water	*Methanosaeta*, *Syntrophus*, *Trichococcus*, *Brevundimonas*, and *Ornatilinea*	Two up-flow UASB reactors, one with aeration in the upper part	79%	Carvalho et al. (2020)

Table 1 (continued)

Dye	Corresponding aromatic amines	Toxicity/ecotoxicity of aromatic amines	Microbiome	Degradation system	Decolorization rate	References
Direct Blue 2B (DB2) 	Benzidine  4-aminobiphenyl 	Exposures to 4-aminobiphenyl and benzidine in the textile dye industries have a historic on cancer of the urinary bladder in humans. Moreover, they can induce neoplasms at multiple organ sites in laboratory animals	*Proteobacteria, Firmicutes,* and *Acidobacteria*	Anaerobic, temperature 38.70 °C, pH 7.57, NaCl concentration 20.10 g L^{-1}	89.2%	Cao et al. (2019), Choudhary (1996) and Airoldi (2002)
Reactive Violet 5 (RV5) 	No aromatic amine formation occurs	It is not applied	*Acidithiobacillus, Acidocella*, *Streptococcus Trichosporon*, *Aspergillus,* and *Clostridium*	Activated sludge treatment and partial Fenton's oxidation	86.1%	Meerbergen et al. (2017), Chung and Chen (2009)

Daily large amounts of residual water containing a high concentration of azo dyes, between 100 and 250 mg L^{-1}, are incorrectly discharged into water bodies (Garcia-Segura and Brillas 2016). To mitigate the impact of azo dyes (colour), their chemical bonds must be broken within the chromophores group structures (Ghosh et al. 2017). Aerobic biodegradation of dyes through the activated sludge process is recognized as an economical and efficient technology. Nevertheless, some drawbacks can cause serious environmental impact, in particular, due to the large amounts of sludge that are inherently generated (Lv et al. 2013). In addition, most dyes and chemicals from the textile process have a low rate of biodegradability. Deraniyagala (2017) reported that the treatment of textile industrial wastewater by activated sludge produces 2000 tons of dangerous sludge, considering a daily flow rate of 4000 m^3 of wastewater. Thus, the activated sludge treatment should be improved, constantly.

Regarding biodegradation investigations of textile effluents, usually they are outlined to enhance the activated sludge microbiome degradation, biosorption (sequestration of dyes from solution by chelation, complexation, precipitation, or ionic interactions), and mineralization (complete oxidation of dyes to H_2O, CO_2, and other inorganic compounds) by varying physicochemical parameters such as pH, temperature, carbon and nitrogen sources, dye concentration, inoculum size, among others (Chen et al. 2003; Moosvi et al. 2005; Kapdan and Erten 2007; Pandey et al. 2007; Khalid et al. 2008; Dhanve et al. 2008; Mullai et al. 2017). However, there are new technologies as MALDI-TOF MS that can assist to reach higher treatment yields.

Dye adsorption process and textile sludge

Adsorption is a wide used wastewater treatment technology, also applied to the textile industry (Ho and McKay 2003; Jain et al. 2003). Intermolecular attraction forces between adsorbate and adsorbent lead to mass transfer, in which the accumulation of contaminants occurs at the interface between phases: gas–liquid, gas–solid, liquid–liquid, or liquid–solid interface (Reisch 1996; Dąbrowski 2001). In this sense, the molecular structure of the adsorbent, medium pH, solute solubility, and temperature significantly affect the adsorption process (Foust et al. 1980).

Regarding adsorption of dyes, there are four main steps: (i) the dye movement from the crude solution to the liquid film or the interface of the adsorbent solid; (ii) its diffusion through the liquid film to the external sites of adsorption; (iii) its inner diffusion through the adsorbent solid pores or capillaries, and; (iv) its adsorption at the available places of the capillary surfaces or walls (Reynolds and Richards 1996).

The most usually used adsorbent for textile wastewater treatment and colour removal is the activated carbon. However, its high cost is promoting the development of low-cost alternative adsorbents (Aksu 2001; Calvo 2001; Wang and Hu 2007; Ju et al. 2008; Smith et al. 2009; Rafatullah et al. 2010). In this sense, waste materials, such as activated sludge, are an interesting alternative since large quantities of sludge are inherently produced (Smith et al. 2009).

The sludge-based adsorbent can be produced by the carbonization of sludge, centrifugation, H_2SO_4 treatment, NaOH treatment, pyrolysis, steam activation. It is worth noting that microbial membranes of sludge affect the adsorbent properties since microbial membranes are negatively charged surfaces (Pavithra et al. 2019). Thus, the control mechanisms of dye adsorption include chelation, complexation, ion exchange, and surface adsorption (Crini 2006; Wang and Hu 2007; Sadhasivam et al. 2007).

The decolourization efficiency of an alternative adsorbent from textile effluent sludge was tested by Vasques et al. (2011) on Reactive Orange 16 (RO16), Reactive Red 2 (RR2), and Reactive Red 141 (RR141) dyes. The absorbent was submitted to a thermal activation at 500 °C followed by the chemical activation with acetic acid. At 25 ºC—equilibrium—it was observed the complete removal of RO16 and RR2. Regarding RR141 and RO16, the adsorption capacity was enhanced with NaCl and Na_2SO_4, respectively.

Sludge from the textile industry was also used as a low-cost adsorbent for Reactive Red 2 dye. A sequential thermal (500 °C for 70 min) and chemical (H_2SO_4, 25 °C for 3 h) treatment were evaluated. The kinetic experiments, the pseudo-second-order model, were performed in batch mode. The adsorption isotherm model was evaluated under different temperature and pH conditions. Maximum adsorption 213.9 mg g^{-1} was obtained with pH 2 and 25 °C (Sonai et al. 2016).

Autoclaved bio-sludge was tested for disperse dye adsorption in sequencing batch reactor (SBR) systems with and without granular activated carbon (GAC–SBR) using textile wastewater (TWW) collected from a central wastewater treatment plant in a textile factory in Thailand; and synthetic textile wastewater (STWW). The GAC–SBR system presented more effectiveness compared with SBR in treating TWW, resulting in a dye decolourization rate of 93.0 ± 1.1%, under the organic loading of 0.18 kg BOD5 m^{-3} (Sirianuntapiboon and Srisornsak 2007).

