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Bacillus Species with Dye-remediation Potential - A Mini Review

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Abstract

Dyes are either natural or synthetic pigments used as colour for different items including textile materials, leather, cosmetics, plastic, paper, printing ink, food, human hair or paintings. The persisting colour and toxic compounds contained in most dyes leads to serious environmental pollution which is unsuitable for the survival of many ecologically important organisms. A wide range of bacterial species have been reported to effectively remediate dyes of various types and classes. This paper reviews bacterial species from the genus Bacillus with the potentiality to remediate synthetic dyes based on published literatures. Bacillus species remediate dyes basically through biosorption and enzymatic action. The most commonly used Bacillus species are Bacillus subtilis, B. cereus, B. megaterium, B. fusiformis, B. odysseyi, B. mycoides, B. paramycoides, B. pseudomycoides, B. flexus, B. cohnii, B. licheniformis, B. spizizenii, B. algicola, B. vallismortis, B. vietnamensis, B. stratosphericus, B. halodurans, B. albus, B. aryabhattai and B. velezensis. Other researches have also proven that mixed cultures of Bacillus species and species from other microbial genera display significant efficiency in the remediation of various dyes. These species produce enzymes and compounds that aid in the breakdown of dyes, thus, reducing their impact to the environment. The use of the aforementioned Bacillus species in the remediation of other dye related environmental pollutants is highly recommended.

Keywords: *Bacillus, Bacteria, Consortium, Dyes, Remediation*

INTRODUCTION

Dyes are natural or synthetic coloured substances that are used to impart colour to various substrates (Kumar *et al*., 2021). They are of various types based on their dissociation in aqueous solutions and can be water-soluble or insoluble depending on their mode of application (Kuberan *et al*., 2011; Sani, 2023). The complex aromatic structure and high stability of dyes makes them very difficult to remediate, thus, their indiscriminate release into the environment may lead to a potent hazard to natural sources like soil, water, flora, fauna, livestock and human population (Sani *et al*., 2018). Synthetic dyes are artificial colourants that are employed in various industrial applications associated with textiles, cosmetics and food processing. They are manufactured through chemical synthesis that results in the production of different varieties of vibrant and long-lasting colours (Sani, 2023). Synthetic dyes often produce a diverse spectrum of colour shades that are highly stable, as such, are preferably used in industrial dyeing than the natural dyes (Ali, 2010). Synthetic dyes have been reported to pose serious damages to the environment due to their persistence, toxicity and undegradable nature. For these reasons, the development of eco-friendly and sustainable dye-remediation strategies were initiated to mitigate the environmental impact of these dyes (Manzoor and Sharma, 2020; Akter *et al*., 2023). The most common dye-remediation strategy is the microbial remediation which involves the use of microorganisms from different species of bacteria, fungi and algae, which proves to be very effective (Sani *et al*., 2021; Panwar *et al*., 2023). Microorganisms are ideally suited to the task of remediating dyes due to their size, adsorption capacity and possession of enzymes that allow them to utilize the dyes as food. Microorganisms have served in nature for billions of years in the breakdown of complex human, animal, and plant wastes maintaining the continuity of life from generation to generation (Rosenberg and Zilber-Rosenberg, 2016). The earth would literally be buried in wastes without the activity of microorganisms and the nutrients necessary for the support of life would be locked up in detritus (Jadhav *et al*., 2010).

Bacteria are unicellular non-nucleated microorganisms that inhabit all types of ecological environments. They show a great diversity in terms of their size, shape and characteristics (Becker *et al*., 2009; Sant'Anna *et al*., 2020).