Haddad et al. (2018) highlighted the optimization of aerobic biodegradation efficiency to reduce the residual adsorbed dye in the final waste sludge. Laboratory and pilot-scale investigations were carried out. The process at pilot-scale was tested under different hydraulic retention times (HRT) of 2–5 days and sludge recycling rates (SRR) of 220–680 m^3 day^{-1}, which achieved the optimal result at HRT of 5 days and a SRR of 0.22 with dye biodegradation efficiency of

95%. These best conditions applied at full-scale reduced the amount of the discharged dyes (89%) significantly.

Water treatment residuals (WTR) in the dried form were used as adsorbents in filtration column tests for the colour removal from a real textile dye wastewater. The process presented a maximum colour removal of 36% in the adsorption process and a decolourization rate in the range of 60–70% in column operation, which generally shows a greater removal. The authors defended the use of WTR as a primary treatment for textile wastewater decolourization (Gadekar and Ahammed 2020).

There are some limitations to applying biomass at an industrial scale, including the accessibility of adsorbents, adsorption sites, adsorbent stability, low adsorption, and desorption rates at specific pH and other environmental factors such as ions and salts. These factors should be improved to make this technology competitive (Li et al. 2019a; Zhou et al. 2019). Regarding emerging advanced technologies used for dye adsorption, the most promising are: magnetic nanoparticles; metal/nonmetal-doped nanostructures; ceramic and modified nanoclays; and carbonaceous nanomaterials such as single and multiwalled carbon nanotubes, carbon quantum dots, and expanded graphite and graphene nanosheets (Fraga et al. 2021). These technologies also present an environmental clean-up perspective and have been attempted to achieve high rates of colour removal efficiency and low cost (implementation and operation) (Anand et al. 2020; Nayak et al. 2020).

Therefore, regarding the dye biodegradation by bacteria culture, the biological adsorption phenomenon interferes on decolourization results, making it difficult to understand biological degradation in details, since adsorption occurs at the same time (Ghosh et al. 2017; Wang et al. 2020). In this sense, Kiayi et al. (2019) investigated this factor through a biosorption test, based on spectrophotometric visualization of the solution from the suspension of bacterial pellets in methanol and water. However, no adsorption interference was detected. Corso and Maganha De Almeida (2009) evaluated the adsorption contribution using different concentrations of isolated biomass (autoclaved and non-autoclaved) to inoculate on dye solution. After 120 h, it was measured absorbances of the supernatants, which revealed high levels of decolourization index. The identification of adsorption in biodecolourization processes was also pointed by Asad et al. (2007) through the gradual decrease of adsorption peaks identified in a decolourization. Besides this verification, the authors made an association between live and inactivated cells, inferring that inactivated cells cannot decolourize an aqueous system by the adsorption process.

The adsorption process is possible due to the cell surface composition from active functional groups (amine, carboxyl, hydroxyl, phosphate, and sulfhydryl) for dye binding (Kapoor et al. 1999; Corso and Maganha De Almeida 2009). Nevertheless, it also depends on the concentration of dye (Ghosh et al. 2017). The presence of these functional groups on the cellular wall provides a negative charge that attracts positively charged molecules as cationic azo dyes or with positively charged groups (e.g. basic red 29, and basic blue 41) (Srivastava and Thakur 2006; Congeevaram et al. 2007). Therefore, the adsorpition must be considered, carefully, in biological treatments.

Activated sludge microbiome

Activated sludge is an association among many organisms in a community, mostly composed of aerobic and anaerobic bacteria. Some bacterial species can flocculate, which favours sedimentation (Paździor et al. 2019). In addition, they can reach high rates of decolourization and mineralization, which leads to low toxic sludge generation and a cost-effective process. Species belonging to the genera *Aeromonas, Bacillus, Proteus,* and *Pseudomonas* are some of the widely investigated bacteria for dye degradation (Mullai et al. 2017).

The azo dyes biodegradation by bacteria generally requires a combination of two stages. First, an anaerobic step responsible for discoloration when azo bonds are broken in the presence of redox mediators through the azo reductase enzyme (Klepacz-Smółka et al. 2010). Then, an aerobic phase promotes the efficient removal of organic compounds. Since the decolourization by pure cultures is associated with the development of aromatic amines (toxic compounds), mixed cultures (Table 1) are often used due to their synergistic metabolisms. This synergy promotes the conversion of toxic intermediates into nontoxic by-products (Yang et al. 2012; Patel 2013; Lotito et al. 2014; Manekar et al. 2014; Ali et al. 2016; Mullai et al. 2017).

Carvalho et al. (2020) evaluated two up-flow anaerobic sludge blanket (UASB) reactors R1 and R2 (with aeration in the upper part), as a comparative system to remove tetra-azo dye Direct Black 22 (DB22). The discoloration and COD removal efficiencies for both reactors were similar (67 e 72% for R1 and 59 e 78% for R2), pointing to no considerable influence of oxygen in R2. DNA extraction (Power Kit Soil®—MO Bio laboratories, Carlsbad-CA, USA), quantification (NanoDrop2000 spectrophotometer—Thermo Scientific, USA), storage at − 20 °C, and Illumina MiSeq with the universal primer 515 F paired with 907R for *Archaea* and *Bacteria* domains, with 20,000 reads and 2 × 300 bp. Microbiome identification of the sludge bed of both reactors was carried out (sequencing), which were similar to each other, that is, *Methanosaeta*, *Syntrophus*, and *Trichococcus* genera. Sequences with less than 150 bp and ambiguous base calls were not considered, and the Operational Taxonomic Units (OTUs) were defined by clustering at 97% similarity. The authors proved that higher salinity in some zones of the reactors promoted some alterations on the microbial community and the association between putative genera *Brevundimonas* and *Ornatilinea* and aromatic amine microaerobic removal.

An investigation of the metagenomic of activated sludge from the common effluent plant of Chennai (India), used in the textile effluent treatment process with mixed azo dyes, was conducted by (Krishnaswamy et al. 2020). The nanopore sequencing was carried out with PCR amplification and barcoding of the sample from the acclimatized sludge used to treat synthetic textile wastewater treatment. After the obtaining and purification of the activated sludge sample, it was amplified with PCR and barcoded. Then, adapters were connected to the amplified fragments constructed a library, which was sequenced using nanopore sequences. The fragments of 16 s rRNA genes were computed, and in the diversity of the organisms was found Actinobacteria, Proteobacteria (abundantly), and Terrabacteria. The Proteobacteria phylum were represented by the *Acidithiobacilia*, *Burkholderiales*, *Betaproteobacteria*, *Neiseriales*, *Nitrosomonadales*, and *Rhodocyclales* genera.

Cao et al. (2019) isolated and developed an indigenous bacteria consortium from a sludge sample of a dying factory for characterizing the active functional microbial communities involved in the degradation of a sulfonated azo dye, Direct Blue 2B (DB2), in a simple batch reactor. The decolourization potential of isolated and combined cultures was analyzed under different temperatures, pHs, dye, and NaCl concentrations, operation modes (static, and agitated). The study obtained 90.74% of maximum decolourization of 100 mg L^{-1} DB2 at 48 h, static condition, with 38.7 °C of culture temperature; initial pH was 7.57, and initial NaCl concentration was 20.10 g L^{-1} predicted by the quadratic model.

To identify the main microorganisms from activated sludge responsible for the degradation of Congo red (CR) and Amino Black (AB) dyes, Zhu et al. (2018) proposed a combined model. Besides identifying the species directly involved in azo dye degradation, the study aimed to reveal the relationship between azo dye degradation and microorganisms through DNA extraction, polymerase chain reaction (PCR), and Illumina Sequencing Analysis, with a multiple linear regression model. The reactions of transformation in each of the six reactor compartments were investigated, and it was verified that degradation intermediates present in each compartment were affecting the microbial communities differently. Concerning the functional species and decolourization process, *Bacteroides* and *Lactococcus* exhibited significant correlations with the azo bond with the t-value of the corresponding regression coefficient larger than 2.0. The study highlighted the occurrence of the decolourization process by anaerobic condition and mineralization under an aerobic environment. The microbial community was significantly affected by the structures of azo dyes and, consequently, their intermediates.

Zhang et al. (2018) investigated activated sludge samples from three typical Chinese municipal wastewater treatment plants: domestic sewage, fine chemical industry, and textile dyeing wastewater. Microbial DNA was extracted by the liquid-nitrogen grinding pretreatment method; metagenomic sequencing and bioinformatic analysis were executed to understand their metabolic potentials. The dominant phyla in every sample included Proteobacteria (12.3–58.5%), Acidobacteria (1.8–35.1%), Chloroflexi (2.8–37.7%). However, were also found in all samples Bacteroidia (0.7–19.2%), Actinobacteria (0.7–6.8%), TM7 (0.1–5.2%), Synergistetes (0.02–5.6%) and Thermi (0.03–7.89%). In the textile dyeing industry wastewater, Nitrospirae (48.68%) and Acidobacteria (34.82%) were prevailing in the oxidation ditch.

A synergic effect of activated sludge treatment and partial Fenton's oxidation for decolourization of azo dye Reactive Violet 5 (RV5) was observed. Pretreatment with Fenton's reagent in 500 mg L^{-1} RV5 aqueous solutions promoted 52.9, 83.9, and 91.3% of colour removal within 60 min to H_2O_2 concentrations of 1.0, 1.5, and 2.0 mM, respectively. Then biological treatment removed 70.2%, on average, of the residual RV5 concentration. An activated sludge microbial community analysis was realized through Genomic DNA using the Power Soil DNA isolation kit (MoBio Laboratories Inc., Solana Beach, CA, USA). Several of the most abundant bacteria were *Acidithiobacillus, Acidocella*, and *Streptococcus*, that presented azo dye reducing abilities. The study also revealed that exposure to RV5 modified a highly-specialized community with degrading activity to azo dye, including *Aspergillus, Clostridium,* and *Trichosporon* species (Meerbergen et al. 2017).

Thus, the wide variety of activated sludge microbiomes mentioned above is directly associated with the complexity of each textile effluent, the structures of the azo dyes, their intermediates, and treatment conditions. However, the microbial community affects directly the decolourisation yield. Thus, it should be investigated deeply.

Screening of bacteria from activated sludge; rapid identification by MALDI-ToF

Usually, microbial identification is carried out using multiple experiments and analytical procedures, for instance, extraction, purification, separation (e.g. through 16S rRNA and 18S rRNA gene sequencing), complex phenotypic, molecular, and morphological characteristics. These methods are costly and often do not provide information on microbial physiology (Padliya and Wood 2004; Kemptner et al. 2009; Kim et al. 2010; Singhal et al. 2015).

In this sense, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) is a technique for a wide range of chemical identification. It can also be used for rapid microbial identification (protein pattern overlay) (Murugaiyan et al. 2012). Generally speaking, a reference library (e.g. MALDI Biotyper) composed of proteomic signals (spectrum) of known microorganisms is used. The spectrum of an unknown sample is instantly matched against the reference library to identify microorganisms by their molecular fingerprint. Its comprehensive database of pathogenic microorganisms, rapid process, relatively higher accuracy, sensitivity, and economy in terms of labour and costs involved lead to advances over other microbial identification methods prevalent in clinical diagnosis. To date, there are some limits to the applicability of MALDI-TOF MS in the area of microbial ecology research due to the deficiency of data on non-clinical microorganisms. In other words, the reference library should be expanded to all microbial species as soon as possible (Singhal et al. 2015; Rahi et al. 2016).

Nevertheless, this technique is becoming increasingly fundamental for microbial characterization and identification, describing new species due to its ability to distinguish at the species level (Lang et al. 2015; Patil et al. 2015; Tong et al. 2015). MALDI-TOF MS technique was already used in a wide range of application, for instance, to distinguish bacterial species of the *Rhizobiaceae* family (Ferreira et al. 2011), to identify bacterial species from the human gut (Lagier et al. 2012), to detect pathogenic bacteria (food security assessment) (Bier et al. 2017; Fröhling et al. 2018), to make faster the urinary tract infection identification (Li et al. 2019b), to identify marine bacterial symbionts (Dieckmann et al. 2005; Vidal et al. 2020).