They are characterized by rapid growth in media containing carbon sources and inorganic salts, enabling them to synthesize all essential macromolecules (Lodish *et al.*, 2013). Most bacterial species are essential in nutrient cycling, food production and environmental clean-up processes (Hassan *et al.*, 2010; Hussein *et al.*, 2019). Some bacterial species are excellent pollutants degraders, thus, are employed to clean-up contaminated environments (Barathi *et al.*, 2020a,b). Bacteria are regarded as nature's recyclers as a result of their potentiality in the transformation of both natural and synthetic chemicals into energy and other raw materials (Jamee and Siddique, 2019). They are also one of the major decomposers in many ecosystems, as they are involved in the breakdown of dead materials into organic matter and nutrients (Hussein *et al.*, 2019). Afrin *et al.* (2021) reported bacteria to exhibit the ability to biosorp dissolved metals, as such are good agents of heavy metals removal in the environment.

A number of bacterial species have been identified with the capability to remove or detoxify pollutants (such as dyes and hydrocarbons) in the environment due to the possession of enzymes and highly effective metabolic pathways (Singh *et al.*, 2015; Dell'Anno *et al.*, 2021). Some of these species include; *Escherichia coli*, *Deinococcus radiodurans*, *Acinetobacter haemolyticus*, *Bacillus*, *Pseudomonas*, *Mycobacterium*, *Alcaligenes*, *Sphingomonas*, *Rhodococcus* and *Aeromonas* species (Darwesh *et al.*, 2014; Ekanayake and Manage, 2020; Bafana, 2022; Hossain *et al.*, 2022).

Mechanisms of Dye Remediation by Bacteria

Bacterial remediation of synthetic dyes involves a high degree of removal and mineralization of harmful compounds which is economically viable, results in minimal production of sludge and is faster than that performed by fungi (Saratale *et al.*, 2011; Mishra *et al.*, 2020; Fletcher *et al.*, 2021; Huda *et al.*, 2022; Panwar *et al.*, 2023). Bacteria mineralize dye by enzymatic action and/or biosorption (Mustapha and Halimoon, 2015; Lellis *et al.*, 2019; Tripathi *et al.*, 2023).

Enzymatic Cleavage

Bacterial enzymatic remediation of dyes involves breaking of the azo bonds (reductive cleavage) by azoreductase and dissociation of other functional groups in the dye molecule by enzymes like peroxidase, laccase, tyrosinase, NADH-DCIP reductase and monooxygenase reductase (Telke *et al.*, 2015; Huy *et al.*, 2020). Some of the azo dyes that can be detoxified and decolourized by bacteria include amaranth, naphthalene, acidic and anthraquinone (Shi *et al.*, 2021). Enzymatic remediation by bacteria occur aerobically, anaerobically, or through both (Mishra *et al.*, 2022). The remediation of dyes under aerobic conditions is not very efficient due to the oxidative stability of most of the dyes resulting to their inability to completely adsorp on activated sludge (Rima *et al.*, 2022). Aerobic bacteria have been reported to metabolize sulfonated azo dyes by producing enzymes that cleave the azo bonds (Franciscon *et al.*, 2012). Sari and Simarani (2019) isolated reductases from *Pseudomonas* sp. KF46 which were used in the aerobic degradation of some azo dyes. *Klebsiella* sp. and *Staphylococcus* sp. also decolourized 90 % of a dye under aerobic condition (Desai, 2017). The aerobic degradation of acid red 151 resulted in the production of aromatic amines and some carcinogenic metabolites (Prasad and Aikat, 2014). In a study involving bacterial aerobic degradation of Para red and Sudan I dye, an oxidative burst occurred due to the formation of some metabolites (Mishra *et al.*, 2022). Most aerobic bacteria require a longer period of acclimatization in the presence of azo compounds to induce the expression of azoreductase, thus, show high specificity to most of the dyes (Cui *et al.*, 2014). Aerobic remediation of dyes in most cases results in the production and release of more toxic substances (Franca *et al.*, 2020). Remediation of dyes by bacteria also occur anaerobically through redox reaction of hydrogen to form methane, carbon dioxide, hydrogen sulfide and other gaseous compounds, subsequently releasing electrons (Ayele *et al.*, 2021). This process involves direct transfer of electrons to the dyes as terminal acceptors in the presence of enzymes and reduction of the dyes through bacterial catabolism. This method of remediation is more efficient and economical than aerobic method, as it is mostly specific and occurs under static conditions (Thangaraj *et al.*, 2021). Reactive red 120 was degraded anaerobically by an unidentified bacterial species (Mishra *et al.*, 2022). In some cases, both aerobic and anaerobic bacterial remediation are employed to completely break down of dyes. Synthetic dyes like disperse blue 79, fast acid red GR and dark red 2B were successfully degraded through the anaerobic-aerobic method (Desai, 2017; Gao *et al.*, 2018; Pereira *et al.*, 2019; Ajaz *et al.*, 2020).