In the context of the textile industry, the MALDI-TOF MS analysis was already used to obtain mass spectra of bacterial proteins from cotton cloth samples contaminated with *Shigella flexneri*, *Escherichia coli*, and *Aeromonas hydrophila*, which are species that could cause illness through the faecal-oral routes. The authors confirmed the technique as a rapid method with a high potential for detecting biomarker proteins recovered directly from clothing samples (Holland et al. 2000).

A *Bacillus* sp. isolated from sediments of distillery unit was found to overproduce laccase with enormous potential for decolourization of various recalcitrant dyes. The enzyme peptide sequences were obtained with MALDI–TOF MS, the spectra were analyzed using MASCOT software (Matrix Science) and compared with the NCBI database for placement of enzyme with known sequences. About decolourization tests, after enzymatic action, there was around 73% decolourization of dye (trypan blue) and 62% of BBR along with the precipitation of dye contents (Kaushik and Thakur 2013). A study developed by Afreen et al. (2017) showed the use of MALDI-TOF MS to bacterial enzyme identification by peptide mass fingerprinting. The enzyme was obtained from *Spirulina platensis* CFTRI, purified, and used in the decolourization of anthraquinone dye Reactive blue 4 (96%) within 4 h.

In this context, MALDI-TOF MS analysis could bring promising results when used to identify activated sludge microbiome. As subtly explored by Mulinari et al. (2020), who used MALDI-TOF MS analysis for species identification of activated sludge, which showed the presence of both types of microorganisms: aerobics (e.g. *Lysinibaciullus fusiformis*) and facultative anaerobic (e.g. *Escherichia coli* and *Kosakonia cowanii*). The MALDI-TOF MS-based biotyping is a remarkable resource. Due to the speed, accuracy, and sensitivity, the wastewater treatment plant can operate with fine adjustments to enhance the biodegradation, for instance, correlates specific dyes with microbial changes. In addition, the MALDI-TOF MS data can be used for more drastic changes, for example, after microbial isolation and identification, the best azo-degrading species could be immobilized and then added into the treatment plant, or it could be growth (ex-situ), then periodically inoculated into the treatment plant.

State-of-the-art and perspectives

The textile industry produces large volumes of recalcitrant effluents, including azo dyes that negatively affect water bodies and their biological activity. The biodegradation of textile industry effluent, in particular azo dyes, by activated sludge stands out due to its high yields of decolourization. The genera *Pseudomonas*, *Bacillus*, *Proteobacteria*, *Clostridium*, *Acidobacteria,* and *Streptococcus* are usually found in activated sludges. However, there are unknown microbial species that should be investigated, besides the seasonality and complexity of textile wastewater composition change activated sludge microbiome, inherently. Thus, the evaluation of isolated cultures from activated sludge can provide insights and significantly enhance biodegradation yield. In this sense, MALDI-TOF MS, a rapid with high accuracy and sensibility technique for microbial identification, is a potential strategy to enhance the biodegradation of azo dye-containing wastewater from the textile industry, in particular identifying microbial species that degrade azo dyes.

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Declarations

Conflict of interest The authors have no conflict of interest to declare.

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References

Afreen S, Shamsi TN, Baig MA et al (2017) A novel multicopper oxidase (laccase) from cyanobacteria: purification, characterization with potential in the decolorization of anthraquinonic dye. PLoS ONE 12:1–20. https://doi.org/10.1371/journal.pone.0175144

Airoldi L (2002) Determinants of 4-aminobiphenyl-DNA adducts in bladder cancer biopsies. Carcinogenesis 23:861–866. https://doi.org/10.1093/carcin/23.5.861

Aksu Z (2001) Biosorption of reactive dyes by dried activated sludge: equilibrium and kinetic modelling. Biochem Eng J 7:79–84. https://doi.org/10.1016/S1369-703X(00)00098-X

Ali I, Kim S-R, Kim S-P, Kim J-O (2016) Recycling of textile wastewater with a membrane bioreactor and reverse osmosis plant for sustainable and cleaner production. Desalin Water Treat 57:1–9. https://doi.org/10.1080/19443994.2016.1172513

Anand KV, Sandy Subala A, Sumathi KS, Antony Lucia Merin S (2020) A review on the removal of dye, pesticide and pathogens from waste water using quantum dots. Eur J Adv Chem Res 1:1–6. https://doi.org/10.24018/ejchem.2020.1.5.14

Asad S, Amoozegar MA, Pourbabaee AA et al (2007) Decolorization of textile azo dyes by newly isolated halophilic and halotolerant bacteria. Bioresour Technol 98:2082–2088. https://doi.org/10.1016/j.biortech.2006.08.020

Bier D, Tutija JF, Pasquatti TN et al (2017) Identificação por espectrometria de massa MALDI-TOF de *Salmonella* spp. e *Escherichia coli* isolados de carcaças bovinas. Pesqui Veterinária Bras 37:1373–1379. https://doi.org/10.1590/s0100-736x2017001200003

Brüschweiler BJ, Merlot C (2017) Azo dyes in clothing textiles can be cleaved into a series of mutagenic aromatic amines which are not regulated yet. Regul Toxicol Pharmacol 88:214–226. https://doi.org/10.1016/j.yrtph.2017.06.012

Calvo L (2001) Upgrading sewage sludges for adsorbent preparation by different treatments. Bioresour Technol 80:143–148. https://doi.org/10.1016/S0960-8524(01)00079-7

Cao J, Sanganyado E, Liu W et al (2019) Decolorization and detoxification of Direct Blue 2B by indigenous bacterial consortium. J Environ Manag 242:229–237. https://doi.org/10.1016/j.jenvman.2019.04.067

Carvalho JRS, Amaral FM, Florencio L et al (2020) Microaerated UASB reactor treating textile wastewater: the core microbiome and removal of azo dye Direct Black 22. Chemosphere 242:51–57. https://doi.org/10.1016/j.chemosphere.2019.125157

Chen K-C, Wu J-Y, Liou D-J, Hwang S-CJ (2003) Decolorization of the textile dyes by newly isolated bacterial strains. J Biotechnol 101:57–68. https://doi.org/10.1016/S0168-1656(02)00303-6

Choudhary G (1996) Human health perspectives on environmental exposure to benzidine: a review. Chemosphere 32:267–291. https://doi.org/10.1016/0045-6535(95)00338-X

Chung Y-C, Chen C-Y (2009) Degradation of azo dye reactive violet 5 by TiO_2 photocatalysis. Environ Chem Lett 7:347–352. https://doi.org/10.1007/s10311-008-0178-6

Congeevaram S, Dhanarani S, Park J et al (2007) Biosorption of chromium and nickel by heavy metal resistant fungal and bacterial isolates. J Hazard Mater 146:270–277. https://doi.org/10.1016/j.jhazmat.2006.12.017

Corso CR, Maganha De Almeida AC (2009) Bioremediation of dyes in textile effluents by *Aspergillus oryzae*. Microb Ecol 57:384–390. https://doi.org/10.1007/s00248-008-9459-7

Crini G (2006) Non-conventional low-cost adsorbents for dye removal: a review. Bioresour Technol 97:1061–1085. https://doi.org/10.1016/j.biortech.2005.05.001

Dąbrowski A (2001) Adsorption—from theory to practice. Adv Colloid Interface Sci 93:135–224. https://doi.org/10.1016/S0001-8686(00)00082-8

Deraniyagala H (2017) Textile colour waste and sustainability. Colour design, 2nd edn. Elsevier, Amsterdam, pp 653–669

Dhanve RS, Shedbalkar UU, Jadhav JP (2008) Biodegradation of diazo reactive dye Navy blue HE2R (Reactive blue 172) by an isolated *Exiguobacterium* sp. RD3. Biotechnol Bioprocess Eng 13:53–60. https://doi.org/10.1007/s12257-007-0165-y

Dieckmann R, Graeber I, Kaesler I et al (2005) Rapid screening and dereplication of bacterial isolates from marine sponges of the Sula Ridge by Intact-Cell-MALDI-TOF mass spectrometry (ICM-MS). Appl Microbiol Biotechnol 67:539–548. https://doi.org/10.1007/s00253-004-1812-2

El M, Salah W, Din E (2016) Biodegradation of Reactive Black 5 by *Aeromonas hydrophila* strain isolated from dye-contaminated textile wastewater. Sustain Environ Res 26:209–216. https://doi.org/10.1016/j.serj.2016.04.014

Elisangela F, Andrea Z, Guimaro D et al (2009) Biodegradation of textile azo dyes by a facultative *Staphylococcus arlettae* strain VN-11 using a sequential microaerophilic/aerobic process. Int Biodeterior Biodegrad 63:280–288. https://doi.org/10.1016/j.ibiod.2008.10.003

Farias S, de Oliveira D, de Souza AAU et al (2017) Removal of reactive blue 21 and reactive red 195 dyes using horseradish peroxidase as catalyst. Braz J Chem Eng 34:701–707. https://doi.org/10.1590/0104-6632.20170343s20160091

Ferreira L, Sánchez-Juanes F, García-Fraile P et al (2011) MALDI-TOF mass spectrometry is a fast and reliable platform for identification and ecological studies of species from family Rhizobiaceae. PLoS ONE 6:e20223. https://doi.org/10.1371/journal.pone.0020223

Ford GP, Griffin GR (1992) Relative stabilities of nitrenium ions derived from heterocyclic amine food carcinogens: relationship to mutagenicity. Chem Biol Interact 81:19–33. https://doi.org/10.1016/0009-2797(92)90024-F

Foust AS, Wenzel LA, Clump CW et al (1980) Principles of unit operations. Wiley New York

Fraga TJM, de Araújo CMB, da Motta Sobrinho MA, Ghislandi MG (2021) The role of multifunctional nanomaterials in the remediation of textile wastewaters. In: Muthu SS (ed) Sustainable technologies for textile wastewater treatments. Woodhead Publishing, Cambridge, pp 95–136

Fröhling A, Rademacher A, Rumpold B et al (2018) Screening of microbial communities associated with endive lettuce during postharvest processing on industrial scale. Heliyon. https://doi.org/10.1016/j.heliyon.2018.e00671

Gadekar MR, Ahammed MM (2020) Use of water treatment residuals for colour removal from real textile dye wastewater. Appl Water Sci 10:1–8. https://doi.org/10.1007/s13201-020-01245-9

Garcia-Segura S, Brillas E (2016) Combustion of textile monoazo, diazo and triazo dyes by solar photoelectro-Fenton:

decolorization, kinetics and degradation routes. Appl Catal B 181:681–691. https://doi.org/10.1016/j.apcatb.2015.08.042

Ghosh A, Ghosh M, Sreekrishnan TR (2017) Bioremediation of chromium complex dyes and treatment of sludge generated during the process. Int Biodeterior Biodegrad 119:448–460. https://doi.org/10.1016/j.ibiod.2016.08.013

Gregory P (2007) Toxicology of textile dyes. In: Christie RM (ed) Environmental aspects of textile dyeing. Woodhead Publishing, Cambridge, pp 44–73

Haddad M, Abid S, Hamdi M, Bouallagui H (2018) Reduction of adsorbed dyes content in the discharged sludge coming from an industrial textile wastewater treatment plant using aerobic activated sludge process. J Environ Manag 223:936–946. https://doi.org/10.1016/j.jenvman.2018.07.009

Harane RS, Adivarekar RV (2017) Sustainable processes for pre-treatment of cotton fabric. Text Cloth Sustain 2:2. https://doi.org/10.1186/s40689-016-0012-7

Ho YS, McKay G (2003) Sorption of dyes and copper ions onto biosorbents. Process Biochem 38:1047–1061. https://doi.org/10.1016/S0032-9592(02)00239-X