Biosorption

Bacteria serve as good biosorbents of dyes, as they require carbon and nitrogen which are main constituents of the dyes. Bacterial biosorption is mainly used for the mineralization of non-degradable pollutants from effluents, such as metal ions and dyes. It is one of the efficient ways of remediating pollutants (Mustapha and Halimoon, 2015).

During biosorption, electrically charged functional groups on bacterial cell surface interact with the dye molecule to form a strong bond, subsequently dissociating to form less harmful compounds (Srinivasan and Viraraghavan, 2010; Tripathi *et al*., 2023). Ito *et al*. (2018) observed that during biosorption, decolourization of dyes starts with the adsorption of the dyes on bacterial cell surface, and then the colour on the stained cells disappears within a period of time depending on the rate of metabolic activity of the bacteria. Ayilara and Babalola (2023) reported that bacterial biosorption of dyes can be achieved either through uptake of the dye molecules into the cytoplasmic matrix of bacterial cells (absorption) or by adhesion/binding of the dye molecules to the bacterial cellular surface (adsorption). During adsorption, bacterial biomass binds to dye molecules which is facilitated by the functional groups contained in the peptidoglycan layer of the bacterial cell wall, thus utilizing the dye molecules as nutrients for cell growth (Tripathi *et al*., 2023). Colour removal of reactive dye Procion blue 2G was achieved through adsorption using immobilized cells of *Pseudomonas aeruginosa* (Saravanan *et al*., 2013). Sani *et al*. (2022) also reported an effective biosorption of five reactive dyes by two bacterial species.

***Bacillus* Species**

Bacillus species are gram-positive or gram variable rod-shaped bacteria belonging to the family Bacillaceae and genus *Bacillus*. The genus has approximately 300 species/subspecies that are mostly motile, haemolytic, aerobic or facultatively anaerobic (Fritze, 2004; Patel and Gupta, 2020). They are widely distributed around all environments due to their physiological abilities and capability to produce dormant endospores that allow them to thrive in adverse conditions (UKSMI, 2018; Celandroni *et al*., 2019; Patel and Gupta, 2020). Due to a constant influx of new species isolated from extreme environments, species in the genus are frequently re-classified based on genome comparison (Zeigler and Perkins, 2008). They grow very rapidly in high densities and can withstand adverse environmental conditions (Pham *et al*., 2023). They exist as either free-living (non-pathogenic) or parasitic (pathogenic) species. Examples of some of the species include; *Bacillus subtilis*, *B. megaterium*, *B. velezensis*, *B. mycoides*, *B. thuringiensis*, *B. odysseyi*, *B. fusiformis*, *B. flexus*, *B. pseudomycoides*, *B. paramycoides*, *B. licheniformis*, *B. amyloliquefaciens*, *B. pumilus*, *B. anthracis* (causes anthracis in humans) and *B. cereus* (causes food poisoning) (Arora, 2020). As a result of their physiological characteristics, production of different varieties of enzymes, antibiotics and other metabolites, *Bacillus* species are used in many processes related to the medical, pharmaceutical, agricultural, environmental and industrial fields (UKSMI, 2018; Celandroni *et al*., 2019; Arora, 2020). A vast number of *Bacillus* species have been reported with effective bioremediation of a wide range of environmental contaminants like dyes, which is mainly achieved through either enzymatic action, biosorption or combination of both processes (Sani, 2023; Pham *et al*., 2023). Bacterial remediation is usually faster than that of other microorganisms due to the rate at which their cells grow and multiply (Akansha *et al*., 2023). Furthermore, the variability in the conditions (either aerobic, anaerobic, facultative anaerobic, anoxic or combination of all) at which the remediation occurs differ with respect to the bacterial species involved (Elizaryev *et al*., 2023).

***Bacillus* Species with Dye-remediation Potentials**

Bacillus species with different physiological characteristics have been reported to have the ability to effectively degrade different classes of dyes (Horitsu *et al*., 1977; Khalid *et al*., 2012; Gul, 2018; Ekanayake and Manage, 2020). *Bacillus* species are extensively used in degradation of dyes and other toxic effluents (Saratale *et al*., 2011; Arora, 2020). *Bacillus* sp. VUS was observed to have remediated navy blue 2G, brown 3REL and orange T4LL (Mullai *et al*., 2017). Karim *et al*. (2018) also observed the ability of two *Bacilli* species to moderately decolourize reactive dyes (Bezema red S2-B, Bezema yellow S8-G and Novacron orange FN-R) at 37 °C within 6 days when tested as individual monocultures. Other strains of *Bacillus* species were employed in the degradation of red B, reactive blue 160, reactive black 5, amido black 10B, Evans blue, Janus green, methyl orange, methyl red, orange G and Metanil yellow dyes which yielded a positive result (Anjaneya *et al*., 2011; Ezhilarasu, 2016; Aydin *et al*., 2021; Sani, 2023). Sriram *et al*. (2013) reported efficient colour removal of reactive yellow - M4G and reactive orange - M2R by a *Bacillus* species within 16 days. Vani *et al*. (2018) used *Bacillus* species to decolourize 92 % of malachite green. *Bacillus* sp. strain CH12 was found to have completely decolourized reactive red 239 dye within four days (Guadie *et al*. 2017).

Bacillus subtilis is one of the earliest and most common *Bacillus* species used in bioremediation of environmental pollutants. For decades, *B. subtilis* and *Staphylococcus aureus* have been used as biosorbents for the removal of reactive dyes. A number of researches have proven that *B. subtilis* is effective in remediation of synthetic dyes (Hu, 1996; Madhuri *et al*., 2018; Adegbite *et al*., 2019; Fidiastuti *et al*., 2020; Barathi *et al*., 2020a; Aydin *et al*., 2021). Saranraj *et al*. (2010) isolated *B. subtilis* from a sample of textile dye effluent and observed its remediating capability against some reactive dyes. The remediation of reactive red M5B, reactive pink MB and reactive purple using *B. subtilis* was also observed by Maheswar and Sivagami (2016).

Colour removal for acid red 337 by *Bacillus megaterium* was reported at 91 % within 24 hrs at optimum temperature of 30 °C and pH of 7. It was also observed to have removed several red dyes from wastewater (99 %) within 10 days (Ewida *et al*., 2019). Similarly, Shah *et al*. (2013) and Shah (2014) observed removal of acid orange dye and five additional azo dyes within 38 hrs under static conditions by *B. megaterium*. *B. megaterium* also degraded and decolourized four azo dyes to 95 % at neutral pH and temperature of 40 °C (Nairr *et al*., 2017). Diez-Mendez *et al*. (2019) revealed that *B. megaterium* was able to partially decolourize eleven synthetic dyes within 48 hrs of incubation (Sani *et al*., 2022). In another study, Tripathi and Srivastava (2012) confirmed 94.4 % decolourization of another azo dye, orange G by *Bacillus megaterium*.