Holkar CR, Jadhav AJ, Pinjari DV et al (2016) A critical review on textile wastewater treatments: possible approaches. J Environ Manag 182:351–366. https://doi.org/10.1016/j.jenvman.2016.07.090

Holland RD, Rafii F, Heinze TM et al (2000) Matrix-assisted laser desorption/ionization time-of-flight mass spectrometric detection of bacterial biomarker proteins isolated from contaminated water, lettuce and cotton cloth. Rapid Commun Mass Spectrom 14:911–917. https://doi.org/10.1002/(SICI)1097-0231(20000530)14:10%3c911::AID-RCM965%3e3.0.CO;2-C

Jain AK, Gupta VK, Bhatnagar A, Suhas (2003) Utilization of industrial waste products as adsorbents for the removal of dyes. J Hazard Mater 101:31–42. https://doi.org/10.1016/S0304-3894(03)00146-8

Ju DJ, Byun IG, Park JJ et al (2008) Biosorption of a reactive dye (Rhodamine-B) from an aqueous solution using dried biomass of activated sludge. Bioresour Technol 99:7971–7975. https://doi.org/10.1016/j.biortech.2008.03.061

Kapdan IK, Erten B (2007) Anaerobic treatment of saline wastewater by *Halanaerobium lacusrosei*. Process Biochem 42:449–453. https://doi.org/10.1016/j.procbio.2006.09.001

Kapoor A, Viraraghavan T, Cullimore DR (1999) 1999 Anoop kapoor bio 1. Bioresour Technol 70:95–104

Kaushik G, Thakur IS (2013) Purification, characterization and USAGE of thermotolerant laccase FROM *Bacillus* sp. for biodegradation of synthetic dyes. Appl Biochem Microbiol 49:352–359. https://doi.org/10.1134/S0003683813040169

Kemptner J, Marchetti-Deschmann M, Mach R et al (2009) Evaluation of matrix-assisted laser desorption/ionization (MALDI) preparation techniques for surface characterization of intact *Fusarium* spores by MALDI linear time-of-flight mass spectrometry. Rapid Commun Mass Spectrom 23:877–884. https://doi.org/10.1002/rcm.3949

Khalid A, Arshad M, Crowley DE (2008) Accelerated decolorization of structurally different azo dyes by newly isolated bacterial strains. Appl Microbiol Biotechnol 78:361–369. https://doi.org/10.1007/s00253-007-1302-4

Khehra MS, Saini HS, Sharma DK et al (2005) Comparative studies on potential of consortium and constituent pure bacterial isolates to decolorize azo dyes. Water Res 39:5135–5141. https://doi.org/10.1016/j.watres.2005.09.033

Kiayi Z, Lotfabad TB, Heidarinasab A, Shahcheraghi F (2019) Microbial degradation of azo dye carmoisine in aqueous medium using *Saccharomyces cerevisiae* ATCC 9763. J Hazard Mater 373:608–619. https://doi.org/10.1016/j.jhazmat.2019.03.111

Kim TW, Kim YH, Kim SE et al (2010) Identification and distribution of *Bacillus* species in Doenjang by whole-cell protein patterns and 16s rRNA gene sequence analysis. J Microbiol Biotechnol 20:1210–1214. https://doi.org/10.4014/jmb.1002.02008

Klepacz-Smółka A, Sójka-Ledakowicz J, Paździor K, Ledakowicz S (2010) Application of anoxic fixed film and aerobic CSTR bioreactor in treatment of nanofiltration concentrate of real textile wastewater. Chem Pap 64:230–236. https://doi.org/10.2478/s11696-009-0115-6

Köchling T, Ferraz ADN, Florencio L et al (2017) 454-Pyrosequencing analysis of highly adapted azo dye-degrading microbial communities in a two-stage anaerobic–aerobic bioreactor treating textile effluent. Environ Technol (united Kingdom) 38:687–693. https://doi.org/10.1080/09593330.2016.1208681

Krishnaswamy VG, Aishwarya S, Kathawala TM (2020) Extrication of the microbial interactions of activated sludge used in the textile effluent treatment of anaerobic reactor through metagenomic profiling. Curr Microbiol 77:2496–2509. https://doi.org/10.1007/s00284-020-02020-4

Kumar N, Sinha S, Mehrotra T et al (2019) Biodecolorization of azo dye Acid Black 24 by *Bacillus pseudomycoides*: process optimization using Box Behnken design model and toxicity assessment. Bioresour Technol Rep 8:100311. https://doi.org/10.1016/j.biteb.2019.100311

Lagier JC, Armougom F, Million M et al (2012) Microbial culturomics: paradigm shift in the human gut microbiome study. Clin Microbiol Infect 18:1185–1193. https://doi.org/10.1111/1469-0691.12023

Lang E, Schumann P, Tindall BJ et al (2015) Reclassification of *Angiococcus disciformis*, *Cystobacter minus* and *Cystobacter violaceus* as *Archangium disciforme* comb. nov., *Archangium minus* comb. nov. and *Archangium violaceum* comb. nov., unification of the families Archangiaceae and Cystobacteraceae. Int J Syst Evol Microbiol 65:4032–4042. https://doi.org/10.1099/ijsem.0.000533

Leão MMD (2002) Controle ambiental na indústria têxtil: acabamento de malhas. SEGRAC Editora e Gráfica, Belo Horizonte

Li W, Mu B, Yang Y (2019a) Feasibility of industrial-scale treatment of dye wastewater via bio-adsorption technology. Bioresour Technol 277:157–170. https://doi.org/10.1016/j.biortech.2019.01.002

Li W, Sun E, Wang Y et al (2019b) Rapid identification and antimicrobial susceptibility testing for urinary tract pathogens by direct analysis of urine samples using a MALDI-TOF MS-based combined protocol. Front Microbiol. https://doi.org/10.3389/fmicb.2019.01182

Lotito AM, De Sanctis M, Rossetti S et al (2014) On-site treatment of textile yarn dyeing effluents using an integrated biological-chemical oxidation process. Int J Environ Sci Technol 11:623–632. https://doi.org/10.1007/s13762-013-0271-7