B. cereus has also been reported to decolourize different azo dyes from textile effluent (Modi *et al*., 2010; Madhuri *et al*., 2018; Adegbite *et al*., 2019; Aydin *et al*., 2021). Maheswar and Sivagami (2016) also observed a positive remediation of reactive red M5B, reactive pink MB and reactive purple using *B. cereus*. Decolourization of azo red dye by bacterial species (*B. cereus*) under optimum conditions was found to be 98 % (Shah *et al*., 2013). Modi *et al*. (2010) reported 97 % decolourization of reactive red 195 by *B. cereus* due to the addition of maltose and peptone as ideal carbon and nitrogen sources during test preparation.

Bacillus velezensis is known for its possession of azoreductase enzymes which are used to decolourize azo dyes of different molecular structures (Bafana *et al*., 2020). Bafana *et al*. (2008) revealed *B. velezensis* to be able to effectively degrade azo dye direct red 28 (DR28) through enzymatic action. *B. velezensis* contains a biopolymer that was isolated and used to decolourize azo dyes by bioflocculation, with the results showing 91 % efficiency (Elkady *et al*., 2017). Similarly, the remediation of five reactive dyes by *B. velezensis* was reported by Sani *et al*. (2022).

Asad *et al*. (2007) isolated *Bacillus firmus* from textile effluent that had the potential to reduce textile azo dyes into simpler and less toxic compounds. CI direct red 80 was degraded by *B. firmus* under anoxic condition within 12 hrs (Ogugbue *et al*., 2012). An effective degradation of reactive blue 160 (RB160) by *B. firmus* isolated from dye-contaminated soil of a textile industry was likewise reported by Barathi *et al*. (2020b). *B. fusiformis* KMK5 also perfectly (100%) mineralized disperse blue 79 and acid orange 10 within 48 hrs (Kolekar *et al*., 2008; Mullai *et al*., 2017; Gul, 2018). Patil *et al*. (2008) observed the culture of *Bacillus odysseyi* SUK3 to have remove the colour of reactive blue 59 completely within 60 hrs. Other notable *Bacillus* species that displayed excellent remediation of various synthetic dyes are presented in Table 1.

Table 1: *Bacillus* Species with Dye-remediation Potentials

Bacillus Species	Environment Isolated	Characteristics	Dye Remediated	Nature of Remediation	Reference
B. mycoides	Caves of Erzurum province	Psychrotolerant bacterium	Amido black 10B, Evans blue, Janus green, methyl orange, methyl red & orange G	90 % decolourization within 72 h	Aydin *et al*., 2021
B. paramycoides	Soil samples in the wood weathering area	Ligninolytic bacterium	Congo red, alizarin red S, methylene blue & Remazol brilliant blue R	Effective decolourization on both solid & liquid media	Rahaya *et al*., 2023
B. pseudomycoides	Domestic wastewater/Industrial effluents		Acid black 24 and a mixture of methylene green, basic violet, acid blue	Decolourization within 24 h and 96 h respectively	Kumar *et al*., 2019; Hossain *et al*., 2022
B. flexus	Textile effluent	Alkaliphilic, halotolerant bacterium	Remazol black, direct blue, acid orange, reactive orange 16 and acid blue 113	Complete decolourization within 24 h	Rani *et al*., 2016; Saini *et al*., 2018; Arora, 2020; Saha and Rao, 2020
B. cohnii		An obligate alkaliphilic bacterium	Direct red-22	95 % decolourization within 4 h at pH 9 & temperature 37 °C	Prasad and Rao, 2013: Arora, 2020
B. licheniformis	Textile effluent		Reactive red 2	Degraded to urea and other metabolites	Sudha and Balagurunathan, 2013

Table 1: *Bacillus* Species with Dye-remediation Potentials (Continued)

Bacillus Species	Environment Isolated	Characteristics	Dye Remediated	Nature of Remediation	Reference
B. spizizenii	Effluent from oil fields	Gram positive, nitrate reducing, dye degrading & biofilm producing	Textile wastewater containing red dyes	Decolourization under static microaerophilic conditions	Gomaa *et al.*, 2023
B. algicola	Sanitary landfill site	Slightly yellowish, gram-positive, filamentous alginolytic bacterium	Yellow azo dye	95 % decolourization	Chukowry *et al.*, 2017
B. vallismortis	Textile industry disposal sites		Malachite green, brilliant green and Aniline blue	Enzymatic degradation	Zhang *et al.*, 2012
B. vietnamensis	Continental slope of the Eastern Arabian sea		Malachite green	Biodegradation	Kabeer *et al.*, 2019
B. stratosphericus	Dye contaminated area		Reactive orange 16	Decolourized and degraded	Akansha *et al.*, 2022/2023
B. halodurans	Sea water	Alkaliphilic protease producing bacterium	Direct red 81, direct orange 34 and acid black 24	Partial decolourization	Prasad and Rao, 2014; Rathod and Pathak, 2018
B. albus	Textile wastewater	Halophilic and alkalophilic bacterium	Reactive black 5	98 % removal from aqueous medium in 38 h	Srivastava *et al.*, 2022
B. aryabhattai	Midgut of *Lasius niger* ant/textile wastewater	Symbionts in midgut of some ant species	Toluidine blue, Remazol brilliant blue, Congo red, acid red 88 and acid blue 193	Enzymatic degradation under aerobic condition	Diez-Mendez *et al.*, 2019: Korcan *et al.*, 2022

Remediation of Synthetic Dyes with *Bacillus* Consortia

Bacterial remediation by pure cultures is rapid but not very effective and leads to the formation of toxic intermediates like aromatic amines (Tony *et al*., 2009). Mixed cultures have been shown to be more efficient in the remediation of wastewater and dyes as a result of the synergistic metabolism of the microbes present that utilize toxic intermediates to form non-toxic by-products (Sharma *et al*., 2023). Remediation of dyes using microbial consortia proves to be a promising technique that can help minimize the impact of synthetic dyes to the environment (Afrin *et al*., 2021). The effectiveness of a microbial consortium during remediation depends on the survival, adaptability and activities of the enzymes produced by the microbes in the mixed culture (Senan *et al*., 2004). In the past years, many studies have developed various consortia containing a combination of species of bacteria, fungi or microalgae which were employed in the remediation of synthetic dyes (Kulandaivel *et al*., 2014; Sharma *et al*., 2023). Microbial consortia have shown high efficiency in dye remediation compared to pure strains. This may be as a result of synergistic metabolic processes by the microbes, in that, each strain in the consortium may tend to target a particular site in the dye molecules or may act on degraded metabolites generated by other strains (Forgacs *et al*., 2004; Khehra *et al*., 2005a; Akansha *et al*., 2023).