Lv G-Y, Cheng J-H, Chen X-Y et al (2013) Biological decolorization of malachite green by *Deinococcus radiodurans* R1. Bioresour Technol 144:275–280. https://doi.org/10.1016/j.biortech.2013.07.003

Manekar P, Patkar G, Aswale P et al (2014) Detoxifying of high strength textile effluent through chemical and bio-oxidation processes. Bioresour Technol 157:44–51. https://doi.org/10.1016/j.biortech.2014.01.046

Meerbergen K, Crauwels S, Willems KA et al (2017) Decolorization of reactive azo dyes using a sequential chemical and activated sludge treatment. J Biosci Bioeng 124:668–673. https://doi.org/10.1016/j.jbiosc.2017.07.005

Moosvi S, Keharia H, Madamwar D (2005) Decolourization of textile dye Reactive Violet 5 by a newly isolated bacterial consortium RVM 11.1. World J Microbiol Biotechnol 21:667–672. https://doi.org/10.1007/s11274-004-3612-3

Mulinari J, de Andrade CJ, de Brandão HL et al (2020) Enhanced textile wastewater treatment by a novel biofilm carrier with adsorbed nutrients. Biocatal Agric Biotechnol. https://doi.org/10.1016/j.bcab.2020.101527

Mullai P, Yogeswari MK, Vishali S et al (2017) Aerobic treatment of effluents from textile industry. Current developments in biotechnology and bioengineering. Elsevier, Amsterdam, pp 3–34

Murugaiyan J, Ahrholdt J, Kowbel V, Roesler U (2012) Establishment of a matrix-assisted laser desorption ionization time-of-flight mass spectrometry database for rapid identification of infectious achlorophyllous green micro-algae of the genus *Prototheca*. Clin Microbiol Infect 18:461–467. https://doi.org/10.1111/j.1469-0691.2011.03593.x

Nayak S, Prasad SR, Mandal D, Das P (2020) Carbon dot cross-linked polyvinylpyrrolidone hybrid hydrogel for simultaneous dye adsorption, photodegradation and bacterial elimination from waste water. J Hazard Mater 392:122287. https://doi.org/10.1016/j.jhazmat.2020.122287

Neumann H-G (2010) Aromatic amines: mechanisms of carcinogenesis and implications for risk assessment. Front Biosci 15:1119. https://doi.org/10.2741/3665

Padliya ND, Wood TD (2004) A strategy to improve peptide mass fingerprinting matches through the optimization of matrix-assisted laser desorption/ionization matrix selection and formulation. Proteomics 4:466–473. https://doi.org/10.1002/pmic.200300567

Pandey A, Singh P, Iyengar L (2007) Bacterial decolorization and degradation of azo dyes. Int Biodeterior Biodegrad 59:73–84. https://doi.org/10.1016/j.ibiod.2006.08.006

Patel SK (2013) Performance evaluation of effluent treatment plant of textile wet processing industry: a case study of narol textile cluster, Ahmedabad. Indian J Environ Prot 33:1002–1008

Patil VS, Salunkhe RC, Patil RH et al (2015) *Enterobacillus tribolii* gen. nov., sp. nov., a novel member of the family Enterobacteriaceae, isolated from the gut of a red flour beetle, *Tribolium castaneum*. Antonie Van Leeuwenhoek 107:1207–1216. https://doi.org/10.1007/s10482-015-0412-8

Pavithra KG, Senthil Kumar P, Jaikumar V, Sundar Rajan P (2019) Removal of colorants from wastewater: a review on sources and treatment strategies. J Ind Eng Chem 75:1–19. https://doi.org/10.1016/j.jiec.2019.02.011

Paździor K, Bilińska L, Ledakowicz S et al (2019) A review of the existing and emerging technologies in the combination of AOPs and biological processes in industrial textile wastewater treatment. Chem Eng J. https://doi.org/10.1016/j.cej.2018.12.057

Pereira ARB, Bueno FL, Santos SC et al (2010) Biodegradação de corantes e efluentes têxteis por fungos. Holos Environ 10:165. https://doi.org/10.14295/holos.v10i2.2156

Rafatullah M, Sulaiman O, Hashim R, Ahmad A (2010) Adsorption of methylene blue on low-cost adsorbents: a review. J Hazard Mater 177:70–80. https://doi.org/10.1016/j.jhazmat.2009.12.047

Rahi P, Prakash O, Shouche YS (2016) Matrix-assisted laser desorption/ionization time-of-flight mass-spectrometry (MALDI-TOF MS) based microbial identifications: challenges and scopes for microbial ecologists. Front Microbiol 7:1–12. https://doi.org/10.3389/fmicb.2016.01359

Reisch MS (1996) Asian textile dye makers are a growing power in changing market. Chem Eng News 74:10–12

Reynolds TD, Richards P (1996) Unit operations and processes in environmental engineering. PWS Publishing Company, Boston

Rittmann BE (2018) Biofilms, active substrata, and me. Water Res 132:135–145. https://doi.org/10.1016/j.watres.2017.12.043

Sadhasivam S, Savitha S, Swaminathan K (2007) Feasibility of using *Trichoderma harzianum* biomass for the removal of erioglaucine from aqueous solution. World J Microbiol Biotechnol 23:1075–1081. https://doi.org/10.1007/s11274-006-9336-9

Salter-Blanc AJ, Bylaska EJ, Lyon MA et al (2016) Structure-activity relationships for rates of aromatic amine oxidation by manganese dioxide. Environ Sci Technol 50:5094–5102. https://doi.org/10.1021/acs.est.6b00924

Sarayu K, Sandhya S (2012) Current technologies for biological treatment of textile wastewater—a review. Appl Biochem Biotechnol. https://doi.org/10.1007/s12010-012-9716-6

Sari IP, Simarani K (2019) Comparative static and shaking culture of metabolite derived from methyl red degradation by *Lysinibacillus fusiformis* strain W1B6. R Soc Open Sci. https://doi.org/10.1098/rsos.190152