Khehra *et al*. (2005b) in a study to decolourize azo dye acid red 88, formed a consortium containing *B. cereus* and three other bacterial species that was inoculated into the dye and monitored for colour disappearance. Direct blue-15 dye was degraded and detoxified by a mixed culture of *B. subtilis*, *B. thuringiensis* along with three other species (Kumar *et al*., 2007). In 2008, Jadhav *et al*. 2008 combined two different microbial species (*Bacillus* and *Galactomyces geotrichum*) and inoculated it in a solution of brilliant blue-G dye of pH 9 at temperature 50 °C. The mixed culture successfully degraded the dye after few hours of inoculation. Dafale *et al*. (2008a,b) develop two separate mixed cultures of *Bacillus circulans* and other bacterial species which were subsequently used in the degradation of reactive black 5 and Remazol black-B. A microbial consortium of *Bacillus*, *Sphingobacterium* and *Pseudomonas* species was reported to have rapidly decolourized textile wastewater compared to their individual monocultures (Tamboli *et al*., 2010). In another study, a mixed culture of *B. vallismortis*, *B. cereus*, *B. pumilus*, *B. subtilis* and *B. megaterium* was used to remediate three synthetic dyes (Patil *et al*., 2010). *B. odysseyi*, *Morganella morganii* and *Proteus* species were combined and deployed in the remediation of Red HE3B dye (Phugare *et al*., 2011). Cui *et al*. (2012) developed a consortium containing three bacterial species (*Bacillus*, *Buttiauxella* and *Klebsiella*) which was used in the remediation of methyl red dye. Another study reported the degradation and decolourization of triphenylmethane dyes with a consortium of *Bacillus* species, *Agrobacterium radiobacter*, *Sphingomonas paucimobilis* and *Aeromonas hydrophila* (Cheriaa *et al*., 2012). Jain *et al*. (2012) in their research revealed the effectiveness of a consortium with four strains of *Bacillus* and two other indigenous bacterial species in the breakdown of reactive violet 5R dye. Congo red dye was also remediated by a mixed culture of *B. subtilis*, *Escherichia coli*, *Staphylococcus aureus*, *Salmonella*, *Proteus* and *Pseudomonas* species (Holey, 2015). The consortium of *B. subtilis*, *B. cereus*, *B. mycoides*, *Bacillus*, *Micrococcus* and *Pseudomonas* species was developed to remediate four dyes (Mahmood *et al*., 2015). The mineralization of three synthetic dyes was achieved by a mixed culture of species of *Bacillus*, *Aeromonas*, *Neisseria*, and *Vibrio* (Karim *et al*., 2018). In another study involving the breakdown of direct black-G dye, a combination of three species (*Bacillus*, *Anoxybacillus* and *Clostridium*) revealed high effectuality (Chen *et al*., 2019). A solution containing a mixture of several azo dyes was remediated with a mixed culture consisting two strains of *B. subtilis* and *B. cereus* (Thiruppathi *et al*., 2021). Afrin *et al*. (2021) made three different consortia by reshuffling four bacterial species (*B. pumilus*, *B. thuringiensis*, *Pseudomonas aeruginosa* and *Enterococcus faecium*) which were employed in the remediation of five dyes under static aerobic conditions. The results showed that the smaller number of species in the consortium, the higher the dye remediation which may be due to a wider enzymatic capability attained by the species (Afrin *et al*., 2021). A newly developed consortium comprising strains of *Bacillus*, *Stenotrophomonas*, *Pseudomonas* and *Alcaligenes* was used in the treatment of reactive red 3 (Shah and Bera, 2021). Another study also showed the efficiency of a bacterial consortium (*B. flexus*, *Pseudomonas aeruginosa* and *Proteus mirabilis*) in the degradation of indanthrene blue RS dye (Mohanty and Kumar, 2021). Kannan *et al*. (2022) combined pure cultures of two bacterial species (*Bacillus* species and *Escherichia coli*) and a fungal species (*Aspergillus niger*) for the complete mineralization of synthetic dyes.

A consortium containing four bacterial strains, *B. tequilensis*, *B. flexus*, *Kocuria rosea* and *Pseudomonas stutzeri* decolourized azo dye acid orange within 23 hrs under static laboratory conditions (Bera *et al*., 2022).

CONCLUSION

In conclusion, several *Bacillus* species have been reported by many researchers to be very effective in the remediation of different varieties of synthetic dyes either as individual pure cultures or in mixed culture with other microorganisms. This has help in the suppression of the impact of these dyes to the environment. The most widely used *Bacillus* species that were reported with potentials to remediate dyes are; *B. subtilis*, *B. megaterium*, *B. cereus*, *B. velezensis*, *B. fusiformis*, *B. odysseyi*, *B. mycoides*, *B. paramycoides*, *B. pseudomycoides*, *B. flexus*, *B. cohnii*, *B. licheniformis*, *B. spizizenii*, *B. algicola*, *B. vallismortis*, *B. vietnamensis*, *B. stratosphericus*, *B. halodurans*, *B. albus* and *B. aryabhattai*. However, the introduction of new biotechnological techniques has resulted in the continuous discovery of new species of *Bacilli* that have the capability to remediate dyes and other environmental contaminants, thus, more species may be reported in the near future.

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