Sen SK, Raut SS, Bandyopadhyay P et al (2016) Fungal decolouration and degradation of azo dyes: a review. Fungal Biol Rev 30:112–133. https://doi.org/10.1016/j.fbr.2016.06.003

Senthilkumar M, Gnanapragasam G, Arutchelvan V, Nagarajan S (2011) Treatment of textile dyeing wastewater using two-phase pilot plant UASB reactor with sago wastewater as co-substrate. Chem Eng J 166:10–14. https://doi.org/10.1016/j.cej.2010.07.057

Singhal N, Kumar M, Kanaujia PK, Virdi JS (2015) MALDI-TOF mass spectrometry: an emerging technology for microbial identification and diagnosis. Front Microbiol 6:1–16. https://doi.org/10.3389/fmicb.2015.00791

Sirianuntapiboon S, Srisornsak P (2007) Removal of disperse dyes from textile wastewater using bio-sludge. Bioresour Technol 98:1057–1066. https://doi.org/10.1016/j.biortech.2006.04.026

Smith KM, Fowler GD, Pullket S, Graham NJD (2009) Sewage sludge-based adsorbents: a review of their production, properties and use in water treatment applications. Water Res 43:2569–2594. https://doi.org/10.1016/j.watres.2009.02.038

Sonai GG, de Souza SMAGU, de Oliveira D, de Souza AAU (2016) The application of textile sludge adsorbents for the removal of Reactive Red 2 dye. J Environ Manag 168:149–156. https://doi.org/10.1016/j.jenvman.2015.12.003

Srivastava S, Thakur IS (2006) Biosorption potency of *Aspergillus niger* for removal of chromium (VI). Curr Microbiol 53:232–237. https://doi.org/10.1007/s00284-006-0103-9

Swati SS, Faruqui AN (2018) Investigation on ecological parameters and COD minimization of textile effluent generated after dyeing with mono and bi-functional reactive dyes. Environ Technol Innov 11:165–173. https://doi.org/10.1016/j.eti.2018.06.003

Tabasum B, Dhagale PR, Nitnaware KM et al (2019) New chemical products formation from textile dye degradation, chitinolytic and antioxidant activity in new strain nbpc5-18 of *Cellulosimicrobium* sp. TH-20. J Environ Chem Eng 7:103114. https://doi.org/10.1016/j.jece.2019.103114

Tomioka K, Obayashi K, Saeki K et al (2015) Increased risk of lung cancer associated with occupational exposure to benzidine and/or beta-naphthylamine. Int Arch Occup Environ Health 88:455–465. https://doi.org/10.1007/s00420-014-0974-1

Tong SYC, Schaumburg F, Ellington MJ et al (2015) Novel staphylococcal species that form part of a *Staphylococcus aureus*-related complex: the non-pigmented *Staphylococcus argenteus* sp. nov. and the non-human primate-associated *Staphylococcus schweitzeri* sp. nov. Int J Syst Evol Microbiol 65:15–22. https://doi.org/10.1099/ijs.0.062752-0

Vajnhandl S, Valh JV (2014) The status of water reuse in European textile sector. J Environ Manag 141:29–35. https://doi.org/10.1016/j.jenvman.2014.03.014

Varanasi U (1989) Metabolism of polycyclic aromatic hydrocarbons in the aquatic environment. CRC Press, Boca Raton

Vasques AR, de Souza SMAGU, Weissenberg L et al (2011) Adsorção dos corantes RO16, RR2 e RR141 utilizando lodo residual da indústria têxtil. Eng Sanit e Ambient 16:245–252. https://doi.org/10.1590/S1413-41522011000300007

Vidal LMR, Venas TM, Gonçalves ARP et al (2020) Rapid screening of marine bacterial symbionts using MALDI-TOF MS. Arch Microbiol 202:2329–2336. https://doi.org/10.1007/s00203-020-01917-9
Waghmode TR, Kurade MB, Sapkal RT et al (2019) Sequential photocatalysis and biological treatment for the enhanced degradation of the persistent azo dye methyl red. J Hazard Mater 371:115–122. https://doi.org/10.1016/j.jhazmat.2019.03.004
Wang B, Hu Y (2007) Comparison of four supports for adsorption of reactive dyes by immobilized *Aspergillus fumigatus* beads. J Environ Sci 19:451–457. https://doi.org/10.1016/S1001-0742(07)60075-8
Wang Y, Jiang L, Shang H et al (2020) Treatment of azo dye wastewater by the self-flocculating marine bacterium *Aliiglaciecola lipolytica*. Environ Technol Innov 19:100810. https://doi.org/10.1016/j.eti.2020.100810
Wong Y, Yu J (1999) Laccase-catalyzed decolorization of synthetic dyes. Water Res 33:3512–3520. https://doi.org/10.1016/S0043-1354(99)00066-4
Xiang X, Chen X, Dai R et al (2016) Anaerobic digestion of recalcitrant textile dyeing sludge with alternative pretreatment strategies. Bioresour Technol 222:252–260. https://doi.org/10.1016/j.biortech.2016.09.098
Yang Q, Wang J, Wang H et al (2012) Evolution of the microbial community in a full-scale printing and dyeing wastewater treatment system. Bioresour Technol 117:155–163. https://doi.org/10.1016/j.biortech.2012.04.059
Yukseler H, Uzal N, Sahinkaya E et al (2017) Analysis of the best available techniques for wastewaters from a denim manufacturing textile mill. J Environ Manag 203:1118–1125
Zhang B, Xu X, Zhu L (2018) Activated sludge bacterial communities of typical wastewater treatment plants: distinct genera identification and metabolic potential differential analysis. AMB Express 8:184. https://doi.org/10.1186/s13568-018-0714-0
Zhou YY, Lu J, Zhou YY, Liu Y (2019) Recent advances for dyes removal using novel adsorbents: a review. Environ Pollut 252:352–365. https://doi.org/10.1016/j.envpol.2019.05.072
Zhu Y, Xu J, Cao X et al (2018) Characterization of functional microbial communities involved in diazo dyes decolorization and mineralization stages. Int Biodeterior Biodegrad 132:166–177. https://doi.org/10.1016/j.ibiod.2018.03.006